UNITED INSTITUTE OF INFORMATICS PROBLEMS
OF THE NATIONAL ACADEMY OF SCIENCES OF BELARUS

PRIP'2025

PATTERN RECOGNITION AND INFORMATION PROCESSING

EMBEDDING THE FUTURE

PROCEEDINGS
OF THE 17th INTERNATIONAL CONFERENCE

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The present volume contains the proceedings of the 17th International Conference on Pattern Recognition and Information Processing (PRIP'2025), held in Minsk, Belarus, on September 16–18, 2025, in a hybrid format. The publication has been prepared by the Conference Organizing Committee in cooperation with the Belarusian Association for Image Analysis and Recognition.

The proceedings are intended for students, graduate and postgraduate researchers, as well as professionals in the fields of machine learning, deep learning, computer vision, artificial intelligence, neural networks and information fusion, signal processing, bioinformatics, pattern recognition and its applications, information retrieval and data management, digital information processing and communications, intelligent analytical systems, embedded systems and software engineering, knowledge-based expert and decision-support systems, and cloud computing technologies and infrastructures.

All contributions included in this volume have undergone multi-stage peer review and are published in the form submitted by the authors. Supplementary materials, including keynote lectures and invited talks, are available on the official Conference website https://www.prip.by/2025/ and the PRIP Conference YouTube channel "PRIP Conference".

The Conference was conducted in full compliance with the Privacy Policy. All participants confirmed their consent to the public dissemination and recording of their presentations for the purposes of the event.

Сборник содержит материалы 17-й Международной конференции по распознаванию образов и обработке информации (PRIP'2025), проходившей 16–18 сентября 2025 года в г. Минске (Беларусь) в гибридном формате. Издание подготовлено Оргкомитетом конференции совместно с Белорусской ассоциацией по анализу и распознаванию изображений.

Представленные труды конференции адресованы студентам, магистрантам, аспирантам, а также специалистам в областях машинного и глубокого обучения, компьютерного зрения, искусственного интеллекта, нейронных сетей и информационной интеграции, обработки сигналов, биоинформатики, распознавания образов и их приложений, информационного поиска и управления данными, цифровой обработки информации и коммуникаций, интеллектуальных аналитических систем, встраиваемых систем и программного обеспечения, экспертных систем и систем поддержки принятия решений, облачных вычислительных технологий и инфраструктур.

Все статьи прошли многоступенчатое рецензирование и публикуются в авторской редакции. Дополнительные материалы, включая пленарные доклады и выступления приглашённых участников, размещены на официальном сайте конференции https://www.prip.by/2025/ и на YouTube-канале «PRIP Conference».

Конференция проведена с соблюдением требований Политики конфиденциальности и защиты персональных данных. Все участники подтвердили согласие на публичное размещение и запись их выступлений в рамках мероприятия.

Editors:

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Alexei Belotserkovsky

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CHAIRMEN'S MESSAGE

From September 16 to September 18, 2025, the United Institute of Informatics Problems of the National Academy of Sciences of Belarus (UIIP) held the XVII International Scientific and Technical Conference "Pattern Recognition and Information Processing", PRIP'2025.

The PRIP Conference has a long history. It started in 1991 as the First USSR All-Union Conference "Pattern Recognition and Image Analysis" in Minsk. PRIP is jointly organized by UIIP, Belarusian State University and Belarusian State University of Informatics and Radioelectronics and up to now it was hold 16 conferences.

PRIP conferences have become well-known and recognized in the scientific world. Information about PRIP is included in all major international databases on image analysis and pattern recognition, including INSPEC. Currently, the PRIP conference is the leading international conference on image analysis and pattern recognition in Central and Eastern Europe and the only conference on this topic in the former USSR, which has international recognition and a high scientific reputation.

This year, the conference had a motto: "Embedding the Future", which emphasizes advances in pattern recognition and information processing in an era of rapid technological advancement.

A total of more than 150 papers from 8 countries were submitted this year. All materials were reviewed by members of the international program committee and independent external reviewers. Based on the review results, 102 papers (written by 254 authors and co-authors) were selected and included in the scientific program of the conference.

The topic of the conference, which usually includes theoretical and applied aspects of computer vision, processing and recognition of signals and images, the use of distributed resources and high-performance systems, this year has been significantly expanded due to the issues of artificial intelligence. Belarusian scientists in this area have their own achievements both nationally and globally within the framework of big projects.

Of course, a feature of this conference was the keynotes made by famous foreign scientists and influencers in the field of R&D and S&T, including professor Minglei Fu from Zhejiang University of Technology (Hangzhou, China), professors Hongqi Fan and Dongdong Li from National University of Defense Technology (Changsha, China), doctor Dmitry Chickrin from Kazan Federal University. This year the coference had a headliner – Segey Markoff (Sberbank, Russia), who is a very experienced speaker and leading visioner in the field of Artificial Intelligence.

Events of this scale and importance would not be possible without the invaluable support of our partners. We extend our deepest gratitude to Veb Technologies (Minsk, Belarus) and InnoTech Solutions (Minsk, Belarus), whose commitment and collaboration have made this conference a reality. Their partnership plays a vital role in fostering innovation, knowledge exchange, and the advancement of our shared goals.

We sincerely thank everyone who took part and helped us hold this large-scale online event in the scientific community of Belarus with international participation in the field of information processing and recognition! We also would like to thank the organizing committee for the excellent work due to which this event took place!

Prof. Alexander Tuzikov and Dr. Alexei Belotserkovsky

Minsk, September, 2025

CONTENTS

THESES OF THE SESSION “LIGHTNING TALKS”

Real-Time Smoke Detection in Video Based on Single-Board Computer

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Abstract. **A real-time smoke detection algorithm is presented. The algorithm includes sequential extraction of smoke features such as directional motion, color, and influence on background objects. The architecture of the developed smoke detection system based on Raspberry Pi 4B single board computer is shown. Comparison with existing single-board computer solutions has shown improvement of detection metrics of the proposed approach and achievement of real-time operation.**

Keywords: **computer vision, smoke detection, single-board computer**

I. INTRODUCTION

Detecting fire at an early stage to minimize damage is an actual problem, while traditional sensors are limited in response speed and range of application. An alternative is the use of closed-circuit television systems (CCTV) that allow visual detection of smoke using computer vision algorithms. In this case, there is no information on air temperature and composition, and the input data is subject to distortions: loss of scene depth, camera noise, optical distortion, and compression artifacts.

Smoke in the early stage is often the dominant visual feature and is characterized by the following properties [1]: vertical bottom-to-top particle motion, changing to chaotic; limited color range in shades of gray; translucency and blurring of background objects; stable source position; and variable shape.

To reduce the load on the central CCTV server, single board computers (SBC) such as Raspberry Pi and Jetson Nano are proposed as intermediate nodes for video stream processing. However, their limited resources require algorithms with low computational complexity based on existing approaches or fundamentally new ones.

For example, in [2], a portable smoke detection system based on Raspberry Pi 4B (RPi 4B) is developed, which consists of a Raspberry Pi camera, video frame processing module, smoke detector, display and alert system. The processing module included applying a 5×5 Gaussian filter to reduce noise and histogram equalization to contrast enhancement. Smoke detection was carried out using an AdaBoost-trained cascade classifier based on Local Binary Pattern (LBP) features. The classifier operated on individual video frames and used a multi-scale detection approach. The classifier was trained on a dataset of 6800 image patches of 35×35 px and 48×48 px images using NVIDIA GTX1080 graphics processing unit (GPU). The software was written in Python using the OpenCV computer vision library. The system is capable of processing 320×240 px (240 p) video at 25 frames per second with an accuracy of 94.7 %. The low resolution of the input data by converting to LBP is dictated by hardware limitations. The low processing power of the Raspberry Pi 4B also prevented the use of classical approaches using artificial neural networks (ANN). Instead, a cascade classifier was used, which demonstrated high accuracy. It should be noted that real-time performance is achieved on low-resolution video frames, which does not allow efficient detection of small or distant objects. It is also a disadvantage that the temporal information between video frames is not taken into account, which could help to improve the detection accuracy.

In [3], a multi-stage smoke detection algorithm is proposed, which includes the following steps: motion extraction using Kalman filter; saturation segmentation in HSV (Hue-Saturation-Value) color space; combining the obtained binary masks by the logical operator “AND”; selecting regions of interest with a sufficiently large area and a certain range of aspect ratio; classifying the regions by a lightweight convolutional neural network (CNN) with an input layer of 50×50×3 and a confidence coefficient of 0.7. The model was trained on a dataset of 14000 images. To suppress false positives, smoke was considered detected if its features were detected for 3 s or more. The software was written in Python using the Keras framework for machine learning. The algorithm was tested on NVIDIA Jetson Nano (JN) and Raspberry

Pi 3 (RPi 3) devices, with an average achieved accuracy of 87.7 % at 55 and 9 frames per second respectively for 240p video frames. A high false positive rate (FPR) should be noted, which could be due to poor timing of the alarm or insufficient generalization ability of the CNN. The performance of the algorithm on the Raspberry Pi 3 does not provide real-time performance, even for low dimensional video frames. Among the features of the approach are the consideration of the temporal component and the presence of pre-processing to reduce the number of computations performed by the convolutional network.

In [4], an ANN based on the YOLOv2 architecture and implemented on an NVIDIA Jetson Nano device was used for fire detection. The software was written in MatLab language using CUDA technology. The model was trained on a dataset of 400 images of size 128×128 px and achieved 96.82 % accuracy on test videos at a processing speed of 21 frames per second. The fire was detected 1–2 s after its actual occurrence. It should be noted that video frames were reduced to extremely small values, but even so, real-time processing speed was not achieved. The algorithm uses NVIDIA's proprietary CUDA technology, which limits the application of the developed method to other SBCs.

In [5], the YOLOv8 architecture with adaptations to the embedded processor Ingenic T41 (IT41) is applied for fire detection: reparameterization, use of the LeakyReLU activation function instead of SiLU to simplify model quantization, training on the COCO dataset and fine-tuning on a specific D-Fire set of 21500 images, minimization of data splitting and merging operations. The model demonstrated 79.4 % mAP at a processing speed of 47 frames per second. Despite the high performance, the optimizations were architecture-specific, and the effectiveness of similar steps when deploying the algorithm on other SBCs may be reduced.

Another approach using YOLO to detect forest fires using UAVs (Unmanned Aerial Vehicle) is discussed in [6]. The YOLOv5 architecture is applied to Raspberry Pi 4B with modifications: replacing the backbone with a lightweight CNN ShuffleNetV2, network thinning and following fine-tuning. The model was trained on a dataset of 24400 240p images using an NVIDIA RTX3050 GPU. The clock frequency of the Raspberry Pi 4B CPU was increased by 33 % via overclocking. The achieved processing speed was 9 frames per second at 92.5 % mAP. Comparison with [5] shows that in [6] the modifications were less platform-specific. A lower processing speed with lower input resolution was demonstrated compared to [5] given the superior processing power of the Raspberry Pi 4B relative to the Ingenic T41. It follows that platform-specific solutions can improve SBC performance in computer vision tasks.

The performance of YOLO and CNN-RCNN architectures in the context of UAV-based fire detection using NVIDIA Jetson Nano was investigated in [7]. The YOLOv5n and YOLOv8n models were used for object detection, while the hybrid convolutional-recurrent CNN-RCNN model performed classification taking into account temporal information. Training was performed on a dataset of 2947 images of 640×640 px. The processing speed on NVIDIA Jetson Nano is not specified, and the achieved detection accuracy was 89 %.

The analysis allows us to conclude that SBCs cannot process high-resolution video in real time, which limits their application in CCTV systems. Nevertheless, the high accuracy of the algorithms proves the prospect of their use for smoke detection tasks. Existing solutions use lightweight trained classifiers and modified ANNs, but this approach does not allow achieving high data processing speed. In order to reduce FPR, a number of algorithms use feature accumulation over several seconds, but most methods use information only from the current video frame and do not take into account the temporal context. The combined use of trained classifiers with computer vision algorithms and the use of platform-specific techniques can increase the performance of smoke detection algorithms.

Thus, the aim of this paper is to create a smoke detection system based on real-time video stream of high resolution IP camera on Raspberry Pi 4B with high accuracy by considering spatial and temporal features and adapting to the hardware platform used.

II. Proposed Method

A. System Architecture

An SBC-based smoke detection system has been developed that consists of a server, IP camera, switch, and remote operator workstation with specialized software that includes tools for viewing the video stream and for control of the server.

The server chosen is a Raspberry Pi 4B based on a 1.8 GHz ARM Cortex-A72 4-core processor with a 64-bit Raspberry Pi OS, which is based on Debian Linux. The device has 4 GB of RAM and provides high-speed data transfer via a gigabit Ethernet port. Hardware encoding and decoding functionality with support for H.264 video compression standard is provided.

The software part of the server consists of three components: an application for smoke detection, MediaMTX media service for publishing the

processed video stream on the network and a control application. The application for smoke detection is implemented in C++ language using OpenCV library functions. The control application is written in Rust language, receives and decodes the input RTSP-video stream (Real Time Streaming Protocol), transmits video frames to the detector and controls it, encodes the output RTSP-video stream, and provides the operator with a control interface.

The architecture scheme of the developed system is shown in Fig. 1.

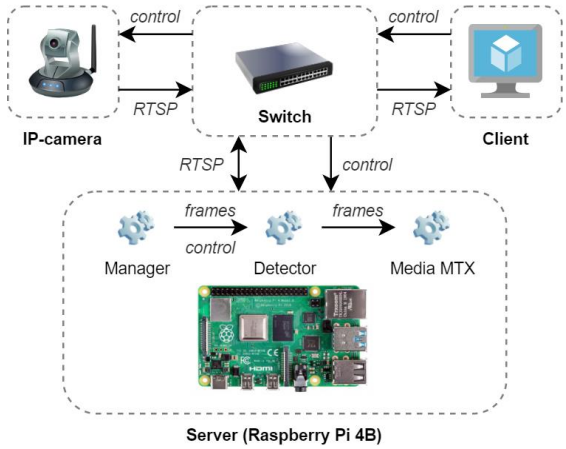

Fig. 1. Elements of the smoke detection system based on Raspberry Pi 4B

B. Smoke detection algorithm

The proposed approach is to sequentially apply computer vision techniques to the original video footage to extract particular smoke features. The order of processing is dictated by two factors: computational complexity and specificity of the feature specifically for smoke. If at the next stage no features are found, the next stages are not triggered, which reduces the load on the computing device. The peculiarity of the algorithm is the division of video frames by a regular grid, in each cell the selected features are averaged. This approach contributes to simplification and acceleration of calculations due to their unification and paralleling.

The algorithm includes the following steps [8].

- Video frame receiving and preprocessing: resizing, cell splitting for further analysis, and histogram normalization for each color channel.
- Building a background model using the MOG2 algorithm [9] based on the preprocessed video frame.
- Extraction of cells with the presence of motion by background subtraction and morphological erosion and dilatation post-processing. Cells with the presence of such objects do not participate in the background model update. If smoke is detected, the update stops completely. This solves the problem of foreground objects appearing in the background model if they are present in the same frame location for a long time.
- Selecting cells with the presence of stable motion during a specified time interval.
- Selection of cells corresponding by color characteristics to smoke. For this purpose the video frame is converted to HSV color space, threshold binarization is applied to S and V channels separately, and then the obtained masks are combined by the logical operator AND.
- Computing the candidate cells of the primary region of interest (RoI) by combining the results of the previous two steps into an array of weights. If a cell in the current iteration contains steady motion and corresponds to smoke in color, its weight in the array becomes maximum. Otherwise, it will decrease to zero at each next iteration with a fixed step. A candidate cell is considered to be any cell in the weight array with a non-zero value. Further processing is performed only for the video frame fragment describing all current candidate cells by a rectangular area.
- The selection of cells for which a significant drop in the energy of high-frequency (HF) components relative to the background model is detected. For this purpose, a two-dimensional wavelet transform is applied [10].
- Selection of cells with a stable drop in the energy of HF components within a defined time interval.
- Selection of cells for which a sufficient contrast reduction relative to the background model is detected.
- Computation of candidate cells for the secondary RoI by combining the candidate cells of the primary RoI and the results of the previous two steps with the logical AND operator. Further processing is performed only for the video frame fragment describing by rectangular area all the obtained candidate cells.
- Selection of cells with the presence of bottom-up directed motion. Using the optical flow algorithm from [11] applied to fragments of the current and previous video frames. The cells are selected, inside which the motion vector is within the specified range of angles and is large enough in amplitude.

- Selection of cells with stable bottom-up directed motion during a specified time interval.
- Combining the results of the previous step and candidate cells of the secondary RoI by the logical operator AND.
- Selection of cells characterized by the presence of all features of smoke by accumulation and comparison with the decision threshold of its presence.

In order to improve performance, different stages of the algorithm are executed on different cores of the central processing unit (CPU). This ensures efficient operation of the data processing pipeline without downtime of computing resources, as shown in Fig. 2.

The tasks were distributed in such a way as to balance their execution time in the corresponding threads on average. Directly the detection algorithm is executed on cores № 2–3, and cores № 0–1 are involved in transmission, encoding and decoding of the video. The tasks were distributed in such a way as to balance their execution time in the corresponding threads on average. Directly the detection algorithm is executed on cores № 2–3, and cores № 0–1 are involved in transmission, encoding and decoding of the video stream.

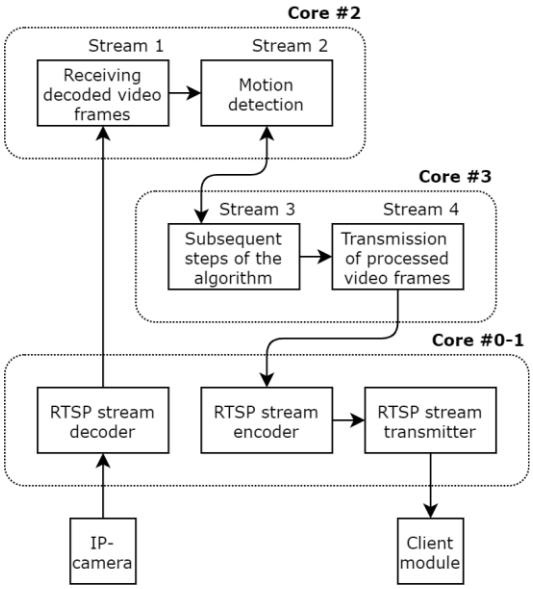

Fig. 2. The principle of task distribution in a smoke detection system based on Raspberry Pi 4B

III. Experimental Results

The system was tested in three load modes.

- No load (mode #1): there are no objects similar to smoke in the scene. Only the first stages of the algorithm are used: motion detection and object selection by color.
- Partial load (mode #2): objects similar to smoke are present in the scene. Smoke areas are absent or occupy a small area of the video frame for a short time. Periodically all stages of the algorithm are activated, but detection is rare and for a short time.
- Full load (mode #3): there is smoke in the scene, and it occupies a significant area of the frame for a long time, which corresponds to the maximum load of all stages of the algorithm.

In order to test the detection quality of the algorithm, a set of recordings of different resolutions up to 1280×720 px (720 p) with smoke and similar objects in the video from sources [12–15], as well as author's recordings was collected. The video files that correspond to the load modes were selected from them and tested.

Testing in all three load modes showed that the developed system processes 25 frames per second at long run times.

Fig. 3 shows examples of detection on video frames from a prepared dataset in the form of a overlay box, within which smoke is assumed to be present.

Fig. 3. Smoke detection on video frames by the proposed algorithm

Table collects the metrics of the considered smoke detection methods and presents the test results of the proposed algorithm in the row «our». The following detection metrics are compared: accuracy (AC), precision (P), FP, false-negative rate (FN) and F_1-score (F_1).

METRICS FOR SMOKE DETECTION SYSTEMS

Method	Hard-ware	*Metrics*				
		FPS (W×H px)	***AC, %***	***FP, %***	***FN, %***	***F_1, %***
[2]	RPi4B	25 (320×240)	94.7	1.1	3.6	-
[3]	RPi3	9 (320×240)	87.7	24.7	4.7	90.6
	JN	55 (320×240)				
[4]	JN	21 (128×128)	96.8	3.4	2.9	95.4
[7]	JN	- (640×640)	89	6.5	2	88
our	RPi4B	25 (1280×720)	97.9	0.26	1.77	97.5

Table shows that the proposed smoke detection algorithm provides relatively high accuracy rates compared to existing solutions that are designed for use at SBCs, and processes higher resolution data.

For each load mode the CPU temperature was recorded every second for one hour from the start of processing. Measurements were made at room temperature for the device in a case with a heatsink. The initial temperature of the CPU is 50 °C. The highest values reached during the measurements are: 58.9 °C for mode #1, 59.4 °C for mode #2, and 60.4 °C for mode #3. The maximum allowable temperature of the Raspberry Pi 4B CPU is limited to 80 °C, which is not reached in any of the load modes.

ACKNOWLEDGMENT

This paper presents a solution to the problem of real-time smoke detection in the form of a system based on a single-board computer Raspberry Pi 4B. The developed architecture includes server and client modules, allows to integrate the system into existing video surveillance networks.

The proposed smoke detection algorithm achieves a detection accuracy of 97.97 % and processes a high quality video stream at 25 frames per second. The use of spatio-temporal analysis of visual features of smoke allowed to reduce the number of false alarms to an average of 2.03 %, which is lower than that of similar solutions. Experiments confirmed the stable operation of the system and absence of overheating during prolonged operation.

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Detection of Oil Pollution in Oceanic Waters

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***Abstract*. Oil spills on the water surface are one of the most destructive forms of water pollution. Such spills have a negative impact on marine and coastal ecosystems, as well as on the health of populations around the world, resulting in significant economic losses, especially in regions dependent on fishing, tourism, and maritime trade. Due to the need to quickly detect and assess the extent of pollution, there is a great demand for fast, accurate and cost-effective methods for monitoring oil spills.**

Traditional spill detection methods are based mainly on satellite remote sensing, such as synthetic aperture radar (SAR), multispectral and hyperspectral imaging, as well as aerial reconnaissance. However, these approaches often require complex preprocessing, manual interpretation by experts, and are limited by weather conditions and image resolution [1]. Modern advances in deep learning and computer vision make it possible to automate image analysis, providing more reliable, scalable, and operational solutions.

This paper presents an automated technology for identifying oil slicks on the water surface using image semantic segmentation. Satellite and ground-based images were processed using the SegNet deep neural network architecture. The model was trained on a labeled dataset consisting of 500 images, augmented with data augmentation techniques. The results demonstrated high accuracy in detecting contaminated areas. Experiments confirmed the model's effectiveness under complex lighting conditions and variations in watercolor. The proposed technology can be integrated into remote sensing and environmental monitoring systems to improve the speed and accuracy of emergency response.

***Keywords*: oil spill, image segmentation, neural networks, environmental monitoring, SegNet**

I. INTRODUCTION

Oil spills remain one of the most serious environmental problems of our time. Such spills damage marine ecosystems, leading to the death of millions of organisms, and negatively affect the economy of coastal regions and human health [2]. The consequences of such incidents can be long-term and affect both local areas and large systems. According to the International Tanker Owners Pollution Federation (ITOPF), 10 oil spills of more than 7 tons occurred in 2024, including 6 major incidents (> 700 tons) and 4 medium-sized (7–700 tons) [3]. High density of marine traffic and difficult natural conditions exacerbate the risk of accidents that can cause significant water pollution, which causes damage to ecosystems, tourism, and international trade [1].

Currently, various spill detection methods are used, for example:

Satellite remote sensing (SAR, multispectral and hyperspectral images). The advantages of this approach are to explore large areas and work around the clock in various weather conditions. The disadvantages of this approach are the high cost and the need for complex preprocessing of the data obtained. Difficulties arise due to false alarms due to algae blooms, noise from waves and reflections.

Aerial and unmanned surveillance. This approach allows for the rapid detection of pollution but is limited in scope and depends on weather conditions.

Ground and ship-based measurements (water samples, visual inspection). This method provides high accuracy locally but is not suitable for rapid monitoring of large-scale incidents due to the need for the physical presence of specialists.

Modern artificial intelligence (AI) technologies have been actively implemented in recent years to solve complex problems of image analysis and environmental monitoring. In recent years, there has been significant demand for the use of AI and deep learning in a variety of industries. This is due to the ability of such technologies to automatically process

large volumes of unstructured data, identify patterns and make decisions without the need for manual intervention.

The use of deep neural networks in remote sensing image processing is considered especially promising. Such algorithms can learn on big data, independently identify signs of pollution, classify objects and segment territories with high accuracy. This reduces the time for analysis, reduces the need for expensive expert assessments and ensures prompt response to environmental incidents.

The advantage of using AI in environmental monitoring is not only its high accuracy, but also its ability to adapt to various conditions. Deep neural network models can consider such complex factors as changes in watercolor, sun glare, weather conditions and the presence of foreign objects (for example, ships or various animals), which makes them more versatile than traditional methods. In addition, modern algorithms can continuously learn from new data, improving their accuracy over time.

In the context of oil spill monitoring, the use of semantic image segmentation based on neural network approaches seems particularly relevant.

This study proposes the use of artificial intelligence methods for automatic recognition of oil slicks on the water surface using semantic image segmentation. The aim of the work is to develop and test a neural network model based on deep learning architecture to solve the problem of accurately identifying oil pollution zones. The approach used is focused on practical application in environmental monitoring and can become the basis for creating automated early warning systems for emergencies related to oil spills.

II. IMAGE SEGMENTATION

A. Basic Concepts

Image segmentation is a key task in computer vision that involves dividing an image into several meaningful segments or regions, each representing a separate object or category. The main goal of segmentation is to provide a simplified representation of the information in photographs and images while preserving its key characteristics for further data analysis. Segmentation allows classification at the level of individual pixels, which distinguishes it from image classification or object detection tasks that operate at a coarser level.

There are three main types of image segmentation that are widely used in computer vision:

Semantic segmentation is a task based on classifying each pixel in an image and determining whether it belongs to a certain class of objects. All pixels that belong to a certain category of objects (e.g., "oil", "water") are given the same label, without distinguishing between individual instances of the same class. At the output of the model, each pixel will be labeled with a label indicating which object or category it belongs to. This approach is especially useful when it comes to understanding the distribution of object categories in an image.

Instance segmentation – Unlike semantic segmentation, this approach not only classifies pixels, but also distinguishes between individual instances of the same class. This approach is used in tasks such as counting and tracking objects in an image.

Panoptic segmentation is a method that combines semantic and instance segmentation. It provides a complete understanding of the scene by assigning pixels both a class label and a unique object identifier. It is suitable for tasks where it is important to distinguish between the background environment and specific objects.

Segmentation is usually performed using deep learning models that can extract hierarchical features from input images. These features allow the model to recognize subtle differences in texture, color, and shape that indicate which pixels belong to different objects or areas.

Recent advances in convolutional neural networks (CNNs), transformers, and encoder-decoder architectures have significantly improved the accuracy and speed of image segmentation, making it possible to apply it in real time and at large scale.

B. Application in Environmental Monitoring

In the field of ecology and environmental monitoring, image segmentation methods are widely used due to their ability to extract the necessary information from the collected data. In particular, segmentation is used to analyze satellite and aerial images to identify pollution, assess the state of vegetation, monitor aquatic and coastal ecosystems, and study changes in the structure of landscapes. Such automated image processing significantly speeds up the analysis, allows processing large data sets and increases the accuracy of identifying environmental problems.

One example of the practical application of segmentation is the detection and monitoring of oil pollution on the surface of oceans and seas. Image segmentation allows you to quickly find pollution zones, determine their area, shape, distribution dynamics and potential impact on the environment. This significantly improves the ability to respond to emergency situations associated with oil spills.

In the context of tracking oil pollution in the waters of the World Ocean, the most rational approach is the use of semantic segmentation. Unlike other methods, semantic segmentation is focused on classifying each pixel of the image according to its belonging to a certain class. The main task here is to accurately determine the spatial distribution of oil pollution, as well as to assess its scale and density.

The use of semantic segmentation ensures the creation of a simplified and visual model, within which all pixels related to the polluted area are combined into a single category. This approach allows for visualization of oil spills in the form of masks suitable for subsequent quantitative analysis and environmental risk assessment. Moreover, semantic segmentation models can be trained on large sets of labeled images and then used in automated monitoring systems in real time.

III. Materials And Methods

A. Dataset

To train the neural network model in this study, a specialized dataset containing 500 labeled oil spill images collected from open sources was used [4]. The images included photographs taken by drones and from ground observation points. The training set included images with varying degrees of pollution, different transparency and color of water, from different viewing angles and in different weather conditions.

However, the number of available labeled images, especially for tasks related to environmental monitoring, is often insufficient to build a robust and well-generalizing model. Therefore, at the pre-processing stage, extensive data augmentation was used – a technique that allows artificially increasing the size of the training set by generating new images based on existing ones. The following augmentation methods were used: random image rotations; horizontal and vertical mirror reflections; varying brightness, saturation, and contrast; random scaling.

The use of augmentation allowed not only to increase the total volume of data several times, but also to significantly increase the model's resistance to noise and unpredictable changes in input data. This is especially important for environmental monitoring tasks, where images may contain glare from sunlight, clouds, traces of shipping, and other distortions. Augmentation also helped prevent the model from overtraining on a limited volume of initial data, providing better generalization ability on new, previously unseen images.

B. SegNet Architecture

SegNet is a semantic segmentation model [5]. This basic trainable segmentation architecture consists of an encoder network, a corresponding decoder network, and a pixel-level classification layer.

SegNet is an image segmentation architecture designed to efficiently recognize objects in an image, making it particularly useful in computer vision-related tasks such as detecting and classifying pollution in satellite imagery. SegNet was introduced in 2015 and quickly gained popularity due to its ability to provide high segmentation accuracy with a relatively small computational load.

SegNet is based on an encoder-decoder architecture. This structure allows important features of an image to be extracted first by the encoder, and then the segmented image to be reconstructed by the decoder. The encoder consists of a sequence of convolutional layers followed by pooling layers that reduce the spatial dimensions of the image while preserving information about its content. During the decoding stage, SegNet uses transform layers that restore the lost spatial information based on the stored indices. The decoder sequentially applies layers similar to the encoder's operational layers to restore the output image size and create the segmentation. SegNet is typically trained using a cross-entropy loss function, which helps optimize the model to ensure maximum accuracy in class segmentation.

Advantages of using SegNet:

1. High accuracy and efficiency in object recognition.

2. Ability to work with images of different resolutions.

3. Low computational requirements compared to more complex architectures such as Fully Convolutional Networks (FCN).

As a result of using SegNet in this work, a model was implemented that can accurately identify and isolate regions affected by oil spills, which greatly simplifies the analysis process.

C. Metrics

To evaluate the model performance, the following metrics were used:

Accuracy – the proportion of correctly classified pixels;

Cross entropy Loss – a loss function characterizing the model error.

The loss function is used to measure the difference between the predicted values (output) and the true values (target). In image segmentation problems, cross-entropy is typically used, which is suitable for multi-

class classification and penalizes the model for incorrect predictions. The formula for cross-entropy is as follows:

$$Loss = -\frac{1}{N}\sum_{i=1}^{N}\sum_{j=1}^{C} y_{ij}\log(p_{ij})$$

N – number of pixels.

C – number of classes.

y_{ij} – true class label for pixel.

p_{ij} – probability predicted by the model for a class.

IV. Results

After training, the model showed good performance in segmenting images containing oil spills. On test examples, the model successfully identified contaminated areas even under varying watercolor, glare, and distance of the oil slick from the source.

Analysis of numerical metrics yielded the following results:

Accuracy = 0.7847.

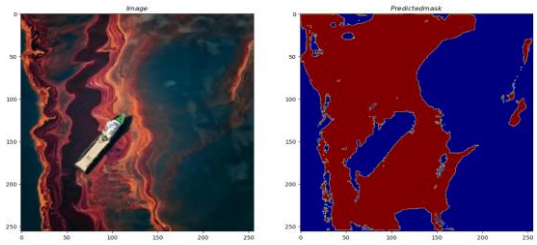
Loss = 0.4482.

The obtained accuracy indicates that almost 78.5 % of all pixels in the test images were correctly classified, which is a good result for the segmentation task, given the high visual variability and limited size of the dataset. The loss function value of 0.4482 indicates a moderate level of errors, which indicates that the model training process was effective and convergence was achieved. These indicators confirm the performance of the model and its readiness for use in applied tasks.

To visually assess the quality of segmentation, use Fig. 1–3. The figures show three representative test cases. Each figure shows the original image on the left, and the predicted segmentation mask obtained by the model on the right.

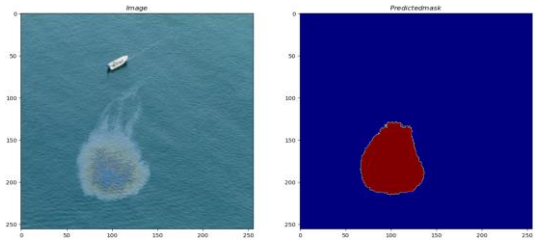
As part of the evaluation of the effectiveness of the developed model, visual experiments were conducted, during which the original images with the applied reference markup (maxa) and the segmentation masks obtained during the model training were compared. For clarity, three illustrative examples were chosen to illustrate both the strengths and limitations of the model.

In the first two images (Fig. 1, 2), the model successfully coped with the task of detecting oil spills. In both cases, the contaminated areas were accurately highlighted. This indicates the ability of the model to accurately interpret visual signs of pollution and ignore background noise, such as light waves or the presence of other objects.



a b

Fig. 1. The input image with an oil slick (a) and the predicted segmentation mask obtained during model training (b). Successful segmentation of a well-defined oil spill under favorable conditions. The model accurately reflects the shape and extent of the contamination with minimal false alarms

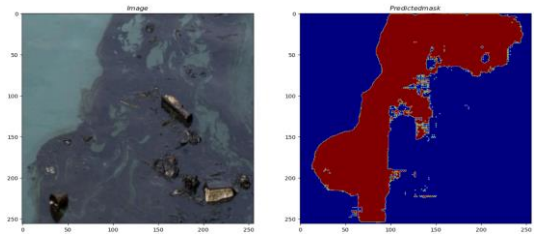


a b

Fig. 2. The input image with an oil slick (a) and the predicted segmentation mask obtained during model training (b). Segmentation of an oil slick with partial overlap and background interference. The model correctly highlights the spill area, despite the complex textures and lighting variations

However, the third example (Fig. 3) shows a situation in which the model encountered certain difficulties. Here, the model incorrectly identifies the area of pollution, which indicates the sensitivity of the model to complex compositions and visual distortions, which can reduce accuracy when processing real data in similar situations.

Nevertheless, even in the third case, the model retained the general structure of the segmentation and highlighted the main areas of the spill. This confirms its potential for practical application in monitoring tasks, especially when used in combination with post-processing or additional error correction algorithms.



a b

Fig. 3. The input image with an oil slick (a) and the predicted segmentation mask obtained during model training (b). A complicated case with unclear borders and dark water spots. The model gives a false negative result, misclassifying the area, which indicates sensitivity to visual distortion. However, the main area of the spill still remains

V. Conclusion

As part of the project, an automated technology for detecting oil spills on the water surface using image semantic segmentation was developed. Implementation of the SegNet architecture demonstrated good accuracy and robustness under various lighting and watercolor conditions.

The resulting model can be integrated into environmental monitoring systems, significantly increasing the speed and accuracy of emergency response to oil pollution incidents.

However, it is worth noting that there is still room for improvement. Segmentation errors highlight the need for further refinement of the model, which may include:

1. Expanding the training dataset to account for different lighting conditions and atmospheric phenomena.

2. Correcting the neural network architecture to improve overall accuracy and reduce segmentation errors.

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Solution of Direct and Inverse Problems of Mathematical Physics Using a New Projection Method Physics Informed Neural Networks (PINN)

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Abstract. **The report discusses a new numerical meshless projection method Physics Informed Neural Networks (PINN), suitable for solving various problems of mathematical physics. The method is based on the approximation of unknowns by neural networks. A feature of the method is the ability to solve nonlinear systems of mixed-type equations without using such classical approaches as linearization, application of a preconditioner. Using a superposition of sufficiently smooth, infinitely differentiable activation functions of a neural network as an approximation of the unknown allows solving such problems on a uniformly generated set of points, which significantly reduces the requirement for computing resources. The method is also suitable for solving inverse and ill-posed problems, including retrospective problems, inverse coefficient problems, inverse boundary value problems, and mixed inverse problems.**

Keywords: **Physics Informed Neural Networks, complex heat transfer, gas dynamics, inverse problems**

I. INTRODUCTION

Numerical solution of mathematical physics equations is a critically important task of modern mathematics, which has a wide range of applications in science and technology. In the context of rapid technological development and increasing complexity of engineering and scientific problems, traditional methods of numerical analysis are often insufficiently effective. Therefore, the development of new, more powerful and universal approaches to solving the problems is becoming a priority area of research. One of such innovative methods is Physics Informed Neural Networks (PINN), which offers a revolutionary approach to solving problems of mathematical physics. This method uses the capabilities of neural networks for approximate calculation of unknown functions, minimizing a special quadratic functional of quality. The functional includes components reflecting the residuals of the equations, as well as boundary and initial conditions. Thus, the model is "informed" about the physics of the process, which allows obtaining a solution to the problem. The advantage of PINN is its versatility – such a network can be applied to a wide range of problems. PINN can handle irregular grids, complex geometry, and high-dimensional problems, making it particularly attractive for practical applications. However, PINN has its limitations. The main drawback is its high sensitivity to training parameters, including the balance between the components of the loss function, the model architecture, and the choice of optimizer. In addition, PINN training can be extremely resource-intensive and unstable, especially in problems with stiff equations or high spatial dimensions. PINN also does not scale well with increasing problem dimension or time interval length, requiring either special modifications or regional decomposition. Nevertheless, PINN remains a powerful tool, especially in situations where traditional numerical methods are either impossible or produce unstable results. It is worth noting that the convergence of the method for many problems remains an open question, which, however, is actively studied in the scientific community. In addition, the PINN method is able to take into account the specific features of inverse and ill-posed problems, which makes it especially useful in complex and non-standard situations. In mathematical physics, inverse problems are encountered in such areas as geophysics, materials science, hydrodynamics and medical diagnostics. The PINN method was first presented in [1] as a new, powerful tool for solving partial differential equations. Since then, it has gained wide recognition and is actively used in various fields, such as mechanics, hydrodynamics, electrodynamics and many others. In addition, [1] proposed a method for time discretization using high-order Runge-Kutta methods, which allows reducing computational costs without loss of accuracy. The papers [2–4] describe the application of the PINN method in solving the Navier-Stokes equations for an incompressible medium. In [1], the authors also present a solution to the inverse

problem of reconstructing unknown parameters and the pressure field from known values of the medium velocity using a neural network approximation of the unknowns. In [3], the PINN method is used to study the solution of the Reynolds equations in a two-dimensional stationary case.

II. Features of the PINN method

Unlike classical numerical methods (e.g., finite difference method, finite element method, or finite volume method), PINN uses a neural network to approximate the solution of a differential equation, minimizing the residual of the equation and boundary conditions. Research shows that artificial neural networks have the ability to approximate various functions. The key role here is played by the theorem on universal approximation [5], which states that neural networks, especially deep ones, can approximate any continuous function with arbitrary accuracy on a compact set if there are a sufficient number of parameters (neurons). The speed of approximation depends on the network architecture, activation function, and learning algorithm. The results of approximation and convergence of the predicted values by the neural network to the exact solution of the boundary differential problem depend on the smoothness of the exact solution and the use of the activation function. Note that the theorem on universal approximation of a smooth function does not guarantee approximation of its derivatives, which are necessary for calculating the residual of the differential operator. Therefore, the activation function must be sufficiently smooth (have continuous derivatives of the required order).

For linear elliptic and parabolic differential equations, there are rigorous proofs of the convergence of PINN [6] to the exact solution, provided that the optimization algorithm minimizes the residual of the differential operator, and the neural network has sufficient approximation ability. In the case of nonlinear equations, there is no study of the convergence of the PINN method. This is due to the impossibility of obtaining an a priori estimate for a number of nonlinear differential operators that relates the norm of the solution error to the norm of the residual of the differential equation. Only for a certain class of problems is such an estimate possible. When choosing an activation function, it is worth considering the stability property of a neural network associated with the vanishing gradient problem. Smoother activation functions are more balanced and less susceptible to the vanishing gradient problem with appropriate initialization of weights. Despite the good properties of smooth activation functions, their use as approximators of exact solutions is limited to consideration of only strong solutions, i.e. those solutions that do not take into account the presence of discontinuities, shock waves, non-smooth coefficients and other features in the system. Empirical results show that the methodology based on PINN often successfully allows constructing new algorithms for finding solutions for a wide range of problems, including problems with the listed features, which stimulates their application and theoretical research.

For the PINN method to work correctly, it is required that all terms included in the residual of the differential operator be of the same order. When working with neural networks, it is a known fact that learning algorithms work better when the input and output data belong to the interval [0, 1]. Therefore, an important part of working with the PINN method is the non-dimensionalization of the equations. In addition to the fact that this allows you to significantly improve the quality of approximation and speed up the calculation process, the dimensionless coefficients also provide important information about the processes occurring in the model. However, non-dimensionalization of the equations in itself does not guarantee that all terms in the loss function will be of the same order. On the contrary, non-dimensionalization of the system can lead to a situation where the term for the residual is several orders of magnitude larger than other terms. To reduce the impact of a large spread of the values of the differential problem parameters on convergence, the method of weighting coefficients ("Self Attention PINN") is used, which can be trained similarly to the model parameters, using gradient descent. This approach allows to weight both a separate term and each point of the training sample separately. Moreover, the selection of each weighting coefficient is equivalent to the question of selecting only one parameter - the training step of the model.

Fourier feature encoding is a method for transforming input data based on the use of periodic functions with different frequencies, in order to improve the approximation capabilities of neural networks when modeling complex, in particular, high-frequency dependencies. The method was first systematically applied in the context of neural network representations of continuous signals and has found wide application in computer vision problems.

Let $x \in \mathbb{R}^d$ be an input vector (e.g., space and time coordinates) fed to the neural network. Using such coordinates directly limits the ability of the model to express high-frequency components of the target function, since standard fully connected architectures are prone to smoothing and do not learn well on functions with abrupt changes.

Fourier encoding maps this vector to a higher-dimensional space using a function γ:

$$\gamma(\boldsymbol{v}) = \{\cos(2\pi \boldsymbol{B}\boldsymbol{v}), \sin(2\pi \boldsymbol{B}\boldsymbol{v})\}^T, \quad (1)$$

where $\boldsymbol{B}$ is a randomly chosen $m \times d$ frequency matrix, m is the number of frequency components (hyperparameter), $\gamma(v)$ is a $2m$-dimensional vector. In case $d = 2$, $v = [x, t]^T \in R^2$, matrix B has size $m \times 2$, then

$$\gamma(x,t) = \begin{bmatrix} \cos(2\pi(B_{11}x+B_{12}t)) \\ \sin(2\pi(B_{21}x+B_{22}t)) \\ \vdots \\ \cos(2\pi(B_{m1}x+B_{m2}t)) \\ \sin(2\pi(B_{m1}x+B_{m2}t)) \end{bmatrix}. \quad (2)$$

A neural network that accepts $\gamma(x,t) = 2\pi(B_{j1}x + +B_{j2}t)$ can construct functions of the form:

$$f(x,t) = \sum_{i=1}^{m} w_j \cos(\gamma(x,t)) + v_j \sin(\gamma(x,t)). \quad (3)$$

Fourier coding can be interpreted as a projection of the input data into a space of basis functions similar to the harmonic basis, but with a finite number of components and random frequencies. This allows the neural network to operate not with the original coordinates, but with their spectral representation, which significantly simplifies the approximation of functions containing both low-frequency and high-frequency components; the number of components m is usually from 32 to 256. Note that the derivatives $\partial\gamma_k / \partial t$ remain in the same class of functions, so the neural network can accurately represent the derivatives after encoding.

However, it should be noted that in a number of problems where the components of the input vector differ significantly in orders of magnitude, the use of the standard approach to Fourier Feature Encoding demonstrates reduced efficiency. This is due to the fact that the same scaling of all variables leads to inadequate coverage of the frequency space and, as a consequence, to a decrease in the expressiveness of the model. To eliminate this problem, anisotropic scaling is introduced, in which the frequency matrix is determined taking into account the individual characteristics of each variable, that is, it is selected or initialized with different scales in the coordinate directions.

III. Numerical solution of the optimal control problem for the motion of a viscous heat-conducting gas using PINN

A numerical solution of the optimal control problem for the unsteady state of a viscous, heat-conducting gas in a one-dimensional case is considered. Control is performed using the gas velocity at the initial time and on the right boundary. For the solution, it is proposed to use the method of physical invariant neural networks (PINN), which consists in approximating unknown functions by neural networks. For this purpose, the problem of minimizing the quadratic functional is solved, which includes terms for the residual equations, boundary and initial conditions, as well as for the inverse problem – additional information.

The mathematical model describing the non-stationary motion of a viscous heat-conducting gas in one-dimensional space together with the boundary conditions has the following form:

$$Sh\,\rho u_t + \rho u u_x = Re^{-1}u_{xx} - p_x, \quad (x,t) \in (0,1) \times (0,1), \quad (4)$$

$$Sh\,\rho_t + \rho_x u + \rho u_x = 0, \; p = k\rho\theta, \quad (5)$$

$$Sh\,\rho\theta_t + \rho u\theta_x = Pe^{-1}\theta_{xx} + \pi k^{-1}(Re^{-1}u_x - p\,)u_x, \quad (6)$$

$$u|_{t=0} = u_0(x), \; \rho|_{t=0} = \rho_0(x), \; \theta|_{t=0} = \theta_0(x), \quad (7)$$

$$u|_{x=0} = u_1(t), \; \rho|_{x=0} = \rho_1(t), \; \theta|_{x=0} = \theta_1(t) \quad (8)$$

$$u|_{x=1} = u_2(t), \quad \theta|_{x=1} = \theta_2(t). \quad (9)$$

Here u, ρ, θ are the velocity, density and temperature of the gas, Sh is the Strouhal number, Re is the Reynolds number, Pe is the Peclet number, k, π are dimensionless parameters, $(x,t) \in (0,1) \times (0,1)$.

The statement (4)–(6) is a direct problem. Let us consider the inverse problem, i.e. we assume that under conditions (7), (9) the unknowns are the velocity at the initial moment of time $u_0(x)$ and the velocity on the right boundary $u_2(t)$. We will look for unknown characteristics such as $u(x,t)$, $\rho(x,t)$, $\theta(x,t)$, $\rho_0(x)$, $u_2(t)$ under some additional condition on the characteristics of the medium. Instead of the optimal control problem, the following extremal problem is considered:

$$J[u_0, u_2] = J_s + \alpha_1 \int_0^1 |u_{0x}|^2 dx + \alpha_2 \int_0^1 |u_{2t}|^2 dt \to \inf, \quad (10)$$

where the observation functional $J_s[u, \rho, \theta]$ describes an additional condition. In this paper, numerical experiments are performed to control the velocity, density and temperature of a gas with medium parameters corresponding to the physical characteristics of real gases at high Reynolds ($Re = 1.5 \cdot 10^7 - -2.4 \cdot 10^8$) and Peclet ($Pe = 3 \cdot 10^7 - 1.6 \cdot 10^8$) numbers. The advantages of the PINN method are shown, which allow calculating complex nonlinear optimal control problems without linearization and solving the adjoint system of equations.

IV. Boundary optimal control of heat-conducting gas motion under radiation conditions

The problem of controlling one-dimensional flow of viscous gas through an interval with a fixed boundary is considered. The flow regime takes into account complex convective radiative heat exchange in the medium. The heat transfer coefficient and the reflection coefficient from the boundary of the region are selected as control.

The mathematical model describing the non-stationary motion of viscous gas taking into account radioactive and convective heat exchange in one-dimensional space together with the boundary conditions has the following form:

$$\rho u_t + \rho u u_x = \mu u_{xx} - p_x, \quad (x,t) \in (0,1) \times (0,1), \quad (11)$$

$$\rho_t + \rho_x u + \rho u_x = 0, \quad p = R\rho\theta, \quad (12)$$

$$\rho(\theta_t + u\theta_x) = a\theta_{xx} + (\mu u_x - p)u_x - bk_\alpha(\theta^4 - \varphi), \quad (13)$$

$$-\alpha\varphi_{xx} + k_\alpha(\varphi - \theta^4) = 0, \quad (14)$$

$$u|_{t=0} = u_0(x), \ \rho|_{t=0} = \rho_0(x), \ \theta|_{t=0} = \theta_0(x), \quad (15)$$

$$u|_{x=0} = u_1(t), \ \rho_{x=0} = \rho_1(t), \ u|_{x=1} = u_2(t), \quad (16)$$

$$-a\theta_x|_{x=0} + \beta(t)(\theta|_{x=0} - \theta_1) = 0, \quad (17)$$

$$-\alpha\varphi_x|_{x=0} + \gamma(t)(\varphi|_{x=0} - \theta_1^4) = 0, \quad (18)$$

$$a\theta_x|_{x=1} + \beta(t)(\theta|_{x=1} - \theta_2) = 0, \quad (19)$$

$$\alpha\varphi_x|_{x=1} + \gamma(t)(\varphi|_{x=1} - \theta_2^4) = 0. \quad (20)$$

The system (11)–(21), unlike (4)–(9), takes into account radiation, the function $\varphi(x,t)$ describes the radiation intensity averaged over all directions, in the system it is described by the equation (14). The boundary conditions (17), (18), (20), (21) in such a problem take into account the influence of the external environment, which we plan to control so that the temperature of the environment at the observation points (the temperature measured by the sensors) takes the specified values. We present a numerical solution of the optimal control problem found using the Physics Informed Neural Network (PINN) method. The functions of velocity, density, temperature, and radiation intensity are sought with boundary control by two coefficients $\gamma(t)$, $\beta(t)$ on the left boundary and two coefficients $\gamma(t)$, $\beta(t)$ on the right boundary. All unknowns are approximated by neural networks. The temperatures at the observation points approach the specified one using optimal control of the boundary coefficients. The case with observation points inside the domain and on the boundaries is considered.

V. Advanced physical neural networks for solving nonlinear retrospective inverse heat conduction problems

Extended Physical Neural Networks for Solving Nonlinear Retrospective Inverse Problems of Heat Conduction.

The EPINN method is used to solve nonlinear retrospective problems in the field of heat conduction. Despite the fact that conductive heat transfer is not complex in the sense of this concept, solving retrospective problems is an extremely important aspect in heat transfer modeling. This problem is especially important in the case of a nonlinear thermal conductivity coefficient in the aggregate when considering composite materials. Consider the heat conductivity equation with a nonlinear coefficient:

$$\frac{\partial\theta}{\partial t} - Fo\nabla(\lambda(\theta)\nabla\theta) = 0, \ x \in \Omega, \ t \in (0,1), \quad (21)$$

where $\lambda = \lambda(\theta) > 0$ is the nonlinear part of the thermal conductivity coefficient, the Fourier number Fo includes the constant part of the heat transfer coefficient, λ_0. For this problem, we will consider the boundary conditions of the Dirichlet type: $\theta|_{\partial\Omega} = = \theta_b(x,t), \ x \in \partial\Omega$.

In the case of a retrospective problem, the initial state of the environment is unknown and must be found. To make the problem solvable, a final (or final) condition is specified:

$$\theta|_{t=1} = \theta_F(x). \quad (22)$$

It is required to determine the temperature value at the initial moment of time $\theta|_{t=0} = \theta_0(x)$. We will consider a two-dimensional problem with a piecewise continuous nonlinear heat transfer coefficient for a material arranged in layers: glass, aluminum. The thermal conductivity coefficients for glass and aluminum were approximated by polynomial functions based on experimental data and have the following form:

$$\lambda_g = 2 \cdot 10^{-9}\theta^3 - 5 \cdot 10^{-6}\theta^2 + 4 \cdot 10^{-3}\theta + 0.1, \quad (23)$$

$$\lambda_a = 10^{-10}\theta^3 - 5 \cdot 10^{-7}\theta^2 + 3.5 \cdot 10^{-4}\theta + 0.9. \quad (24)$$

To solve the retrospective ill-posed problem (21)–(24), we used neural network technology. EPINN. Innovative EPINN technology takes into account physical laws and can adapt to various conditions. The method is used to approximate functions and solve inverse problems where it is necessary to restore initial conditions or equation parameters. The method includes self-adaptive weighting coefficients and anisotropic coding of Fourier features.

Numerical modeling showed that the restored initial approximation is close to the specified one, and the resulting final distributions with the specified initial condition and the restored one differ by no more than 20 %.

VI. Conclusion

The paper presents a numerical calculation of the parameters of direct and inverse problems of viscous gas motion control. Natural parameters of the medium characteristic of turbulent flows were considered. However, due to the complexity of the Navier-Stokes equations model for a compressible medium, the calculations were performed in the case of one-

dimensional gas motion. In the future, it is planned to investigate the possibility of applying the developed technique to a multidimensional case. The possibility of solving the inverse problem of controlling one of several unknown functions describing the state of the system is shown. The advantage of using the PINN method to solve the inverse problem for a highly nonlinear system of equations is the absence of the need to linearize the system and solve the optimality system, as well as the possibility of solving the problem on a relatively small amount of training data, while classical methods require a very small step of the computational grid. It is shown that the use of the method does not require excessive computing resources for operation.

ACKNOWLEDGEMENTS

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Application of Algorithms for Selection and Analysis of Multicollinear Input Features in Solving Inverse Problems of Exploration Geophysics

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Abstract. **One of the main problems in exploration geophysics is restoration of distribution of some physical value inside the thickness of the earth by the values of physical fields measured on its surface. Such inverse problems are well solved with machine learning methods. However, such methods are often sensitive to the number of input features; so, reducing the input dimensionality is required. In this study, we compare use of several feature selection methods when solving an inverse problem of magnetotelluric sounding, and make some conclusions on their proper use.**

Keywords: **inverse problems, feature selection, neural networks, gradient boosting, exploration geophysics, magnetotelluric sounding**

I. INTRODUCTION

When solving EG IP using numerical and machine learning (ML) methods, the problem of high dimensionality and multicollinearity (linear relationship) of input features becomes especially relevant. This phenomenon has a significant impact on the accuracy, stability and interpretability of the obtained solutions, especially when working with real geophysical data, which are often described by hundreds or thousands of input features.

Thus, the aim of this paper is to study and compare various methods for selecting informative features to improve the accuracy, stability and interpretability of EG IP solutions.

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II. PHYSICAL STATEMENT OF THE PROBLEM

A. Parameterization Scheme

In this paper, the magnetotelluric sounding (MTS) problem is considered as a problem with the specified characteristics (high input dimension and multicollinearity of input features). This MTS IP consists of reconstructing the distribution of electrical conductivity in the Earth's interior based on the values of the electromagnetic field components measured on its surface. To implement the IP solution using ML methods, it is necessary to move from a continuous description of the geological section to a discrete description by setting an initial distribution with a limited number of determined parameters, i.e. by defining a so-called section parameterization scheme, within which the creation of the dataset and training of ML models will be carried out. The parameterization scheme used was a 4-layer 2D model corresponding to the Norilsk region section. It is shown in Fig. 1 and is described in more detail in [1].

The parameters to be determined were the values of the depths of the layer boundaries h(y) along the section, with the thickness of each layer for each y being greater than zero.

The depths for each training dataset pattern were set randomly within given ranges. Then the DP was solved using the finite difference method. In this case, six components of the electromagnetic field were calculated: the real and imaginary parts of the impedance tensor Z (Z_{YX} – H-polarization and Z_{XY} –

E-polarization) and the Wiese vector W_{ZX}. The calculation was performed for 13 frequencies in the range from 0.001 to 100 Hz [1].

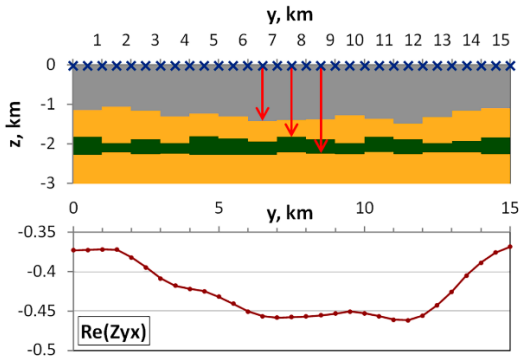

Fig. 1. Since direct methods of studying a geological section, such as drilling, are extremely expensive and provide information only at individual points, the solution of inverse problems (IP) occupies a central place in modern exploration geophysics (EG): it allows us to interpret measurement data and to reconstruct the physical parameters of the geological environment. In contrast to the direct problem (DP), in which expected geophysical responses are calculated based on a known geological model, IPs aims to reconstruct the unknown structure of the Earth's interior based on actually recorded data (e.g. gravimetric, seismic, magnetic, electrical or electromagnetic). An example of the geological section within the considered parameterization scheme (top), and the corresponding Re(Zyx) component (at one frequency) of the fields used in this study (bottom). Markers (×) are measurement points of geophysical fields (pickets), arrows are the positions of the depths of the lower boundaries of geological layers

B. *Data Used*

The dataset used in this work was obtained by repeated DP solution: a total of 30 000 patterns were calculated.

The input dimension of the problem was:

*6 field components (taking into account the complex representation of the data) * 13 frequencies * 31 measurement points (pickets) = 2 418 features.*

The total output dimension of the problem was:

3 layers × 15 depths = 45 parameters.

Due to the geometry and physics of the problem, many features are correlated with each other, which is confirmed by the heatmaps of correlations (Fig. 2), and this is an additional argument in favor of using feature selection methods.

III. Methodological Statement of the Problem

A. *Output Dimensionality Reduction*

To reduce the output dimension of the problem, the methods of autonomous and group determination of parameters was used [2]. In the case of autonomous determination, the original problem with N outputs is divided into N single-output problems, with a separate single-output neural network (NN) being constructed for each problem. At the same time, simultaneous determination of several parameters by a neural network with several outputs, also known as the multi-task learning approach, in some cases allows improving the quality of the problem solution [2–6]. For this approach to be effective, the number of simultaneously determined parameters should be small, and the parameters combined into a group should have similar dependencies on the input features [2]. For the IP considered in this paper, this is realized with vertical grouping of the parameters to be combined, i.e., when determining the depths of blocks (from different layers) located directly above each other. Thus, when using the multi-task approach, one model simultaneously determined 3 parameters.

In this paper, the study was conducted for the central vertical, taking into account the equivalence of tasks within one layer. A total of 3 parameters were considered, corresponding to 3 layers.

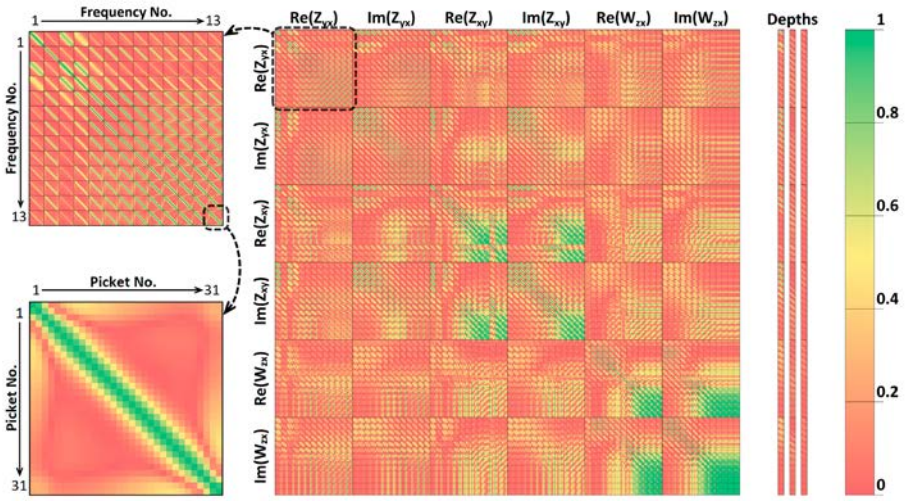

Fig. 2. Heatmap of absolute values of cross-correlation of input features with input features and with target variables

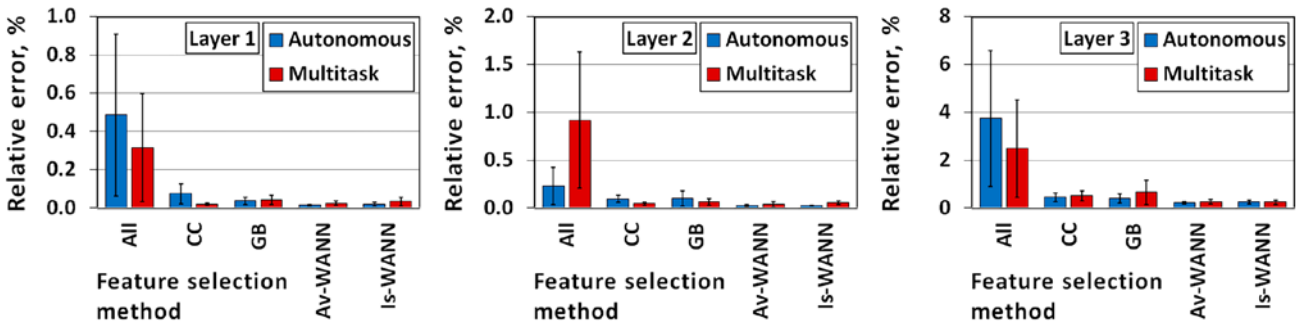

Fig. 3. Dependence of the relative error of the solution of the inverse problem on the feature selection method: All – all features, CC – selection by cross-correlation, GB – selection by gradient boosting, Av-WANN – weight analysis of neural network by average, Is-WANN – weight analysis of neural network by intersection

B. Using Neural Networks

In this paper, a multilayer perceptron (MLP), which is known to be a universal approximator, was chosen to solve the inverse problem. The architecture was a single-output or 3-output MLP with 32 neurons in the single hidden layer. To reduce the influence of weight initialization, 5 identical neural networks with various starting weights were trained in each case under consideration. To prevent overtraining of the neural network, the early stopping method was used on the validation sample - training was stopped after 10 epochs without improving the quality of the solution on this sample. Adam [7] was chosen as the optimization algorithm.

C. Datasets

The original dataset was split into training, validation, and test sets in the ratio of 70:20:10. The set sizes were 21 000, 6 000, and 3 000 patterns, respectively.

D. Feature selection methods

Traditionally [8, 9], methods for selection significant features are divided into filter methods, embedded methods and wrappers. Wrapper methods are the most computationally expensive, and when the problem size is several thousand features, their use without additional tricks [10] is difficult, so in this study only filter and embedded methods were considered.

E. Filter Methods

In this study, the absolute value of cross-correlation was used as the metric by which the selection was carried out. From the initial set, the feature with the largest absolute value of correlation with the target variable was selected. Then, such a threshold was selected that 750 features were included in the final set. NNs were trained on the selected features

F. Embeded Methods

The embedded methods used were the weights analysis of the trained NN (WANN) [11, 12] and the analysis of the importance of gradient boosting (GB) features [13].

In the case of WANN, two approaches were used:

- Averaging the weights for each feature with subsequent selection of the 750 most significant ones.
- Selection of the 750 most significant features for each of the five NNs and removal of those features, which fell into less than 3 of the 5 sets of significant features, from the original set.

In the case of selection based on the analysis of the GB-based importance of features, five GB models were trained on the original data set, then the importance of each feature was determined for all models, and the values of the importance were averaged across the models. The final set was formed from 750 features with the highest significance.

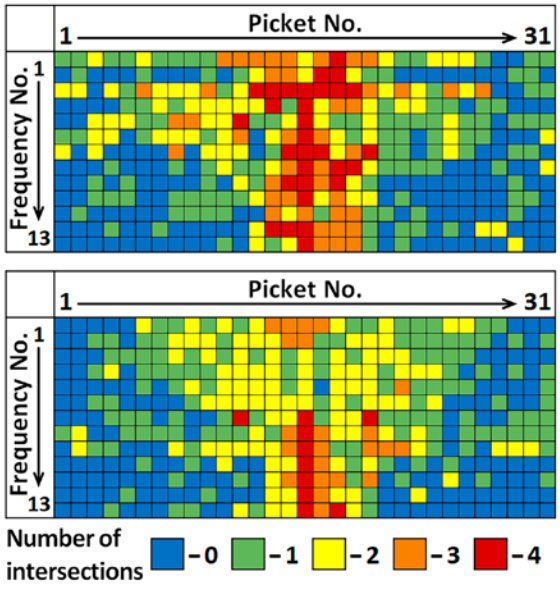

Fig. 4. Heat map of distribution of significant features by frequencies, pickets and components of electromagnetic fields. Top - Re(Z_{YX}), bottom - Im(Z_{YX})

IV. Results

Fig. 3 was obtained by comparing the significant features identified by all previously described methods. It can be argued that the best selection method among those presented is WANN based on significance averaging. In addition, MLP with three outputs in some cases coped better with solving the problem, which is consistent with the results obtained in [2].

Fig. 4 displays the results of WANN based on intersection of significant feature sets. The significant features are predominantly located closer to the central picket, for which the task of determining the depth of the layers was initially set. The greatest contribution to training was made by the real components of the fields at low frequencies.

V. Conclusions

Based on the results of the study, the following conclusions can be drawn:

- Solving the inverse problem of magnetotelluric sounding using any of the presented feature selection algorithms gives better results than solving this problem on the full set of input features.
- Group determination of parameters can be an effective method for reducing errors in solving multiparameter inverse problems using NN.
- The most effective method was based on the analysis of NN weights and subsequent averaging of significance values.
- Real field components make a greater contribution to model training than imaginary ones.
- Lower frequencies make a greater contribution to model training than higher ones (as higher frequencies penetrate earth worse due to skin effect).

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Strategy for Building Multi-Step Forecasting Models

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***Abstract*. This article presents a multi-step semantic network model, which aims to statistically analyze cause-and-effect relationships between events and make necessary predictions. The model uses statistical probabilities of events of the first, second, and third steps and is based on statistical data or expert assessments. The multi-step semantic network model can be used both for predicting natural disasters and for analyzing political and economic scenarios.**

***Keywords*: multi-step event models, statistical and expert data, modeling of natural disasters**

I. Introduction

Multi-step forecasting models describe a forecasting structure in which the forecast is developed step-by-step at different steps. Each step uses a different data source, modeling, or analysis method, and the results are sequentially built on each other.

Natural disasters – such as earthquakes, landslides, floods, or mudslides – are caused by many interrelated factors, such as geological, hydrological, climatic, and other characteristics. In addition, one cataclysm often causes another catastrophic event (the second step), which causes a third event (the third step), and so on. If it is possible to create an appropriate mathematical model for each cataclysm, then such events can be predicted using a system of interconnected, multi-step models. Thus, each model represents a specific cataclysm, and the entire system provides an analysis of their interaction.

A system of similar models can be visually represented in the form of extended semantic networks, where each vertex reflects the most appropriate model or a combination of several models for a particular cataclysmic event. The connections (edges) between the vertices express the chance of transition between steps, expressed in probability percentages - that is, the probability of one catastrophe developing into another. The calculation of such probabilities is based on the statistics of long-term observations. If the depth of the data is insufficient, experts are involved in the process, whose assessments fill or fill in the information gap.

The advantage of the extended semantic network is that its individual vertex can itself represent an independent subnet, which further increases the accuracy of the analysis.

The following types of data can be integrated into the multi-step approach:

- Meteorological, geophysical, and satellite data;
- Expert assessments;
- Existing statistical data.

Combining such multi-sector data creates the conditions for more complex and accurate forecasts.

II. Literature Review

Hybrid forecasting approaches include the work [1], which proposed a GA-PSO-BP hybrid model for seismic risk assessment, which combines a genetic algorithm, particle swarm optimization, and a feedback neural network. Their model showed high performance in predicting seismically vulnerable urban areas.

In [2], the integration of multi-factorial data into artificial intelligence models is discussed. Their study focused on combining geophysical and geological data using deep learning models, which increases the prediction accuracy.

Deep learning hybrid models are used in [3], who proposed a hybrid model of CNN–GRU architecture for earthquake timing prediction, which outperforms other alternatives in prediction accuracy

In [4], review emergency optimization models that combine expert judgment, statistical analysis, and AI modeling to refine response strategies.

New approaches that combine multivariate data analysis and AI models offer new opportunities in

seismic risk management, both in terms of improving forecast accuracy and response efficiency.

There are articles on multifactor prediction systems and how to take each factor into account [5]. We call these factors antecedents, and of course, multifactor is actually a set of antecedents, and these are not models based on the sequence of different events.

III. Three-Step Semantic Network Model

As we have already noted, the increasing interconnectedness of global and local processes in the modern world has created a need to create models that can logically and predictably structure complex events. This goal is served by a multi-step semantic network — a model that describes events and their interconnections at different steps. The corresponding semantic network for three-step forecasting models is shown in Fig. 1.

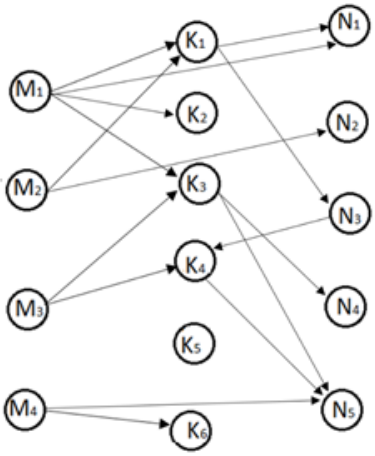

Fig. 1. A network corresponding to a three-step forecasting model

Let us consider the structure and elements of this model. The model consists of three steps:

- First-step events (M) — initial triggering factors (e.g., earthquake, political elections).
- Second-step events (K) — intermediate events that develop as a result of first-step events.
- Third-step events (N) — final consequences that may be caused either directly or by second-step events.

The edges connecting the vertices (events) are filled with the probabilities between them, either by statistical observation or expert assessment.

For example:

- M_1 (earthquake) → K_1 (tsunami) = 60 %,
- K_1 → N_1 (coastal damage) = 70 %,
- M_1 → N_1 = 30% (independently without tsunami).

This means that M_1 can cause N_1 both directly and through a second step (intermediate link).

Methodology: Probabilities are calculated based on the analysis of statistical data, or in cases where statistical data are not available, by expert assessment (Delphi method, fuzzy logic, etc.).

Two main approaches are defined:

- Deterministic network, where all nodes have an exact probability.
- Stochastic/probabilistic network, which combines estimation uncertainty and a range of options.

In the scheme presented in Fig. 1, we write down the percentages of all the peaks, which are calculated over several years of observations in one specific place, for example, Tbilisi, the Vera River Gorge, etc. We will obtain the following semantic network (Fig. 2):

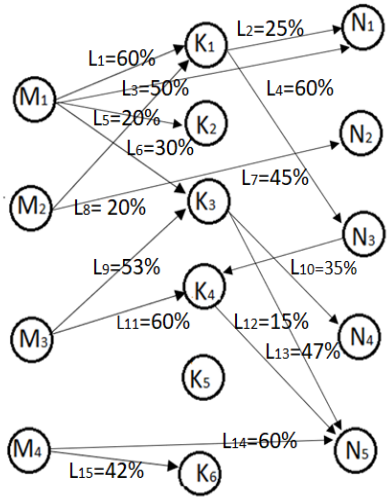

Fig. 2. Semantic network corresponding to three-step forecasting models

In this semantic network, one event can be connected to another from both sides, which means that a third-step event can cause both another and its own step event. In the figure: $N_2 \rightarrow K_5$, $N_3 \rightarrow K_4$, $N_5 \rightarrow K_5$ connections.

A third-step event (e.g. column N) can be not only a fixed event, but also a forecasting subnetwork itself – that is, N_1 can be transformed into a new first-step event in another system. This gives us a multilayer forecasting network that is used to forecast complex processes.

We can consider a special case of a multi-step model – a two-step forecasting model (Fig. 3), which is based on a hybrid forecasting model and then evaluates the event (denoted as K_i) resulting from the interaction between them. These models combine both statistical analysis and expert knowledge.

Methodological part. Each circle in Fig. 3 represents a hybrid forecasting model, obtained on the basis of the method developed by us. Thus, each circle represents not just one model, but a combined hybrid structure of models, the principles of construction of which are discussed in the work [6–9]. For example, model M_1 may denote a hybrid system created by intersecting different flood forecasting models. This group includes several models. As a result of the analysis of the intersection of pairwise or triple forecasts, the option that gives the smallest forecast difference and the highest accuracy is obtained.

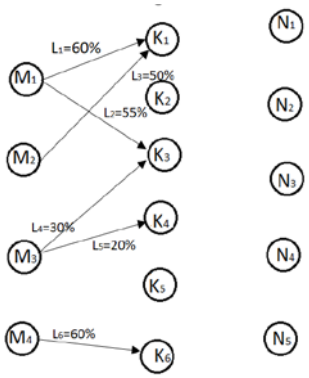

Fig. 3. Network structure of two-step forecasting models

Similarly, model M2 may reflect a hybrid of ice melt forecasting models. Ultimately, a set of models from M1 to Mn is formed, which was selected according to pre-established criteria.

IV. Examples of Use

A. Natural disasters

For example, M_1 was a flood, and N_3 is the Shovi tragedy. M_1 directly caused N_3. In this case, we do not know the intermediate event, that is, we do not know the sequence of events that took place – that the ice melted from the glacier, that the water flowed and accumulated. Then the landslide developed. So sometimes we may not know the events of the second step. N events - the events of the third step are already completed events. We will not have to consider more steps. We know the initial and completed events, but we may not know the intermediate events.

That is, the flood (M_1) may cause the landslide (K_1) in turn causes the Shovi tragedy (N_1). If the intermediate link is unknown, it becomes possible to estimate the direct impact ($M_1 \rightarrow N_1$).

Let's provide diagrams and tables for a multi-step semantic network, which will help you visually perceive the model, allowing you to better see the connections between events.

This Table I will help us to quantitatively assess the connections, including direct and indirect influences.

TABLE I. Probability Matrix Between Events

	K_1	**K_2**	**N_1**	**N_2**	**N_3**
M_1	60 %		90 %		40 %
M_2		80 %		85 %	
K_1			70 %		
K_2				60 %	30 %

B. Politics and Economics

The model under consideration is not only for predicting natural disasters. It can be used, for example, for jointly predicting politics and economics. For example, M_1 may denote the parliamentary elections in the USA, M_2 may be the Russian-Ukrainian war, M_3 may be the assistance of European countries to Ukraine, and M4 may be the attitude of Hungary towards the Russian-Ukrainian war. M_1 caused the event K_1 – Trump's coming to power. K_2 may be the development of Ukrainian minerals. To what extent will this lead to N_1, which is the security of Ukraine, and the events of the third step, N_1–N_6. N_2 may be the end of the Russian-Ukrainian war, N_3 – the victory of Ukraine in the Russian-Ukrainian war. That is:

M_1 – US parliamentary elections;
K_1 – Trump's election as president;
N_1 – Change in Ukraine's security step.

TABLE II. Probability Matrix Between Events

Case	**M Event**	**K Event(s)**	**N Event**	occurred?	Note
#001	M_1 (flood)	K_1 (landslide)	N_3 (Shovis tragedy)	✔	Full chain known
#002	M_1	?	N_3	✔	K unknown
#003	M_2 (election)	K_2 (Trump)	N_1	✔	Multi-step model structure for landslide prediction

C. One more example

Step I – Long-term climatic and geological risk analysis.

Inputs:

- Geological maps, slope gradients, soil type.
- Climatic trends (semi-centennial precipitation, temperature).

Output:

- Identification of general landslide zones (regional map).

Step II – Short-term hydrometeorological assessment.

Inputs:

- Precipitation amount in the last week, soil moisture, snowmelt.
- Forecasted rainfall in the next 72 hours.

Output:

- Locally elevated risk zones (e.g. specific village or valley).

Step III – Real-time observation and rapid modeling.

Inputs:

- Sensors on the slope (slope velocity), drones, satellite images.
- Population reports (crowdsourced data).

Output:

- Instant landslide Hazard prediction and algorithmic alarm triggering.

Step IV – Economic and human risk assessment.

Data:

- Population in the risk zone, infrastructure layout.
- Result.
- Modeling of damage scenarios and priority evacuation plan.

Summary.

Using this model, it is possible to:

- Identify the risk in advance.
- Confirm the expected threat through observation.
- Take appropriate measures in a timely manner.

V. Main results

- **The need for complex analysis in multi-step forecasting.** It was found that forecasting based on only one source or model cannot provide an effective assessment of events. Real conditions require multi-faceted data integration, since processes are closely interconnected. A multi-model hybrid approach reduces forecasting error and increases reliability.
- **The role of previously identifiable precursors in forecasting.** We have studied the circumstances that precede critical events and can be used as a basis for forecasting. For example, geophysical or thermal changes can indicate an impending earthquake, which increases the predictive ability of the model.
- **Using co-intersections of forecasting models to improve forecasting.** Combining models in pairs or groups based on different characteristics provides more reliable results than using them separately. Such a method provides a qualitative improvement in the forecast.
- **Quantitative assessment of the probability of forecast success.** The performance of each model was assessed by the number of correct and incorrect forecasts. The obtained reliability indicators were combined at the pairwise step, which allows the researcher to identify optimal combinations for maximum results.
- **Optimization of the number of models to reduce material costs.** Although the use of more increases accuracy, it also requires more resources. Therefore, it is recommended to select 2–3 models that provide forecasts with greater reliability.
- **Implementation of a multi-step data fusion model.** A system is presented that combines information from different sources – both quantitative (statistics) and qualitative (expert assessments). This hybrid structure increases the accuracy of the probability of forecasting.
- **The importance of combining expert knowledge with models.** It is noted that in cases where statistical data are limited, the use of expert assessments is critical. Their integration into formal models improves the decision-making process under uncertain conditions.
- **The role of decision support systems in forecasting.** It is important that the obtained analytical results are easily understandable for decision-makers. The presented system provides practical interpretation of the forecast and possible operational response.
- **Practical validation of models in real scenarios.** The study used simulation of existing cases, which helps to test the reliability of the model in a practical environment and establishes its applicability in real situations.

VI. Conclusion and prospects

The presented scheme is an effective framework for determining and predicting cause-and-effect relationships between events at different steps. Its universality allows it to be used in many areas. Future development of the model includes the integration of automated data collection algorithms and the inclusion of machine learning modules.

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Leveraging Semantic Prior for Image Super-Resolution

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***Abstract*. Image super-resolution (SR) is a classical task that recovers high-resolution (HR) images from low-resolution (LR) images. Existing methods have advanced through learning LR-HR pairs mappings via deep networks for single image priors, but often leads to over-smoothed reconstructions. Recent studies have attempted to introduce external semantic priors, yet the full potential of such priors remains underexplored due to insufficient interaction between semantic information and reconstruction tasks, as well as inadequate dive in semantic prior utilization. This paper provides a method for fully leveraging large-model semantic priors, offering new insights for advancing super-resolution research. The Core of our method is a Semantic Prior Fusion Unit (SPFU) with two innovations. Specifically, we propose a Channel Enhancement Module (CEM) to refine instance-level masks generated by Segment Anything (SAM) through channel-wise feature enhancement, and a Semantic Fusion Module (SFM) to establish a multi-level interaction path between semantic priors and image features. Those components can dynamically select effective semantic information and successfully incorporate semantic priors into SR tasks. The proposed method can be fine-tuned to adapt to mainstream SR networks, demonstrating significant performance improvements over baseline models on benchmark datasets.**

***Keywords:* Image Super-Resolution, Semantic Prior, SAM, Channel Attention**

I. INTRODUCTION

As a fundamental low-level computer vision task, image super-resolution (SR) aims to reconstruct high-resolution (HR) images from their low-resolution (LR) counterparts. Over the past decade, various learning-based methods [2–4] have been developed to learn the mapping between LR-HR image pairs, and significantly outperformed traditional SR algorithms [1, 5, 6]. However, due to the ill-posed nature of SR, the key to performance improvement hinges on acquiring more precise image priors to constrain SR results [1, 2, 25].

Recently, researchers have explored integrating external priors to assist SR, such as semantic prior [7, 13], explorable prior [8, 24] and text prior [9]. Among these efforts, semantic priors have garnered significant attention. Prior researches [7, 10–12] demonstrate the potential benefits of semantic priors acquired from segmentation for image reconstruction tasks. These semantic priors aggregate texture and color characteristics of objects within images. Essentially, semantic prior integration enhances reconstruction performance by leveraging rich knowledge encoded in segmentation results [11, 12], enabling deeper contextual understanding to guide the reconstruction process.

In this work, we investigate semantic prior utilization to enhance SR models. We propose a Semantic Prior Fusion Unit (SPFU), comprising a Channel Enhancement Module (CEM) and a Semantic Fusion Module (SFM). The CEM clusters semantic information from SAM outputs by instance, achieving fine-grained semantic alignment. Simultaneously, the adjusted semantic encodings interact and fuse with image features through the SFM. What's more, our unit can be easily inserted into conventional model for fine-tuning. Experimental validation across multiple SR networks demonstrates the effectiveness of our approach.

II. RELATED WORK

A. Image Rstoration with Semantic Priors

Early efforts implicitly incorporate semantic priors by designing tailored loss functions, such as perceptual loss [14, 15] and adversarial loss [7, 14], which enforce alignment between restored images and semantic constraints. However, these methods lack explicit communication between semantic priors and the image restoration (IR) task, and the black-box nature of networks make it difficult to verify the precise utilization of semantic priors. Subsequent works [17, 18] extract intermediate features from semantic segmentation networks as explicit semantic priors, integrating them into the feature representation space of IR models. While these methods achieve significant performance improvements by explicitly leveraging semantic priors,

they require annotated training data tailored to the specific reconstruction task. Recent attempts [10, 13] exploit the exceptional zero-shot generalization and strong robustness of Segment Anything Model (SAM) [16], but overlook systematic processing of SAM-derived semantic priors. This neglect results in insufficient interaction between semantic guidance and image features. Our framework enables effective interaction between semantic priors and the IR task while ensure rigorous utilization of semantic information.

B. SAM and Its Robust Generalization

As a foundational model for image segmentation, SAM is trained on billions of data, exhibiting remarkable zero-shot generalization without requiring pre-annotated inputs. Furthermore, by adjusting parameterized sampling strategies, SAM can generate semantic information at optional granularities, from coarse object-level segmentations to fine-grained part-level segmentations. This adjustable segmentation granularity is particularly valuable for IR tasks, as it enables the incorporation of richer semantic priors during reconstruction [10]. By harmonizing multi-scale semantic cues with image features, SAM provides a versatile prior bank that adaptively supports diverse reconstruction objectives.

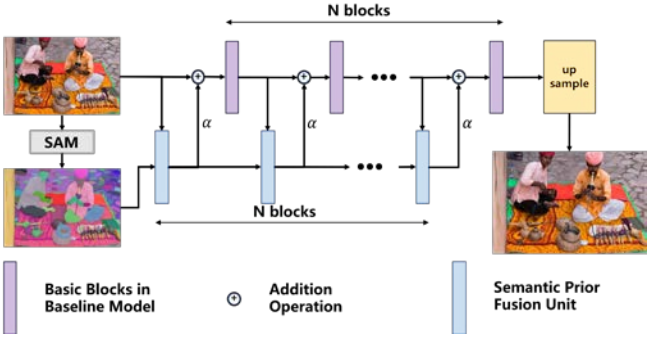

Fig. 1. Illustration of our proposed method. Our proposed method involves integrating semantic masks obtained from SAM into semantic prior fusion unit (SPFU), which combine the semantic priors from SAM or perceding SPFU with intermediate features from baseline's building basic blocks of existing SR methods. The ouput will be weighted and added to next building basic blocks, as well as given to later SPFU

III. METHOD

A. Mathematical Formulation

In general, the mask generation process by SAM can be formulated as:

$$M_{LR} = g_{SAM}(I_{LR}, \theta), \tag{1}$$

where I_{LR} denotes the LR image, θ represents adjustable SAM hyperparameters, g_{SAM} is the mapping process of SAM to generate image masks, and $M \in (S, H, W)$ is the output mask set. Here, S means the number of masks which is non-fixed and equals the number of instances segmented by SAM.

The operation of our designed unit is formulated as:

$$F^i_{SPFU} = \begin{cases} g^i{}_{SPFU}(F^{i-1}_{SPFU}, F_{img}) & \text{if } i>1, \\ g^i{}_{SPFU}(M, I_{LR}) & \text{if } i=1, \end{cases} \tag{2}$$

where $g(\bullet)$ denotes the *i-th* building block generating the next feature map, and g^i_{SPFU} represents the *i-th* SPFU block in the proposed scheme. The first SPFU takes the LR image I_{LR} and semantic prior M as inputs, while subsequent units process the intermediate feature maps F_{img} and outputs from the preceding SPFU.

B. Details of SPFU

The SPFU comprises two submodules: a Channel Enhancement Module (CEM) and a Semantic Fusion Module (SFM). When processing input features and semantic features, the CEM first performs semantic selection on M via a channel attention mechanism. Simultaneously, the input features and semantic priors are concatenated along the channel dimension and preliminarily fused through a base block f. This base block f consists of sequential operations: a 3×3 convolution, ReLU activation, and another 3×3 convolution. The intermediate result from the f-transformed features is multiplied with the semantic features to inject semantic guidance. After another f-block processing, a residual connection is applied. Finally, the output is element-wise multiplied with the channel attention-refined semantic prior, concentrating the fusion on the most informative semantic regions. By iteratively repeating SPFU, semantic information is progressively integrated into the network.

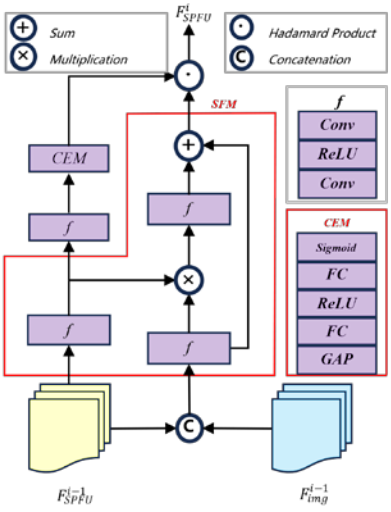

Fig. 2. Illustration of the SPFU, where FC means full connection layer, GAP means global average pooling. This unit takes image features from preceding backbone block and semantic priors from preceding SPFU

IV. EXPERIMENT

A. Experiment Setting

Datasets & Metric: We used DIV2K train set [19] as the training dataset which contains 800 HR images. Additionally, classic benchmark datasets including Set5 [20], Set14 [21], Urban100 [22], Manga109 [23] and DIV2K validation set (with 100 HR images differ from train set) [19]were employed to evaluate SR performance. And we used PSNR as validation metric.

Baseline Models: We selected VDSR [3] as the baseline model to demonstrate the effectiveness of our network architecture under general conditions. Furthermore, the lightweight SR model IMDN [4] was utilized to validate the efficacy of the unit. Our SPFUs were incrementally integrated after the base components of each network to achieve progressive fusion.

Training Configuration: LR images were cropped into 48×48 patches and HR images were cropped following scale factor and LR patches, with random data augmentation applied, including horizontal and vertical flipping and 90° rotation, each with 50 % probability. The batch size was set to 8. We employed the Adam optimizer with β_1=0.9, β_2=0.99, and weight decay=0.99. The initial learning rate was set to 1×10^{-4}, halved every 5000 iterations until convergence. The baseline model was trained on a single RTX 3090 GPU.

B. Quantitative and Qualitative Results

Table I presents a quantitative comparison between methods trained with and without the SPFU on benchmark datasets for SR. Our proposed module achieves superior results. The results demonstrate that existing SR methods augmented with the SPFU significantly outperform their corresponding baselines. For instance, on the Urban100 dataset under ×3 SR, VDSR fine-tuned with our method attains 27.35 dB (PSNR), whereas the same baseline network achieves only 27.14 dB (PSNR). Notably, the performance improvements across datasets matches our expectation.

To give an example, the Urban100 predominantly contains buildings with distinct foreground-background separation that can produce masks with higher precision and differentiation compared to other datasets. The integration of such precise masks further amplifies the efficacy of SPFU, explaining why our method exhibits more pronounced gains on Urban100 as well as Manga109 than on other datasets. The improvement (denoted by Δ) introduced by our module demonstrate that our method successfully integrates semantic priors into baseline model in a sufficiently effective manner and leverages them to improve image quality.

C. Ablation study

We conducted experiments to separately validate: *a)*the effectiveness of our proposed module; *b*) the optimal values of its weighting coefficients (denoted by α); and *c*) the impact of segmentation granularity in SAM-generated masks. For the ablation study, we trained the VDSR model on the DIV2K dataset under a 3× down-sampling task and evaluated it using Urban100 set.

TABLE I. ABLATION STUDY

SPFU variants		**Impact of params**			
structures	**PSNR**	**weights**	**PSNR**	**granularity**	**PSNR**
w/o concatenation	27.15	0.1	27.18	Coarse	27.32
w/o CEM	27.30	0.5	27.31	Fine	27.35
w/o SFM	27.19	1	27.35	-	-
standard	27.35	10	27.15	-	-

TABLE II. QUANTITATIVE COMPARISON OF BASELINE METHODS AND THEIR SPFU-TUNED VARIANTS IN TERMS OF PSNR FOR SR TASK

Methods	Scale	Set5 [20]	Δ	Set14 [21]	Δ	Urban100[22]	Δ	Manga109[23]	Δ	DIV2K[19]	Δ
VDSR [3]	×2	37.53	-	33.03	-	30.76	-	-	-	33.66	-
	×2	37.6	**+0.07**	33.12	**+0.09**	30.87	**+0.11**	29.12	-	33.74	**+0.08**
	×3	33.66	-	29.77	-	27.14	-	-	-	30.09	-
	×3	33.71	**+0.05**	29.82	**+0.05**	27.35	**+0.21**	24.48	-	30.19	**+0.1**
	×4	31.35	-	29.77	-	25.18	-	-	-	28.17	-
	×4	31.45	**+0.1**	29.78	**+0.01**	25.22	**+0.04**	21.13	-	28.29	**+0.12**
IMDN [4]	×2	37.91	-	33.59	-	32.13	-	38.78	-	-	-
	×2	37.92	**+0.01**	33.64	**+0.05**	32.18	**+0.05**	38.87	**+0.09**	33.86	-
	×3	34.32	-	30.3	-	28.15	-	33.58	-	-	-
	×3	34.36	**+0.04**	30.35	**+0.05**	28.34	**+0.19**	33.82	**+0.24**	30.93	-
	×4	32.18	-	28.61	-	26.03	-	30.43	-	-	-
	×4	32.19	**+0.01**	28.62	**+0.01**	26.19	**+0.16**	30.64	**+0.21**	28.95	-

a) The effectiveness of SPFU:

We test our proposed module to see its effectiveness by designing these ablation study: *w/o concatenation*: Instead of concatenating the generated mask semantics with image features, we directly feed them into the SPFU terminal; *w/o CEM:* We remove the CEM and substitute it with standard convolutional modules; *w/o SFM:* We discard the SFM and replace it with direct residual connections; *standard:* Standard SPFU.

Experimental results are presented in the left of Table II. When directly inputting semantic segmentation priors without concatenating, the network outputs demonstrate unmeasurable improvement, indicating that semantic information cannot directly enhance the reconstruction capability of SR models. This improvement also decreases when lacking fine-grained adjustment of semantic features. The network performance degrades in the absence of our feature fusion module. Without prior aggregation and adjustment of semantic information, the network essentially fails to gain improvement, suggesting that the model becomes confused by the raw SAM data and consequently ignores this module. This indicates that our designed channel enhancement module effectively mitigates the problem where instance-specific information in SAM outputs obscures categorical information.

b) Impact of weight α:

Since we add SPFU outputs with image features as the input of next building basic blocks, we naturally dive into the impact of weights. From small to large we test four kinds which show in the middle of Table II. It is demonstrated that whether too large or too small cannot balance the building blocks of baseline model and our SPFU, leading to a decrease of reconstructed image quality. The best performance gets when α equals 1.

c) Impact of segmentation granularity:

Intuitively, the accuracy and granularity of semantics generated by SAM can influence SPFU's performance. Therefore, we investigate the effect of segmentation granularity on the network.We adjust the *points-per-side* parameter in SAM, which controls the sampling density of the image, allowing flexible selection of granularity – from coarse instance-level to fine-grained part-level. Through experiments, we set 8×8 and 24×24 to represent coarse and fine granularity, respectively. The resulting feature channels are standardized to 64 and 128 dimensions via padding or truncation ("more removed, less supplemented"). Consequently, only adjusting the input channel number of the first convolutional layer is needed. Observations show that fine-grained segmentation improves the performance, further validating the impact of fine-grained semantic prior.

V. Conclusion

In this work, we propose a unit that effectively integrates semantic priors into SR networks, addressing the critical issue where category information in the output of SAM is obscured by instance-specific data while enabling efficient interaction between semantic priors and image features. Our method can be seamlessly inserted into existing networks through fine-tuning, eliminating the need for full model retraining and ensuring efficient module deployment. Furthermore, we systematically explore utilization strategies for semantic priors derived from large vision models, with this study demonstrating their unrevealed potential.

For future research, we will investigate more efficient semantic fusion mechanisms and interpretability of semantic representations and their underlying principles in enhancing network reconstruction. We believe those researches represent a promising direction for exploration.

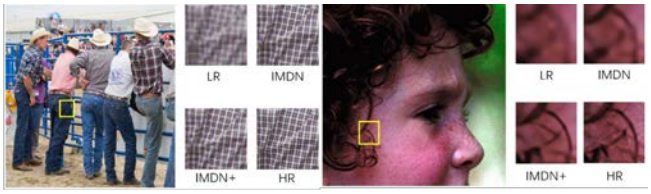

Fig. 3. Visual comparisons on ×4 image super-resolution for IMDN and IMDN with SPFU variant (which is denoted as IMDN+). Left: from DIV2K [19] validation dataset. Right: from Set 14 [21]dataset.Zoom in for better comparsion

Fig. 4. Visual comparisons on ×4 image super-resolution for VDSR andVDSR with SPFU variant (which is denoted as VDSR+). Left: from Urban100 [22] dataset. Right: from Manga109 [23] dataset.Zoom in for better comparsion

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Multimodal Person Emotion Analysis System Based on Shared Transformer Architecture

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Abstract. **Traditional psychological assessment relies heavily on human observation and interpretation, which is vulnerable to subjectivity, bias, fatigue, and inconsistency. To address these limitations, this study presents a multimodal emotion recognition system, offering psychology professionals a standardized, objective, data - based tool. It integrates facial expression, audio, and video of emotional states, reducing misdiagnosis and over – diagnosis risks. Initial tests under real – world conditions show its potential to offer reliable emotional insights and enhance diagnostic accuracy.**

Keywords: **multimodel, Transform, Emotional analysis**

I. INTRODUCTION

Emotion recognition is a key area in AI. It can improve human-computer interaction and help with psychological and psychiatric assessments. But traditional methods, which depend on manual observation and subjective interpretation, are error-prone due to human factors.

Multimodal emotion recognition, which integrates information from facial expressions, speech, and body language, has emerged as a promising approach. It overcomes the limitations of single-modal recognition and boosts the accuracy and reliability of emotion recognition. When a person speaks, their facial expressions, tone of voice, and word choice all convey emotions. Analyzing these multimodal signals together provides deeper insights into their emotional state.

The Transformer – based architecture offers significant benefits for multimodal emotion recognition [1, 5]. Its self - attention mechanism models global dependencies by directly computing associations between arbitrary sequence positions, capturing long - range temporal relationships. For multimodal fusion, the Transformer uses a cross - modality attention matrix to dynamically adjust feature contributions and learnable modality - specific embedding vectors to distinguish data sources, achieving efficient emotional feature integration. The self - attention calculation is fully parallelizable, reducing computational complexity and boosting training/inference speed.

This paper introduces a new multimodal emotion recognition framework using a unified multimodal encoding scheme based on a shared Transformer architecture [1]. It processes and fuses emotional features from facial, video, and audio data. A progressive training strategy is adopted to ensure stable model learning and effective multimodal information fusion.

The framework has three innovative aspects. First, it implements hierarchical feature extraction for different modalities. For audio features, it uses a cascaded CNN structure and spectrum attention mechanisms. Second, it proposes a contrastive learning framework that maximizes mutual information between representations of the same emotion across different modalities and learns temporal consistency of emotional states. Third, it employs a multi - task learning strategy combining emotion classification loss, recognition rate prediction loss, and contrastive loss, enabling the model to learn more comprehensive and discriminative features.

II. THE PROPOSED SYSTEM

During the feature extraction phase, the system processes different data modalities using specialized deep networks. For facial images, a lightweight ResNet-18 [2] extracts 512 - dimensional spatial features, reducing computational complexity via depth - wise separable convolutions while capturing facial muscle movements and shape changes. Video sequences are handled by a 3D ResNet [3, 4], yielding 1024 - dimensional spatiotemporal features; its 3D convolutional kernel processes both spatial and temporal video dimensions to capture dynamic behaviors and emotional expressions. As for audio signals, they're first converted into 128 - D Mel-spectrograms. Then, a frequency - band attention module enhances emotionally sensitive areas, and cascaded 1D CNNs extract acoustic features like pitch and loudness changes.

The extracted features are fed into a 6 - layer Transformer encoder, each layer having 8 - head self - attention and a feed - forward network. Modality - specific embedding vectors and positional encoding

enable the model to differentiate modalities and retain sequence info. The encoder's output is fused via cross - modality attention, which dynamically adjusts modality weights for efficient emotional feature integration. The emotion understanding module has three layers: a basic emotion recognition layer for identifying seven emotions, an emotion intensity assessment layer using a Sigmoid function to predict intensity values, and a complex emotion state inference layer with a bidirectional LSTM and temporal attention mechanism to generate natural - language descriptions of emotion - transition processes.

Model training consists of four stages: basic audio - emotion recognition on EmoDB using supervised learning, phoneme - level feature enhancement by incorporating EmoDB's lablaut - annotated phoneme - level information via multi - task learning, advanced feature learning using self - and contrastive attention to capture long - term dependencies and enhance feature representation, and model evaluation and optimization based on test - set performance, error - case analysis, and confusion - matrix review.

With its hierarchical feature representation, the model can abstract from local to global features, effectively capturing multi - scale emotional features. The contrastive experiments highlight the Transformer model's advantages, showing higher accuracy in image, audio, and video modalities than CNNs and RNNs, better cross - modality fusion performance, and improved training/inference efficiency.

III. Mathematical Methodology

A. Face Image Feature Extraction

The face image feature extraction module uses ResNet-18 [2] to extract spatial features from face images. After preprocessing steps like cropping and normalization, the image data goes through convolutional layers. The convolution operation, $F = = \mathrm{Conv}(X; W, b)$, along with ReLU activation, generates feature maps. The fully connected layer of ResNet-18 outputs a feature vector encoding key visual features such as facial expressions, providing essential information for emotion recognition.

B. Video Sequence Feature Extraction

The video sequence feature extraction module leverages 3D ResNet [3] to capture spatio-temporal features from video sequences. The 3D convolution operation, $F = \mathrm{Conv3D}(X; W, b)$, extracts features considering both spatial and temporal dimensions. Residual connections, $F_{res} = F + X$, help alleviate the gradient vanishing problem. The 3D ResNet outputs a feature vector that combines dynamic and static visual information from the video, reflecting emotional variations over time.

C. Audio Signal Feature Extraction

The audio signal feature extraction module [4] begins with computing Mel-Frequency Cepstral Coefficients (MFCC) to highlight emotion-related information. The MFCC calculation involves framing, FFT, applying a Mel filter bank, and DCT. Additionally, 1D CNN processes the MFCC features, with the operation expressed as $F = \mathrm{Conv1D}(X; W, b)$. These operations transform the audio signal into a feature vector rich in emotional information (Fig. 1).

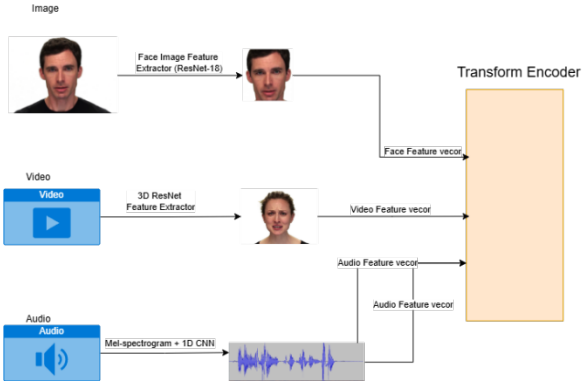

Fig. 1. Pictures, videos and audio are processed and transmitted to the transformer encoder

D. Transformer Encoder

The Transformer encoder [1] module integrates features from face, video, and audio modalities (Fig. 2). Modality-specific learnable embedding vectors, $E_{\text{modal}} = W_{\text{modal}} \cdot F + b_{\text{modal}}$, and position encoding, $(F_{\text{pos}} = F + \text{PositionalEncoding}(pos))$, are used to preserve the unique characteristics and positional information of each modality. Cross-modal attention mechanisms dynamically adjust feature importance weights by calculating correlations between different modalities

$$\text{Attention}(Q, K, V) = \text{Softmax}\left(\frac{QK^T}{\sqrt{d_k}}\right)V,$$

generating a comprehensive feature representation for subsequent emotion recognition.

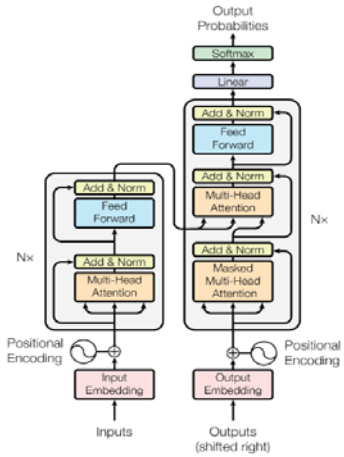

Fig. 2. The transformer encoder is used for multimodal fusion analysis

E. Multi-level Emotion Understanding Module

The multi-level emotion understanding module consists of three sub-layers: basic emotion recognition, emotion intensity assessment, and complex emotion state inference (Fig. 3). The basic emotion recognition layer uses the Softmax function, $p_{\text{basic}} = \text{Softmax}(W_{\text{basic}} \cdot F + +b_{\text{basic}})$, for emotion classification. The emotion intensity assessment layer employs a linear transformation with an activation function, $I_{\text{pred}} = \sigma(W_{\text{intensity}} \cdot F + b_{\text{intensity}})$, for regression prediction. The complex emotion state inference layer also uses the Softmax function, $p_{\text{complex}} = \text{Softmax}(W_{\text{complex}} \cdot F + b_{\text{complex}})$, for multi-class classification of complex emotions, providing comprehensive emotion recognition results.

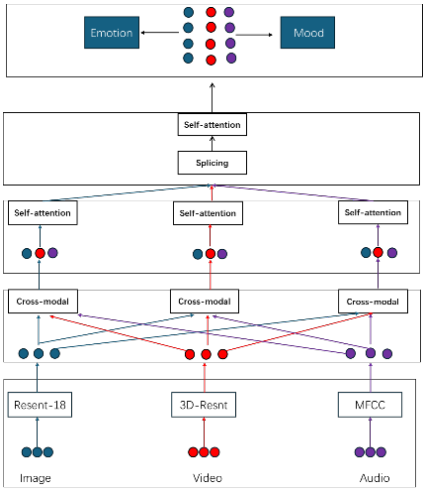

Fig. 3. Multimodal emotion and sentiment analysis architecture

F. Multi-task Learning Loss Function

The multi-task learning loss function module jointly optimizes emotion classification, emotion intensity prediction, and cross-modal feature alignment. The cross-entropy loss, $L_{\text{cls}} = -\sum_{i=1}^{C} y_i \log(p_i)$, measures the discrepancy between predicted and actual emotion categories. The mean squared error loss, $L_{\text{reg}} = |r_{\text{pe}} - r_{\text{tu}}|^2$, calculates the difference between predicted and actual intensity values. The contrastive loss

$$L_{\text{contrast}} = -\log\left(\frac{\exp(\text{sim}(h_i, h_j)/\tau)}{\sum_{k \neq i} \exp(\text{sim}(h_i, h_k)/\tau)}\right),$$

enhances the correlation between features from different modalities. These loss functions are linearly combined into the overall loss function, $L_{\text{total}} = L_{\text{cls}} + +\alpha L_{\text{reg}} + \beta L_{\text{contrast}}$, to improve the overall performance and generalization ability of emotion recognition.

IV. Experimental Results

A. Datasets

EmoDB is a German emotional speech database created by the Communication Science Institute at Technical University of Berlin. It consists of 535 speech samples from 10 professional actors (5 male and 5 female), covering seven emotions: anger, disgust, fear, happiness, sadness, neutrality, and boredom.

RAVDESS is an audio-visual emotional performance dataset developed by Ryerson University in Canada (Fig. 4). It includes performances of 24 actors (12 female and 12 male), each performing 60 different emotional segments, resulting in a total of 1,440 files. The actors performed two lexically matched statements, expressing a variety of emotions including calm, happy, sad, angry, fearful, surprised, and disgusted. Emotions were performed at two intensity levels (normal and strong), and there was also a neutral expression.

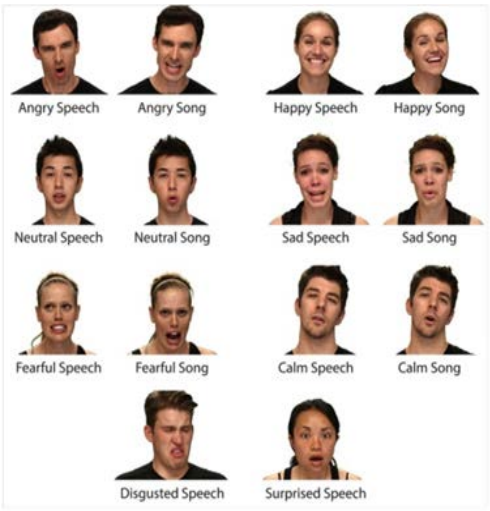

Fig. 4. Example of frames seen in RAVDESS

CREMA-D is a multimodal emotional dataset obtained through acted performances and crowdsourced annotation. It contains performances of 91 actors (48 male, 43 female, aged 20–74, from diverse races and ethnicities), totaling 7,442 samples. Actors performed from 12 sentences, each presented in six emotions (anger, disgust, fear, happiness, neutrality, sadness) and four intensity levels (low, medium, high, and unspecified). Details of datasets are given in Tabl. I.

TABLE I. Emotions considered in each databases

Database	Emotions	Resolution	Cues	Persons
RAVDESS	8, (anger, calm, disgust, fearful, happiness, neutral, sadness, surprise)	1920×1080	Audio and voice	24
EmoDB	7, (anger, disgust, fearful, happiness, neutral, sadness, surprise)	1280×1024	Audio and voice	10
CREMA-D	6, (anger, disgust, fear, happiness, neutral, sadness)	480×360	Audio and voice	91

B. Experiments

Each dataset was divided into two subsets: a training set consisting of 80 % of the samples and a test set comprising the remaining samples (Fig. 5). The number of units in the LSTM layer was set to 16 and was trained for 100 epochs using the Adam optimizer. An adaptive learning rate was employed during training, with values adjusting between 1e−03 and 1e−05 based on the network's specific requirements. The number of outputs in the softmax layer corresponds to the number of emotions in the dataset. Fusion strategies Multimodal AE and Embracement, described in Section 4.2, are based on trainable models, namely an AE and EmbraceNet. Therefore, they must be trained.

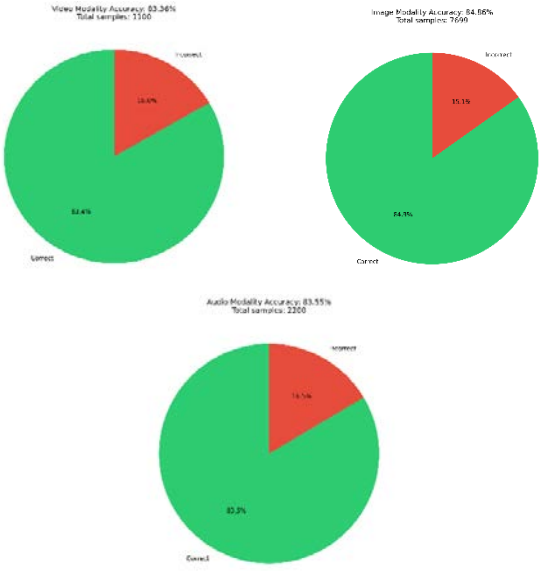

Fig. 5. The pictures from left to right are the results of Video, image and Audio respectively

C. Results

The performance of the multimodal emotion recognition system varies across different modalities. The audio modality achieves an accuracy of 83.55 %, correctly classifying 1,838 out of 2,200 samples, with 362 misclassified. The image modality shows the highest accuracy at 84.86 %, correctly identifying 6,534 out of 7,699 samples, while 1,165 are misclassified. The video modality has an accuracy of 83.36 %, with 917 correct classifications out of 1,100 samples and 183 errors.

Overall, the image modality performs best in most emotion categories, especially in recognizing happiness and neutral emotions. The audio modality's lower accuracy may stem from the difficulty in extracting audio features. The video modality's accuracy is similar to the audio modality, possibly due to information loss during feature fusion.

To enhance system performance, it is recommended to improve feature extraction methods, particularly for emotions that are easily confused, to better capture key features. Additionally, strengthening the contrastive learning framework can enhance cross-modal feature alignment by maximizing mutual information between different modalities. Optimizing the multi-task learning strategy and balancing the loss functions for emotion classification, recognition rate prediction, and contrastive learning can boost the model's generalization and robustness. Finally, developing datasets with more real-world scenarios can improve the model's practical performance.

D. Comparison

The performed analysis compares Transformer, CNN, and RNN models in multimodal emotion recognition across image, audio, and video modalities. The Transformer model performs best overall. It excels in image modality with 84.9 % accuracy, showing strong ability in capturing spatial features. In audio modality, it achieves 83.5 % accuracy, effectively extracting long - term dependencies. For video modality, it leads with 83.4 % accuracy, indicating effective multimodal information processing.

CNN performs well in image modality (80.1 % accuracy) but declines in audio (75.3 %) and video (73.4 %), struggling with temporal dependencies. RNN underperforms, with 77.3 % in image, 70.5 % in audio, and 70.4 % in video, likely due to limitations in spatial processing and multimodal integration (Tabl.II).

TABLE II. COMPARISON OF RESULTS

Model	Image Modality Accuracy	Audio Modality Accuracy	Video Modality Accuracy
Our approach	84.9 %	83.5 %	83.4 %
CNN	80.1 %	75.3 %	73.4 %
RNN	77.3 %	70.5 %	70.4 %

Our approach outperforms CNN and RNN in all modalities, proving robust and adaptable. Its ability to capture spatial and temporal features makes it ideal for multimodal tasks. CNN's sequential data handling limits its effectiveness, while RNN falls short in multimodal integration. Overall, Transformer-based approach is the most promising for advancing multimodal emotion recognition technology.

V. CONCLUSION

This study presents a multimodal emotion recognition system aimed at improving the objectivity and accuracy of traditional psychological assessments. By integrating facial expression, audio, and video recognition, the system captures subtle emotional cues often missed in manual evaluations, offering psychology

professionals a comprehensive and standardized tool. The system uses a unified framework where facial, video, and audio data are processed via a shared Transformer architecture. This architecture is selected for its superior ability to handle both spatial and temporal features in multimodal tasks compared to CNN and RNN models. A progressive training strategy is applied to ensure stable learning and effective multimodal information fusion. Key innovations involve hierarchical feature extraction, utilizing cascaded CNN structures for audio features, spectral attention for spectral enhancement, and self-attention for temporal modeling. Furthermore, a contrastive learning framework is employed to maximize mutual information across different modalities, and a multi - task learning strategy jointly optimizes emotion classification and recognition rate prediction. Experiments on the EmoDB, RAVDESS, and CREMA-D datasets show the system's effectiveness. The Transformer model surpasses CNN and RNN models in all modalities, achieving 84.9 % accuracy for images, 83.5 % for audio, and 83.4 % for video, highlighting its robustness and adaptability across different data types.

The study concludes that the proposed system represents a significant advancement in multimodal emotion recognition. Future research will focus on optimizing multimodal fusion strategies and developing more complex datasets to boost the system's real - world application performance.

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Encoding and Information Protection Algorithms in Digital Communication Channels

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***Abstract*. In the modern era of ubiquitous digital communication, ensuring the reliable and secure transmission of data is a fundamental requirement. This paper explores the theoretical basis and practical implementation of encoding and information protection algorithms used in digital communication channels. It focuses on the role of source and channel encoding, error detection and correction techniques, and cryptographic methods. Furthermore, it examines challenges posed by high-speed communication networks and evolving security threats, highlighting solutions such as forward error correction (FEC), convolutional codes, turbo codes, and encryption standards. The integration of these techniques is essential for building robust, efficient, and secure communication systems.**

***Keywords:* digital communication, error correction codes, channel encoding, data integrity, information security**

I. Introduction

Digital communication systems have become indispensable in our daily lives, enabling services such as internet browsing, mobile telephony, video streaming, and machine-to-machine communication. However, the digital nature of information introduces vulnerabilities, such as noise in transmission channels and the threat of unauthorized access. To address these issues, encoding (for efficient and reliable transmission) and information protection (for confidentiality and integrity) algorithms are employed. This paper provides a comprehensive overview of the encoding and protection mechanisms used in digital communication channels, from classical theory to modern applications in wireless networks, satellite communications, and cybersecurity.

II. Fundamentals of Digital Communication

Digital communication refers to the process of transmitting digital data between two or more devices using various transmission media such as copper cables, fiber optics, or wireless radio frequencies. These systems convert information into binary format (a sequence of 0s and 1s), which can be efficiently processed, stored, and transmitted over long distances. However, the transmission of digital signals is subject to several challenges. One major issue is the presence of noise and distortion in the communication channel, which can lead to signal degradation and errors in the received data. In wireless channels especially, interference from other sources and signal fading due to environmental conditions can severely affect performance. Additionally, weak signal strength may result in partial or complete data loss. Security concerns are also critical, as digital data can be intercepted, modified, or stolen during transmission. Threats such as eavesdropping, unauthorized access, and data tampering require strong protective measures. To address these challenges and ensure accurate and secure communication, digital systems implement a combination of encoding and protection techniques. Source encoding is used to compress and efficiently represent data for transmission, while channel encoding introduces redundancy that allows for error detection and correction. Cryptographic methods are employed to protect the data's confidentiality and integrity, making sure that it remains secure even if intercepted. These three techniques – source encoding, channel encoding, and cryptographic protection – form the core of a reliable and secure digital communication system (Fig. 1).

Fig. 1. Basic Digital Communication System

III. Source Encoding

Source encoding, also known as data compression, is the process of representing information in a compact form to reduce the amount of data that needs to be transmitted or stored. This is especially important in digital communication systems, where efficient use of bandwidth is critical. By eliminating redundancy and irrelevant information, source encoding allows the same

message to be transmitted using fewer bits. The main goal is to preserve the integrity and meaning of the original data while minimizing its size. One of the most well-known techniques in this area is Huffman coding, which assigns shorter binary codes to more frequently occurring symbols and longer codes to less frequent ones, thus reducing the average length of the encoded message. Another popular method is arithmetic coding, which encodes the entire message into a single fractional number between 0 and 1, often achieving better compression ratios for large data sets. Run-length encoding is a simpler approach that replaces sequences of repeated characters or numbers with a single value and count, which is especially useful for compressing simple graphics or binary images. Source encoding is essential in various applications, including audio and video compression, file storage, and transmission over networks with limited capacity. For example, formats such as JPEG for images, MP3 for audio, and MPEG for video rely heavily on source encoding principles. In modern communication systems, effective source encoding not only reduces the burden on transmission channels but also improves overall system efficiency by lowering storage requirements and speeding up data exchange.

IV. Channel Encoding: Error Detection and Correction

In digital communication systems, the transmission of data over physical channels is inherently susceptible to various types of noise and interference, which can result in bit errors. These errors pose significant challenges to the integrity and reliability of data transmission. To mitigate this issue, channel encoding techniques are employed, which introduce controlled redundancy into the transmitted data to enable the detection and correction of errors at the receiver's end.

Channel encoding is a core aspect of digital communications, complementing source encoding and encryption by ensuring that the data received is as close as possible to what was originally transmitted, even in the presence of disturbances in the transmission medium. There are two primary objectives of channel encoding: error detection, which identifies the presence of errors, and error correction, which reconstructs the original data without the need for retransmission.

Several types of error control codes have been developed and adopted in modern systems:

A. Hamming Codes

Hamming codes are among the earliest and most fundamental error-correcting codes. They are capable of detecting up to two simultaneous bit errors and correcting single-bit errors. These codes are relatively simple to implement and are often used in memory systems and applications where computational efficiency is critical. Hamming codes use a set of parity bits inserted at positions that are powers of two to check specific combinations of data bits.

B. Reed-Solomon Codes

Reed-Solomon (RS) codes are non-binary cyclic error-correcting codes particularly effective in burst-error environments. They are widely used in storage devices (CDs, DVDs), digital television, and satellite communications. RS codes work over finite fields and are capable of correcting multiple symbol errors, making them suitable for systems where data is transmitted in blocks rather than as individual bits.

C. Turbo Codes

Turbo codes represent a breakthrough in channel coding, providing performance close to the Shannon limit. They consist of two or more convolutional encoders connected in parallel and separated by interleavers. Decoding is performed iteratively using soft-input soft-output (SISO) decoders. Due to their high error-correcting capability, turbo codes are employed in 3G/4G mobile communication systems, satellite links, and deep space communication.

D. Low-Density Parity-Check (LDPC) Codes

LDPC codes are modern linear block codes characterized by sparse parity-check matrices. They were first proposed in the 1960s and later rediscovered due to their exceptional performance. LDPC codes allow for parallelizable and highly efficient decoding through belief propagation algorithms. They are a key component in the 5G communication standard due to their near-capacity performance and scalable implementation potential.

To evaluate the effectiveness of these codes, a common metric used is the Bit Error Rate (BER) as a function of the Signal-to-Noise Ratio (SNR). BER is defined as the number of erroneous bits received divided by the total number of transmitted bits, while SNR quantifies the signal strength relative to background noise. The relationship between BER and SNR for various coding schemes reveals their robustness in maintaining data integrity under noisy conditions.

The following simulation visualizes BER versus SNR for three typical error correction codes – Hamming, Turbo, and LDPC. Although the results are illustrative and not based on real code implementations, they demonstrate the comparative performance trends of the different schemes (Fig. 2).

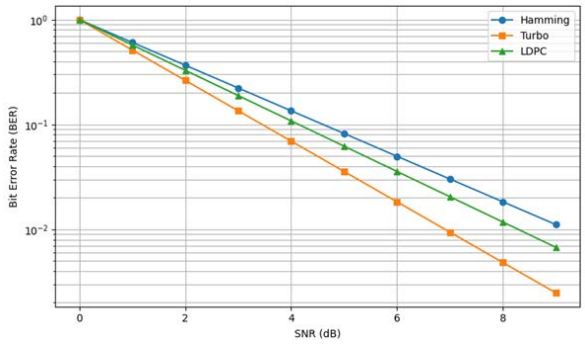

Fig. 2. BER vs SNR for Different Coding Schemes

As illustrated in the above plot, LDPC and Turbo codes significantly outperform the Hamming code in high-noise environments, maintaining lower BER values across increasing SNR levels. This demonstrates their suitability for modern high-performance communication systems where data accuracy and reliability are paramount.

In summary, the evolution of error-correcting codes from simple Hamming codes to sophisticated LDPC schemes reflects the technological advancements in communication theory. As digital communication networks continue to scale in complexity and data rates, the role of efficient and robust channel encoding remains central to ensuring seamless and secure information exchange.

V. Cryptographic Information Protection

While encoding ensures reliability, cryptography ensures confidentiality, integrity, and authentication of transmitted data. Cryptographic methods are crucial in protecting data from unauthorized access and manipulation during transmission. Symmetric encryption algorithms, such as the Advanced Encryption Standard (AES), use the same secret key for both encryption and decryption, making them highly efficient but dependent on secure key distribution. In contrast, asymmetric encryption algorithms like RSA and Elliptic Curve Cryptography (ECC) use a pair of public and private keys, enabling secure key exchange and digital signature implementation. Hashing algorithms such as SHA-256 convert messages into fixed-length hash values that serve as digital fingerprints, essential for verifying data integrity and authenticity in digital signatures and message authentication codes (MACs). End-to-end encryption ensures that only the sender and recipient can read the transmitted messages, providing an additional layer of security, especially in communication apps like Signal and WhatsApp. Together, these cryptographic techniques provide a multi-layered defense against threats such as eavesdropping, data tampering, and identity spoofing.

VI. Practical Applications and Analysis of Encoding and Protection Algorithms in Digital Communication Systems

To better understand the performance of encoding and protection algorithms in real-world scenarios, numerical simulation and analysis provide valuable insights (Fig. 3). One widely studied metric is the Bit Error Rate (BER) as a function of the Signal-to-Noise Ratio (SNR), which measures how effectively a coding scheme can correct errors introduced by the communication channel. Simulations comparing Turbo codes and LDPC codes reveal their relative strengths under varying channel conditions. Turbo codes, used extensively in LTE, typically achieve a BER of 10^{-5} at an SNR of approximately 5 dB for code rates around 1/3 (Tabl. I). LDPC codes, implemented in 5G systems, demonstrate improved performance by reaching the same BER at lower SNR values near 3.5 dB, indicating greater error correction efficiency (Tabl. II). However, LDPC decoding generally requires higher computational complexity, which is offset by advances in hardware acceleration.

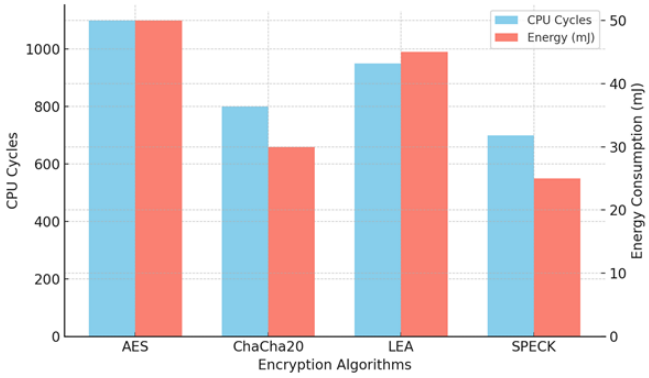

Fig. 3. Encryption Algorithm Performance

TABLE I. BER vs. SNR Table (Code Rate ≈ 1/3)

SNR (dB)	Turbo Code BER	LDPC Code BER
2.0	1.0×10^{-1}	8.0×10^{-2}
3.0	5.0×10^{-2}	2.5×10^{-2}
4.0	8.0×10^{-3}	5.0×10^{-3}
5.0	1.0×10^{-4}	2.0×10^{-5}
6.0	5.0×10^{-6}	5.0×10^{-7}

TABLE II. IoT Encryption Performance

Algorithm	CPU Cycles/Byte	Energy/Byte (µJ)
AES-128	2000	50
TinyAES	1200	30
SPECK	1000	25

In the realm of encryption overhead, IoT devices often face stringent resource constraints. Performance analysis shows that lightweight encryption algorithms such as TinyAES or SPECK consume roughly 30–50 % less CPU cycles and energy compared to standard

AES, making them more suitable for battery-powered devices. However, the trade-off lies in their reduced cryptographic strength, necessitating careful security assessment based on the application context.

VII. 5G Encoding and Encryption Integration

The 5G New Radio (NR) protocol employs LDPC codes for data channels, supporting flexible block lengths from 384 to 8448 bits and code rates ranging from 1/5 to 8/9. LDPC base graphs are selected based on the data block size, with iterative belief propagation used for decoding. Rate matching ensures the encoded data fits the transmission bandwidth, and iterations are tuned for performance and latency (Fig. 4). This flexibility enables 5G to meet diverse use cases including enhanced mobile broadband (eMBB), ultra-reliable low-latency communications (URLLC), and massive machine-type communications (mMTC).

Encryption in 5G relies on AES-CTR mode for user-plane encryption, combined with AES-CMAC or 128-NEA3 for integrity protection. These functions operate at the Packet Data Convergence Protocol (PDCP) layer. Keys are derived from master session keys defined in 3GPP TS 33.401, with periodic updates ensuring sustained security. Data flow begins with encryption and integrity protection at PDCP, then proceeds through MAC segmentation, LDPC encoding, modulation, and wireless transmission. The receiver reverses this process, validating and decrypting data before delivery.

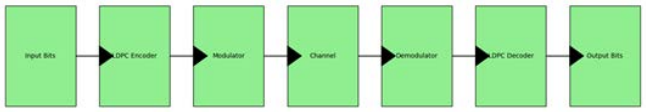

Fig. 4. LDPC Encoding and Decoding in 5G

VIII. Conclusion

This paper has provided a comprehensive analysis of encoding and information protection algorithms within digital communication channels. By delving into foundational principles, exploring modern error detection and correction techniques, and comparing various encryption algorithms under practical performance metrics, the study offers a broad yet detailed perspective of the current state of digital data integrity and confidentiality. We introduced comparative plots of Bit Error Rate (BER) versus Signal-to-Noise Ratio (SNR), as well as CPU usage of encryption algorithms, to quantify both the reliability and efficiency of different protection methods. The use of LDPC and Turbo codes, combined with advanced cryptographic methods like AES and RSA, was highlighted to reflect the balance between data security and computational overhead. Moreover, the integration of encoding and encryption mechanisms in emerging 5G architectures was diagrammatically presented to provide insight into the structural complexity and efficiency of next-generation communication systems. This structural visualization helps bridge theory and real-world deployment.

What distinguishes this work from prior studies is the combined evaluation of both encoding and encryption techniques in a unified performance framework. The inclusion of visual representations and simulation data using Python strengthens the paper's applicability to both academic research and engineering practice. By aligning theoretical discussions with practical Python simulations, the study contributes a reproducible and extendable methodology that can support further research in network security and signal processing. Future research may explore the combination of quantum-safe cryptographic algorithms with modern channel coding to address the security concerns in quantum-enabled networks.

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Grid-based Pedestrian Tracking with Long-term Shortcut Edge

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Abstract. **Multi-object tracking (MOT) has gained significant attention for its various applications like human behavior analysis for assisted living. Conventional grid-based tracking methods usually suffer from detection failures since temporally successive connections can't resist such transitory errors, while long-term connections build shortcuts and help to cross failure gaps. We re-formulate the grid-based method with the proposed deep metric based long-term shortcut edge for multi-object tracking, where a Siamese CNN is utilized to produce the similarity information. We verify the proposed long-term shortcut edge strategy in experiments on some widely-used datasets. The long-term shortcut edge could boost the MOTA by nearly 16 %. Comparison experiments with other popular methods indicate the performance advantage of our tracking method, enabling more accurate and continuous monitoring of daily activities.**

Keywords: **Multi-object tracking, data association, grid-based tracking**

I. INTRODUCTION

Multi-object tracking has gained significant traction in recent years, with its applications extending to various domains, including activity analysis [1–3], aerial surveillance [4] and human behavior analysis for assisted living, where real-time tracking of multiple individuals is essential for monitoring daily activities and detecting potential health issues. Multi-object tracking is a challenging task due to various problems, such as occlusions, unstable appearance, and trajectory mutual.

The most popular paradigm for multi-object tracking is 'tracking-by-detection', which identifies objects using an object detector in each video frame and then associates them with trajectories across video frames. In this work, we also utilize this paradigm considering its advantage of being resistant to divergence and demonstrating impressive results.

Among numerous multi-object tracking algorithms, grid-based methods have garnered attention for their ability to efficiently reduce computational costs, rendering the method suitable for limited resource environments. This stems from their adoption of spatiotemporal discretization in association, which transforms nearly infinite association possibilities into finite discrete options. This approach transforms the data association challenge into a structured grid network by discretizing both space and time within the area of interest. Subsequently, it generates a convex problem formulated as an integer linear programming task, yielding a globally optimal solution. The graph's unique configuration enables the avoidance of premature decisions based on incomplete evidence and simplifies the handling of temporary occlusions.

For the conventional grid-based tracking, since only the temporally successive connections (links between t and t+1) are considered, detection failure could easily cause a connection gap and lead to identification switches or trajectory fragmentation. We introduce a long-term shortcut edge to facilitate more robust tracking and reduce identification switches. As shown in Fig. 1, we present two representative instances caused by detection failures, including trajectory fragmentation (L=2) and identification switches (L=4,5). The color of the node and edge indicates the probability. A deeper color means a higher detection probability or similarity. We believe that both node (detection) and edge (motion permission and similarity) information is necessary for correct tracking. Detection failures happen in nodes (L=2,4,5 and t=4), which leads to a low probability of nodes and a low similarity response. The green dot lines indicate the proposed long-term shortcut edges, which serve as shortcut links and fill the gaps.

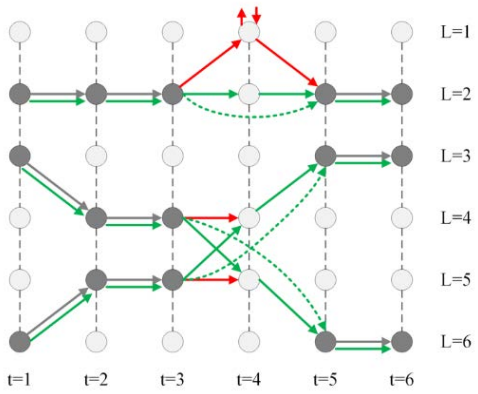

Fig. 1. Long-term edge (green dot lines) to resist detection failures. Green solid arrow lines are the ground truth tracks, while red arrow lines are erroneous tracks

Meanwhile, we integrate appearance similarity data into the grid network's edges to enhance tracking robustness. We employ a compact Siamese neural network as our similarity metric, which is an effective network first used in person re-identification. This network processes pairs of images and generates similarity scores between them.

II. Related Works

A. Grid-based Tracking

Grid-based tracking is an effective and efficient method for multi-object tracking that has been extensively studied in recent years. In this method, grid locations are encoded as nodes [5–9]. [5] proposed the K-shortest path algorithm to solve complex grid network problems.

However, [5] and [6] actually only take into account the information of detection location and neglect other important cues like appearance. Intuitively, the ignored appearance information could further improve the tracking performance. We try to integrate appearance similarity information into the edge of the grid network to facilitate robust tracking.

Recent neural networks for person re-identification show strong discriminative ability, with siamese CNNs gaining attention for their robust yet simple architecture. These networks process two inputs through shared-weight layers that merge at specific points. Siamese topologies fall into three main categories based on fusion points:

1) Parallel branches with identical structures process inputs separately, feeding top-layer features into a cost function to learn class-separable manifolds [10];

2) Top-layer outputs from parallel branches are concatenated, followed by additional layers and a softmax loss function [11];

3) Input patches are stacked as a unified CNN input, also using softmax loss [12].

III. Method

A. Formalization

As shown in Fig. 2, the approach of grid-based tracking involves dividing the relevant physical area into K discrete locations and the time interval into T instants. For each location k, let $N(k) \in \{1, \ldots, K\}$ represent the neighborhood of k, i.e., the locations that an object at k at time t can reach at time t+1. Thus, a directed graph with KT vertices is used to represent every location at every instant. The edges of the graph correspond to allowable object motions. In other words, there is a single edge from (t,i) to (t+1,j) if and only if $j \in N(i)$.

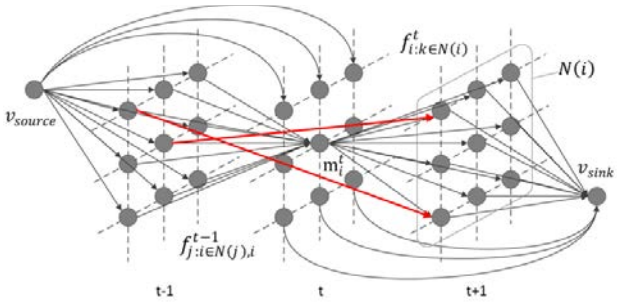

Fig. 2. Grid-based tracking with shortcut edge (red line)

Each vertex of the graph is labeled with a discrete variable m_i^t, which denotes the number of objects located at i at time t. Similarly, each edge is labeled with a discrete variable $f_{i,j}^t$, representing the number of objects moving from location i at time t to location j at time t+1. For example, $f_{i,j}^t = 1$ indicates that an object remains at location i between times t and t+1.

B. Multi-object Tracking Framework

The tracking procedure consists of two phases: building a grid model and solving the path. We present the procedure for building the grid model, which comprises two stages: producing nodes and edges. To conclude, we employ KSP [5] to resolve the grid network and extract trajectories.

The first stage involves building grid nodes, which requires a grid model map. We adopt the popular 'tracking-by-detection' paradigm, where object detection is performed individually in the beginning. We generate a grid model map and match each detection box with a grid location (m_i^t) based on its foot point position. However, not every grid location will have a corresponding detection. For the empty nodes without detection responses, we assign a default score to them. These detected locations are subsequently fed into the grid-based tracking module for the construction of corresponding nodes.

In our grid model, we utilize two types of edges: neighbor edges (black lines in Fig. 2) and long-term shortcut edges (red lines in Fig. 2). The neighbor edges are the neighborhood connections commonly used in conventional grid-based methods, but we integrate them with deep metrics. Upon obtaining the detections and their associated grid locations, we identify pairs with neighboring relationships and input them into a Siamese neural network to compute appearance similarities, which are then utilized to calculate the neighbor edge scores.

Additionally, we also generate a set of candidate long-term shortcut edges and use the Siamese network to measure their similarities. We apply a similarity threshold to filter out only the high similarity edges, which are then preserved as the long-term shortcut edges for global optimization.

C. Appearance Similarity based Long-term Shortcut Edge

We argue that long-term shortcut edges can improve the performance of grid-based tracking. Conventional grid networks only connect nodes with adjacent time steps, meaning that a node at time k can only connect to nodes at k+1 and not to nodes at k+n where n>1. This limitation can cause the trajectory flow formed by neighbor edges to be easily broken when an intermediate edge makes a mistake.

To reduce the number of edges and required computation, we consider appearance similarity and spatio-temporal constraints when generating the long-term shortcut edges. For two nodes connected by a long-term edge, we have the following spatio-temporal constraints: both nodes must have detection responses, the time difference between the nodes should be less than a maximal value, t_{max_diff}, and there must exist a path from one node to the other formed by the neighborhood edges.

We combine the long-term shortcut edges with a Siamese Convolutional Neural Network (CNN)-based appearance similarity measure to evaluate these edges. Only edges with a score higher than S_{th} are preserved.

We assign a probability score to each edge using a tiny Siamese network. A Siamese neural network comprises two identical weight paths within a convolutional neural network, designed to differentiate between similar objects. We input detection patches from two locations into the Siamese neural network and train it to calculate similarity probabilities.

Instead of randomly sampling negatives, we collect negatives based on spatio-temporal topological relationships, where negative pairs represent possible association results under our tracking framework. We use a common contrastive loss for training, which is robust against appearance variations.

The network architecture consists of inputting two RGB images concatenated into a 6*width*height tensor. This input is subsequently processed through a series of three convolutional layers (7*7 Conv 64, 3*3 Conv 128, 3*3 Conv 256), followed by three fully connected layers with dimensions 2048, 1024, and 512 respectively.

Additionally, we add a batch norm layer after each of the convolutional layers. Ultimately, a softmax layer generates similarity probabilities. This process allows us to incorporate the similarity measurement results from the Siamese network into the grid-based tracking formulation.

IV. Experiments and Evaluation

In this section, we present several experimental results to validate the proposed algorithm quantitatively.

A. Datasets and Metricss

Two popular datasets are used for the fair evaluation, including PETS09 [13] and a sequence known as AVG-TownCentre [14].

We use CLEAR-MOT [15] as the evaluation metrics. CLEAR-MOT includes the multiple object tracking accuracy (MOTA), multiple object tracking precision (MOTP), etc. MOTA is a score which combines false positives, false negatives and identity switches (IDSW) of the output trajectories. MOTP measures the alignment accuracy between the positive trajectories and the ground truth trajectories in terms of the average distance. Besides, the average number of false alarms per frame (FAR), the total number of false positives (FP), the total number of false negatives (FN), track fragmentations (FM), and identity switch (IDSW) are also presented. In addition, the average amount of false alarms per frame (FAR), the total amount of false positives (FP), the total amount of false negatives (FN), track fragmentations (FM), and identity switch (IDSW) are also shown.

B. Implementation Details

To train the Siamese similarity network, positive(same identification) and negative(different identifications) pairs of object image patches should be collected and prepared. When cropping the image patches, naturally there are two ways, namely, bounding boxes of ground truth or detection from an object detector. We use detection results for training rather than ground-truth because it's is more similar to practical data. Detection results(bounding boxes) of all images are generated by a modified ACF detector [16]. Using munkres' algorithm(with overlap threshold 0.5)

to solve the matching between ground-truth and detections, we label those detections with the ground-truth identification number. Siamese network is trained with the training part of PETS09 datasets, which are excluded from testing.

C. Comparison with Other Methods

To evaluate the capability of the proposed tracking method under the common circumstance, we compare it with other popular multi-object tracking methods. The same detection input as the comparison methods is used to produce fair results. Notice that since detection results have a massive impact on tracking performance, the comparison between association algorithms with different detection conditions is meaningless.

We use some widely used datasets including PEST2009 and AVG-TownCentre. Same public detections are used for all methods in testing for fair comparisons. The results from TBD [19], TC_ODAL [20],RNN_LSTM [18], DCO_X [21], SMOT [17], CEM [22] and ours is presented in Table. CEM and DCO_X utilize multiple cues like motion model, which could significantly improve tracking performance for such still scene with predictable moving objects, while our method only uses appearance information and produces the similar performance.

In our experiments, the proposed method demonstrates superior tracking performance across multiple evaluation metrics for sequences PETS and AVG-TownCentre according to MOTA. These results collectively highlight the proposed method's effectiveness in addressing critical challenges in multi-object tracking, solidifying its dominance in the evaluated scenarios

V. CONCLUSION

In this work, we re-formulate the grid-based with a long-term shortcut edge term, and utilize a Siamese CNN to produce the similarity information. The experiment verifies the strength of the proposed method. We conclude that long-term shortcut edge improves the performance of tracking.

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TABLE I. PERFORMANCE COMPARISON BETWEEN OUR METHOD AND OTHER METHODS WITH SAME DETECTION INPUT

Dataset	**Method**	**MOTA(↑)**	**MOTP(↑)**	**IDSW(↓)**	**FN(↓)**	**FP(↓)**	**REC(↑)**	**PRC(↑)**
PETS S2L2	SMOT	34.4	70.0	251	5602	475	41.9	89.5
	TBD	35.5	69.2	523	4355	1340	54.8	79.8
	TC ODAL	30.2	69.2	284	5375	1074	44.2	79.9
	CEM	44.9	70.2	150	4506	657	53.3	88.7
	DCO X	33.5	85.3	243	860	1657	79.3	66.5
	Ours	45.8	70.0	231	3938	1057	59.2	84.4
TownCentre	SMOT	15.0	70.0	76	5404	599	24.4	74.4
	TBD	10.5	69.7	176	5200	1020	27.3	65.6
	TC ODAL	1.6	68.9	26	6111	899	14.5	53.6
	CEM	-2.6	68.9	186	4979	2170	30.3	50.0
	DCO X	8.2	69.9	30	5766	763	19.3	64.4
	RNN_LSTM	13.4	68.8	299	4682	1206	34.5	67.1
	Ours	18.1	69.0	147	4501	1203	37.0	68.8

Features of Electrical Fluctuations Wavelet Transform for Hydrogen Fuel Cell Diagnostics

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Abstract. **Proton Exchange Membrane Fuel Cells (PEMFC) are one of the most promising components for the hydrogen energetics. Maintaining high efficiency and reliability of PEMFC requires online monitoring of technical state and predicting of the critical modes development at early stages. One of the most effective tools for solving this problem is fluctuation-noise diagnostics. It is shown that this approach allows obtaining diagnostic information without disturbing the operation of the PEMFC. The main problem in this area is the development of algorithms that do not require long accumulation of measurement signals, since this reduces the operativity of decision-making and the accuracy of the spectral characteristic assessment. The paper shows that an effective approach to solving the problem is to use Morse wavelets. It is shown that the approach used potentially allows detecting incorrect water balance, slow charge transfer, high diffusion loses. The speed of decision-making should be significantly increased to a time interval of 5–10 seconds. The proposed approach can be used as a basis for the development of modern systems for monitoring, diagnostics and control of operating modes of PEMFC based power plants.**

Keywords: **fuel cell, wavelet transform, electrical fluctuations, diagnostics**

I. INTRODUCTION

One of the most promising components for future hydrogen energetics is Proton Exchange Membrane Fuel Cell (PEMFC) due to the unique combination of characteristics: high power density, environmental friendliness, low operational temperatures, solid electrolyte, etc. However, the complexity of the internal processes of PEMFC and the need to manage them lead to the fact that in order to meet high reliability requirements [2, 3]: a service life of 40,000 hours while maintaining a generated power level of more than 80 % of the nominal. To achieve the specified requirements, it is necessary to implement systems for monitoring and diagnosing critical operating modes and faults at early stages of development. Such systems must ensure continuous monitoring of physical and chemical processes in the PEMFC during operation.

There are several different approaches for technical condition monitoring: polarization curve analysis [4, 5], electrochemical impedance [6, 7] and electrical fluctuation-noise characteristics [8–11]. The last approach has a particular interest, since it does not require the organization of any specialized disturbance of PEMFC operation mode. Potential of this direction of diagnostic tools development are proved by the first results related with diagnostics of PEMFC stacks [12, 13]. However, despite the fairly large number of works on the diagnostic properties of fluctuation-noise characteristics of PEMFC, the issue of adapting these approaches to real operation condition has not been fully studied yet. One of the main issues here is the problem of increasing the efficiency of diagnostic decision-making. The article discusses the possibility of applying the wavelet transform to improve probabilities of fluctuation-noise diagnostics.

II. ELECTROCHEMICAL NOISE OF PEMFC

During operation of any electrochemical systems, including solid polymer fuel cells, the electrical voltage and current randomly change around the average values of V_0 and I_0, determined by the current operating mode:

$$V_{FC} = V_0 + u(t), \quad (1)$$

$$I_{FC} = I_0 + i(t). \quad (2)$$

Such random deviations $u(t)$ and $i(t)$ are electrochemical noise and fluctuations of voltage and current, respectively. The characteristics of noise and fluctuations can change due to changes in operating modes and the technical condition of PEMFC [8–12]. When PEMFC operates under a constant electrical load (Fig. 1), there is a simple relationship between the stochastic deviations of current and voltage:

$$i(t) = u(t)/R_L, \quad (3)$$

where R_L is a load resistance.

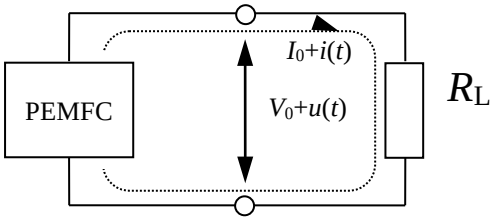

Fig. 1. PEMFC electrical fluctuations

The main technical difficulties in studying electrical fluctuations and noise are the need to perform high-precision measurements over wide frequency ranges and a large dynamic range as well as complex structure of the measurement signal requiring special algorithms to identify and estimate the diagnostic features.

III. Wavelet Analysis

The information properties of the electrical fluctuations are occurring during the operation of a fuel cell are used for the prediction the changes in the mode of operation of a fuel cell. The possibility of this approach follows from [14, 15], in which it is shown that the characteristics of electrical fluctuations are dependent on the technical state of the fuel cell.

Applying wavelet transform allows allocating local features and analysis of the fine structure of the signal, and thus ensures higher quality of diagnostics than currently suggested systems.

The possibility of applying wavelet transform to the analysis of electrical fluctuations of a fuel cell is considered on a model experiment [16]. Then this method is used to analyze the experimental data.

Wavelet transform of the signal is based upon its decomposition of the signal by scaling and translation, and converts signal to two-dimensional representation of a one-dimensional signal, where the frequency and coordinates become as independent variables.

One of the important components of the wavelet transformation is the choice of the mother wavelet. It is proposed to use a generalized Morse wavelet, which has the ability to instantly estimate the frequency and phase of the signal [14, 15]. The Morse wavelet is an analytical wavelet, the resolution parameters of which depend on the wavelet bandwidth

$$p^2 = \beta\gamma . \qquad (4)$$

With this increase in p, the resolution properties of the wavelet in the frequency domain increase, which occurs due to an increase in the number of oscillations of the real and imaginary parts of the wavelet (Fig. 2).

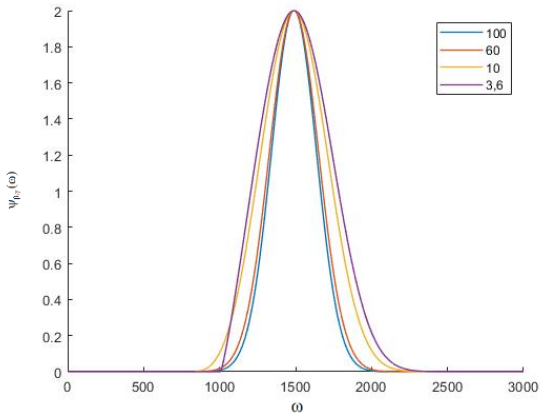

Fig. 2. Morse wavelet in the frequency domain at $p^2 = 100,\ p^2 = 60,\ p^2 = 10,\ p^2 = 3{,}6$ (top to bottom)

The processing of electrical fluctuations by the methods of wavelet transform is carried out in the following sequence:

1. Direct discrete wavelet transform: decomposition of a signal into approximating and detailing coefficients in the basis of orthogonal wavelets with subsequent zeroing of the approximating coefficients to highlight the signal trend;

2. Signal recovery using detail coefficients using inverse discrete wavelet analysis;

3. Continuous wavelet transform and calculating the informative features in the form of sum of wavelet coefficients' absolute values.

When analyzing voltage fluctuations of a fuel cell using direct discrete wavelet transform, it is necessary to remove the trend component of the signal while retaining the maximum information in the noise component of the signal, since only this component is subjected to further analysis. It is assumed that the fluctuation and noise component contains the diagnostic features of the technical state and critical operation modes of the PEMFC membrane-electrode assembly. For the detrending procedure based on the discrete wavelet transform, orthogonal wavelets with a compact carrier are used.

The use of the Daubechi 2 wavelet for removing the trend component allows saving diagnostic information, which is subsequently, analyzed using a continuous wavelet transform. It is proposed to use the criterion of maximum dispersion of the reconstructed signal to select the optimal wavelet of the discrete wavelet transform. It was determined that the maximum dispersion of the reconstructed signal is achieved using the Daubechi 2 (db2) and Symlet 2 (sym 2) wavelets.

Experimental studies of diagnostic signals were carried out for the PEMFC, the membrane-electrode unit of which with an effective area of 5 cm^2 is made of a proton-exchange film Nafion 112, hydrophobized carbon-graphite fabric electrodes coated with a catalytic layer with a platinum load of 0.5 mg/cm2 on a Vulcan XC-72 carrier. The experimental setup from Fuel cell technologies, Inc. allows us to select the oxidizer type: air or oxygen and set seven operating parameters: cell temperature, fuel η_A and oxidizer η_C humidity, fuel Q_A and oxidizer Q_C volumetric flow rate, pressure at the outlet of the anode P_A and cathode P_C gas transport channels. The measurement of electric current and voltage are carried out with dedicated high sensitive equipment.

Fig. 3 shows the fluctuations of a fuel cell operating under a load of 1 Ohm on the upper graph. The lower graph shows the signal after performing the trending procedure with the discrete wavelet transform. When performing a discrete wavelet transform, the signal is decimated, but the diagnostic properties of the signal do not change.

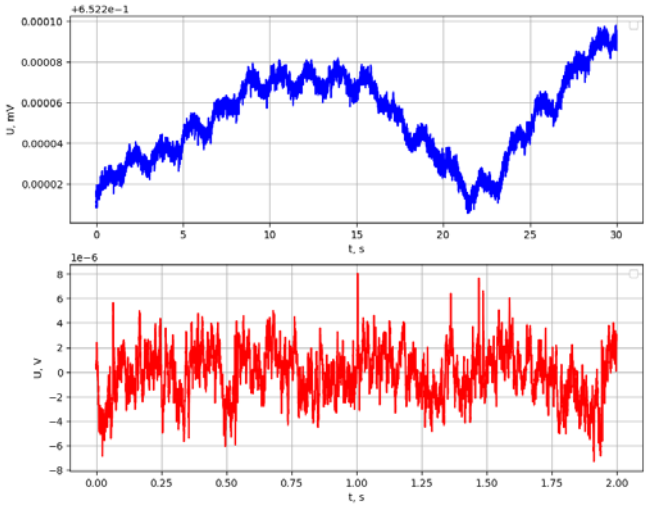

Fig. 3. Electrical fluctuations PEMFC with R_H=1 Ohm (upper), detrended signal (down)

On the next step a continuous wavelet transform is performed using the Morse wavelet with parameter p^2=9.

The scalogram of the wavelet coefficients for R_L=1Ohm is shown in Fig. 4. It can be seen that the values of the wavelet coefficients are significantly higher at low frequencies than at high frequencies. Comparison the scalogram presented in Fig. 4 with one (Fig. 5) measured for R_L=0.4Ohm shows significant difference. It means that the Morse wavelet based scalogram are sensitive to the variation of internal structures of fluctuation depending on the operational mode.

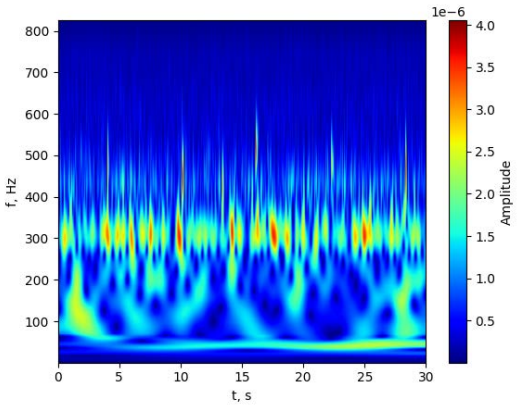

Fig. 4. Scalogram of the wavelet coefficients (mother wavelet – Morse, p^2=9) for load resistance R_L=1Ohm

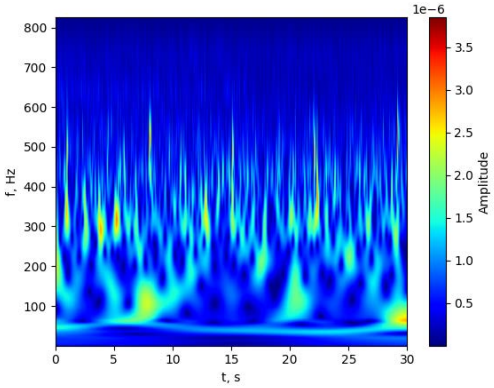

Fig. 5. Scalogram of the wavelet coefficients (mother wavelet – Morse, p^2=9) for load resistance R_L=0.4Ohm

The more detailed investigation of this fact was done for a series of measurement for different load resistances (Fig. 6) using the following approach. The obtained wavelet coefficients were summed up by their absolute values depending on the scale factor a, which are proportional to the frequency.

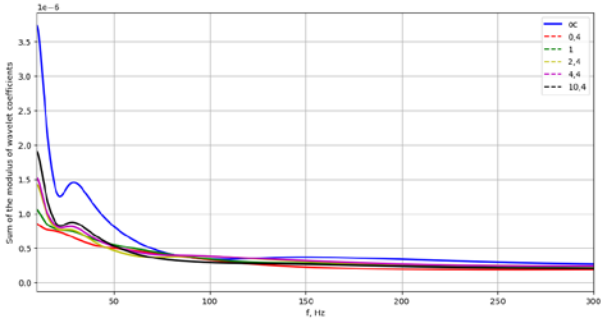

Fig. 6. The modulus of the sum of wavelet coefficients with R_H=∞, R_H=0.4, R_H=1, R_H=2.4, R_H=4.4, R_H=10.4 Ohm

Fig. 5 shows distribution of the modulus of the sum of wavelet coefficients depending on the frequency at different values of the fuel cell load. The analysis of Fig. 5 shows that the wavelet coefficients depend on electrical operation points in a complex way and reflect the basic internal physical and chemical

processes within PEMFC. Spectral characteristics show different behavior in distinct frequency ranges. The more detailed analysis of this behavior requires the additional invesigations.

The results obtained in frame of this paper shows that the Morse wavelet-based analysis is a promising way to study diagnostic features of PEMFC electrical fluctuations. The sensitivity of the received spectrum to the operation condition and the results for more classical Fourier analysis [8–11] proves the prospectivity of the corresponding investigations.

CONCLUSION

Electrical fluctuation noise analysis is one of the most prospective diagnostics approaches for PEMFC since it has high information content and does not require perturbation of operation mode. This approach needs special tools for effective data processing and diagnostic features retrieval. The existing techniques of data processing requires the long procedure of data accumulation.

The wavelet analysis is an appropriate tool for electrical fluctuation data processing to solve problem of PEMFC technical state online monitoring. The established is the fact that the Morse wavelet provides sensitivity to operation mode of PEMFC and could be considered as a potential basis for signal processing module of the diagnostics system. The sensitivity to the PEMFC operation mode is demonstrated on the basis of different load resistances. Change the load resistance induces variation of current which defines the intensity of internal physical and chemical processes. The proposed data processing procedure allows us to detect the corresponding difference. The further wors will be focused on the topic of identification of specific diagnostic features allowing detection of incorrect water balance, diffusion and charge transfer processes slowing down.

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Detailed Foot Keypoint Completion and 3D Human Skeleton Estimation Based on Multi-Model Fusion

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Abstract. **This paper proposes a 3D human skeleton estimation method based on multi-model fusion. It utilizes the full-body skeleton keypoints generated by the HRNet model and the foot keypoint detection results from MediaPipe. A multi-head attention mechanism is then employed to generate 17 3D skeleton nodes. In this experiment, the 2D-to-3D ratio mapping and direction estimation of foot posture are used to complete the foot skeleton reconstruction. By leveraging the 2D-to-3D proportional relationship of the legs and the skeletal topology structure, the 3D coordinates of the foot keypoints are calculated, resulting in a complete 3D skeleton model with 21 keypoints. Experimental results demonstrate that the proposed method significantly enhances the detail restoration in the foot region while maintaining the overall skeleton estimation accuracy. This method does not require additional 3D foot annotation data, offering good applicability and robustness, and providing an effective solution for complete 3D human skeleton estimation.**

Keywords: **3D Human Skeleton Estimation, Foot Keypoints, HRNet, MediaPipe, Multi-Head Attention, 2D-to-3D Ratio Mapping**

I. INTRODUCTION

3D human skeleton estimation is a critical research area in computer vision, with broad applications in motion analysis, virtual reality, medical rehabilitation, and pose recognition. By accurately locating human keypoints and modeling the 3D spatial structure, it is possible to achieve a comprehensive understanding of human motion states, providing technical support for various real-world applications [17]. However, existing 3D skeleton estimation methods typically focus on modeling major joints such as the head, torso, and limbs, while paying less attention to detailed estimation in the foot region. Keypoints such as toes and the sole are often ignored. This incomplete skeletal structure limits the performance of 3D human pose estimation in fine-grained tasks, especially in applications requiring detailed foot motion analysis, such as posture correction and gait analysis. To address the shortcomings of current methods in foot region estimation.

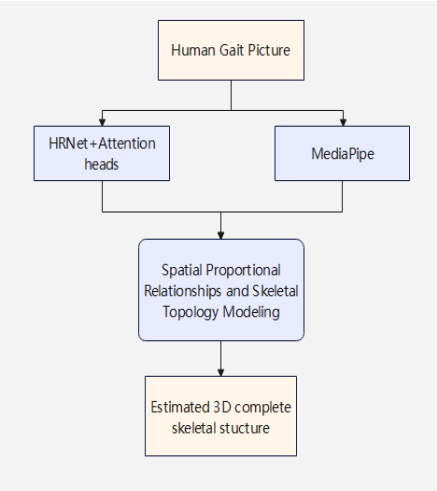

Fig. 1. Structure of the 3D Lower Limb Skeleton Estimation Model

From Fig. 1, it can be understood that the method based on multi-model fusion leverages the advantages of HRNet and MediaPipe to complete the reconstruction of 3D foot skeletal structure through 2D-to-3D proportional mapping and directional estimation. The specific steps include using HRNet to perform full-body skeleton pose estimation on video sequences, generating 2D and 3D skeleton sequences with 17 key points as the base skeletal structure. Utilizing MediaPipe for refinement of the foot region, extracting 2D skeletal key points of the left and right feet including toes, soles.

Calculating the 3D coordinates of the foot key points by using the proportional relationship between the 2D and 3D distances of the legs (from knee to ankle), and completing the spatial information of the foot skeleton with directional vectors and depth assumptions. Finally, fusing the estimated foot key points with the 3D skeleton generated by HRNet to produce a complete 3D skeleton model with 21 key points.

II. Related Work

A. HRNet in Human Skeleton Estimation

HRNet, short for High-Resolution Network, is a deep learning model that performs exceptionally well in human skeleton detection tasks. Its core idea is to leverage multi-scale fusion of high-resolution features to accurately locate key points of the human body. The model structure can be seen in Fig. 2.

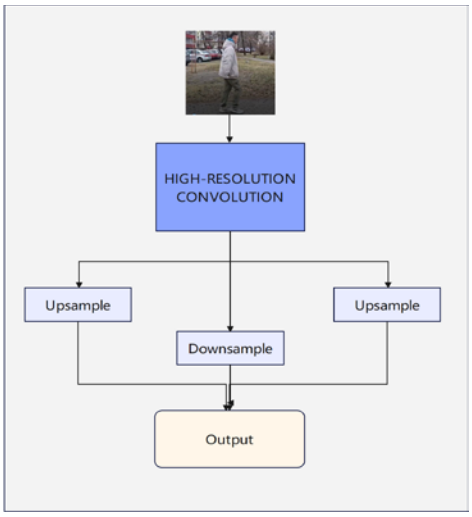

Fig. 2. Generating high precision 17 2D skeletal keypoints

HRNet maintains high-resolution feature maps throughout the network, avoiding excessive downsampling, which enhances its ability to detect detailed regions such as hands and feet. Through its multi-branch network structure, HRNet can simultaneously capture global information and local features, maintaining high accuracy even under complex pose variations. It has been widely applied in both 2D and 3D skeleton estimation tasks. For example, in some studies, the combination of HRNet with regression modules has further improved the prediction accuracy of 3D skeletal coordinates. That HRNet's output typically focuses on general skeletal key points, such as the 17 key points defined in the COCO dataset [13], leaving room for improvement in modeling finer details like the feet. This opens up significant opportunities for future research. In HRNet, cross-resolution feature fusion is achieved through both upsampling and downsampling methods. The formula for cross-resolution feature fusion is [11]:

$$X_s^{(t+1)} = \sum_{j=1}^{S} W_{s,j} \cdot \text{Resize}\left(X_j^{(t)}\right). \quad (1)$$

Represents the process of upsampling or downsampling features to align multi-scale features. The formula indicates that, during the $t+1$ iteration, the features X of the s layer are obtained by adjusting $X_s^{(t+1)}$ from all layers to the same scale as the $X_j^{(t)}$ layer. weighted summation is then performed on all the features adjusted by $Resize$. Through this feature fusion mechanism, HRNet achieves information exchange between features of different resolutions, preserving high-resolution details while low-resolution global semantic information.

B. Multi-Head Attention Generating 3D Skeletons

Multi-head attention understands the relationships between elements in the input sequence from different perspectives. By introducing multiple "heads" (attention heads), the model can capture different levels or types of semantic information. Multi-head attention generates multiple 3D hypotheses on the time series and skeletal key points. Multi-head attention generates the structure of a 3D skeletal model as shown in Fig. 3. The module further enhances the modeling of dynamic relationships in time series by utilizing cross-frame attention to capture motion trends. The input is a sequence of 2D keypoints $X \in \mathbb{R}^{T\times J\times 2}$, where T represents the number of time frames, J is the number of keypoints, and 2 represents the 2D coordinates. The core formulas are primarily based on the multi-head attention mechanism and the temporal modeling module. First, the input data is mapped to a high-dimensional feature space through a linear embedding layer, and then multi-head attention is used to model the global dependencies between keypoints and the spatiotemporal interactions through the following formula [12]:

$$\text{MultiHead}(H) = \text{Concat}(\text{head}_1, \text{head}_2, \ldots, \text{head}_h)W_O, \quad (2)$$

$$\text{head}_i = \text{Attention}\left(HW_Q^i, HW_K^i, HW_V^i\right). \quad (3)$$

Q, K, and V represent the query, key, and value vectors, respectively, while Wq, Wk, and Wv are learnable weight matrices [14]. The role of multi-head attention is to capture the global relationships between keypoints, with each head focusing on different feature patterns. The number of attention heads, H, significantly impacts the model's performance. Heads higher number of heads can capture richer features but also increases computational overhead.

The temporal modeling module is designed to capture dynamic changes in sequential data and to model the dependencies between different time frames.

It uses 1D convolution to capture the local dynamic relationships within the time series. The effectiveness of temporal modeling is reflected in the smoothness of motion over short time frames. The formula for temporal modeling is as follows [10]:

$$Y = \mathrm{MLP}(H_{\mathrm{time}}). \tag{4}$$

The features processed through multi-head attention and temporal modeling are mapped to 3D space to predict the 3D coordinates of each keypoint. Here, **MLP** (a multilayer perceptron) is used to reduce the high-dimensional features down to the 3D coordinate space.

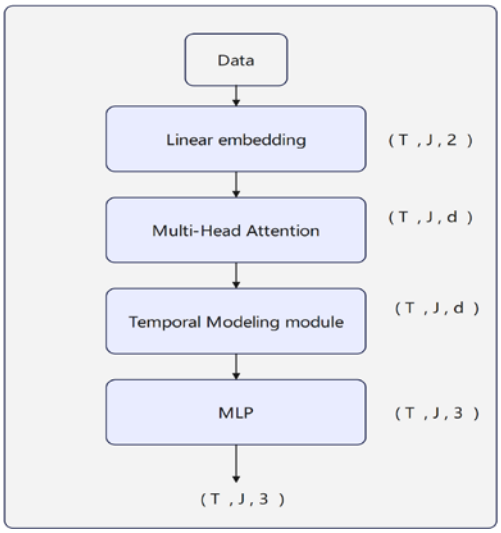

Fig. 3. 3D bone generation at 17 key points

The multi-head attention mechanism, high-precision 3D skeletal pose predictions can be achieved by leveraging spatial structural information and temporal information from consecutive frames, resulting in 17 skeletal key points.

C. Application of MediaPipe in Foot Keypoint Detection

MediaPipe is a real-time computing framework-based human pose estimation system capable of detecting detailed information, including 33 key points, for hands or feet in monocular images. The MediaPipe foot module can detect regions such as toes, soles, and heels. Its key characteristic is efficiency, as MediaPipe is designed as a lightweight network suitable for real-time processing [15], performing exceptionally well on mobile devices [5].

Compared to full-body pose estimation models like HRNet, MediaPipe provides more precise modeling of foot details, offering additional key point location information. By using MediaPipe for 2D lower-limb estimation, four skeletal key points of the left and right foot (soles and toes) can be filtered, combined with the 17 skeletal key points from HRNet. The combination of the two models estimates a total of 21 skeletal key points for 2D human pose estimation [5].

HRNet achieves very high prediction accuracy, estimating 17 key points, while MediaPipe estimates only 4 key points with slightly lower overall accuracy compared to HRNet. However, MediaPipe is a lightweight model with very fast detection speed. Therefore, we can ultimately achieve high-accuracy 2D pose estimation for 21 key points by combining the two [16].

D. Modeling Spatial Proportional Relationships and Skeletal Topology

Skeletal topology is an important prior in human skeleton estimation. The human skeleton has a fixed connection structure (such as the connections between the knee and ankle, and between the ankle and toes), and this topology follows certain geometric proportional relationships in space [2]. Leveraging this prior information can effectively reduce depth ambiguity problems in monocular 3D skeleton estimation. Spatial proportional relationships refer to the relative distances between human joints, which exhibit a certain invariance in proportions in both 2D and 3D space. For example, the 2D and 3D distances from the knee to the ankle satisfy the following proportional relationship formula [8]:

$$R = \frac{|P_{3D}(\mathrm{knee}) - P_{3D}(\mathrm{ankle})|}{|P_{2D}(\mathrm{knee}) - P_{2D}(\mathrm{ankle})|}. \tag{5}$$

Skeletal topology modeling constrains and optimizes the connection relationships between human joints, ensuring that the generated 3D skeletal model adheres to human anatomical principles [9]

$$\vec{d}_{\mathrm{toe}} = k \cdot \vec{d}_{\mathrm{heel}}. \tag{6}$$

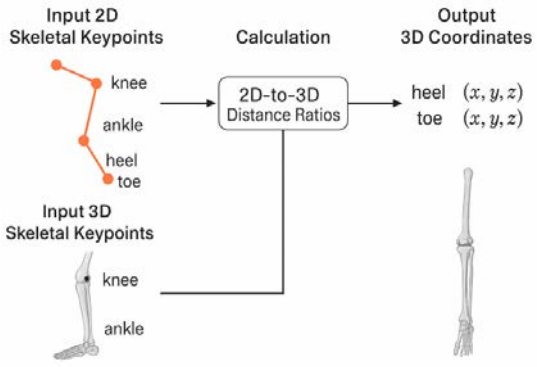

Fig. 4. Skeletal Topology for Lower Limb Pose Estimation

Skeletal topology modeling involves constraining and optimizing the connection relationships between human joints to ensure that the generated 3D skeletal model conforms to human anatomical principles. The relative positions between the toes and the sole of

the foot should satisfy the following geometric relationships. Here, $\vec{d}_{toe}$ and $\vec{d}_{heel}$ represent the directional vectors of the toes and the heel, respectively, and **k** represents the proportional constant. The depth optimization of the directional vectors is aimed at refining the depth information of the key points on the foot.

As shown in Fig. 5, the estimated lower limb key points, combined with the original 17 skeletal nodes [4], form a 3D gait estimation model with 21 human body key points.

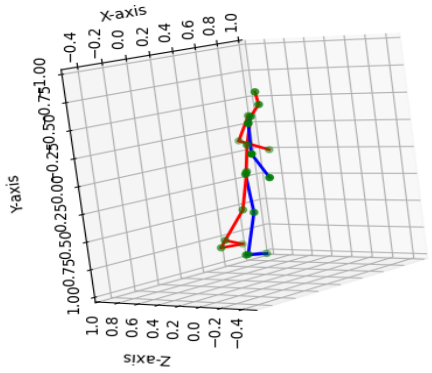

Fig. 5. Estimated 21 node skeleton

By combining multiple models, high-precision 3D estimation was achieved without the need for labeled data to estimate 21 key points of the human skeleton. This enables accurate lower limb detection, providing more detailed information about the lower limbs for applications such as medical diagnostics.

III. Experimental Analysis

The estimated lower limb joint points combined with the original 17 skeletal nodes to form 21 3D estimates of human gait can be seen in Fig. 5. The experiment was completed to estimate 21 skeletal gaits without the 3D labelled data of the foot.

Accuracy Error Analysis for Joints in Different Models

Keypoint region	**Model for this experiment(mm)**	**HRNet(mm) [1]**	**MediaPipe(mm) [3]**
Full-body skeleton	42.5	35.2	54.2
The upper body	33.8	33.8	53.1
Joints of the foot	59.6	NO	NO

Due to the lack of real 3D foot annotation data, it is not possible to directly evaluate the accuracy of the generated 3D skeletal model. From Table we performed error analysis by re-projecting the generated 3D skeletal data onto the 2D plane and comparing it with the real 2D keypoint data. The experimental results demonstrate that the proposed method achieves detailed 3D reconstruction capability in the foot region while maintaining high accuracy in overall skeletal pose estimation. The average EPJPE (Error Per Joint Position Estimation) for the foot region is 59.6 pixels. Below are the EPJPE error results for different keypoint regions:

The experimental results show that this method outperforms the MediaPipe model but is slightly less accurate than the HRNet model. However, this approach does not require additional 3D foot annotation data and can achieve detailed estimation of the foot as well as accurate estimation of other skeletal parts. By combining HRNet and MediaPipe, the method significantly enhances the detailed reconstruction capability in the foot region, providing an effective solution for complete 3D human skeleton estimation.

IV. Conclusion

This paper proposes a 3D human skeleton completion method based on spatial proportional relationships and skeletal topology. By integrating HRNet and MediaPipe models and leveraging 2D-to-3D proportional mapping and directional vector calculations, the method successfully reconstructs the 3D coordinates of foot key points and optimizes the overall skeletal structure through topology constraints. Experiments demonstrate that the proposed approach outperforms existing methods in both foot region detail and overall skeleton estimation accuracy, achieving an MPJPE of 42.5 mm. The key contributions include generating a complete 21-keypoint skeletal model through multi-model fusion, introducing spatial proportional relationships and directional vector optimization for foot key points, and enhancing model consistency with skeletal topology constraints. Notably, the method achieves high-precision completion without requiring additional 3D foot annotation data. Despite its effectiveness, reliance on depth assumptions and proportional relationships may limit performance in dynamic scenarios or when 2D predictions involve significant errors. Future work will explore physical constraints, kinematic models, multi-view data fusion, and high-quality 3D foot data to improve robustness. This method enhances skeletal model completeness and offers valuable tools for motion analysis, virtual reality, and gait detection applications.

V. Acknowledgment

This work was supported by the China Scholarship Council. Thanks Alexander Nedzved for his invaluable guidance throughout this research. Specifically, Professor Nedzved provided critical insights during the experimental design phase, helping to refine the approach for multi-head attention and 2D-to-3D ratio

mapping. His expertise was instrumental in overcoming key challenges, such as the reconstruction of foot skeletons and the accurate estimation of 3D skeleton nodes. His thoughtful suggestions and problem-solving strategies greatly contributed to the success of this study.

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System of Machine Vision Algorithms for Detecting and Eliminating Speckle Noise in Ultrasound Images Using a Convolutional Neural Network

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***Abstract*. Ultrasound image visualization plays an important role in medical diagnostics, but the presence of speckle noise significantly complicates diagnostics and analysis, reducing the quality of ultrasound (US) image visualization in medical practice. This paper proposes a method for removing speckle noise based on the use of an autoencoder. A multi-layered convolutional architecture is used to suppress noise and restore diagnostically significant details. Positive results in noise removal are demonstrated. The article presents an approach to noise level classification using metrics such as PSNR, SSIM, MSE, ERGAS, and UQI.**

***Keywords:* Ultrasound images, machine vision, medical image processing, speckle noise, neural networks, autoencoder, noise reduction**

I. INTRODUCTION

In medical imaging, ultrasound images are some of the most common diagnostic methods due to their availability, safety and information content. However, a significant drawback of this method is the presence of speckle noise, which degrades the quality of images and reduces the legibility of anatomical structures [1–3]. There exist various approaches to eliminating noise in ultrasound images, e.g. classical methods such as median and Gaussian that partially reduce noise, but often lead to the loss of important image details limiting their use in clinical practice [4]. In recent years, deep neural network models, including autoencoders, have shown high efficiency in image restoration tasks [5–7].

To solve the problem of eliminating speckle noise in ultrasound images, the authors developed a system of algorithms based on convolutional autoencoder. As part of the study, an autoencoder architecture adapted for working with ultrasound images was created, and it was trained on a dataset containing artificially noisy images. The quality of the restoration was assessed using the PSNR, SSIM, MSE, ERGAS and UQI metrics. In addition, a noise level classification method was developed, allowing images to be divided into «strong», «medium» and «weak» categories based on the analysis of quality metrics.

II. DESCRIPTION OF A SYSTEM OF MACHINE VISION ALGORITHMS FOR NOISE DETECTION AND ELIMINATION

A. Architecture

An autoencoder is a type of neural network model designed for data compression and reconstruction tasks. In our case, an autoencoder is used to remove noise and restore images while preserving important structural elements. The main advantages of autoencoders are their ability to filter noise without losing important details and to adapt to different types of noise found in real data.

The encoder compresses the input image into a compact representation (called the latent space or bottleneck). In our implementation, the encoder receives a 1024×1024×1 grayscale image and uses multiple convolutional layers to extract key features from the image.

• Convolutional layers (Conv2D): Each convolutional layer contains 128 filters with a 3x3 kernel, a ReLU activation function, and a 'same' alignment type. This allows the feature map dimensionality to be preserved at each stage, which helps the model extract features from low-level features (edges, textures) to high-level features. The formula for convolution is as follows:

$$Y[i, j] = \sum_{m=0}^{M-1} \sum_{n=0}^{N-1} X[i + m, j + n] * W[m, n], \quad (1)$$

where X[i, j] is the input image, W[m, n] is the filter (convolution kernel) of size M×N, a Y[i, j] is the result of the convolution.

• MaxPooling2D: After each convolutional layer, a pooling operation is used with a 2×2 kernel and 'same' padding. This reduces the size of the feature map by selecting the maximum value in each window, preserving key information, and helping the model learn a more efficient representation of the data. For example, after the first layer, the image size is reduced from 1024×1024 to 512×512.

The decoder, in turn, restores the image from the compact representation. It consists of layers that increase the size of the image to its original state, trying to minimize the error between the original and the restored image. The following elements are used for this:

• UpSampling2D: Increasing the image dimension is done through upsampling. For example, if the input image is 64×64, then upsampling increases its size to 128×128, and then to the original 1024×1024. Formally, upsampling can be expressed through interpolation:

$$Y[i, j] = X\left[\frac{i}{s}, \frac{j}{s}\right], \quad (2)$$

where s is the magnification factor (in this case s = 2).

• Convolutional layers (Conv2D): they are used to restore textures and fine details lost during the encoding stage. The convolution formula is similar to that used in the encoder.

• Final layer: The final layer is a convolutional layer with a single filter and a sigmoid activation function that normalizes the pixels of the output image to a range between 0 and 1:

$$\sigma(x) = \frac{1}{1 + e^{-x}} . \quad (3)$$

ReLU activation function is used as follows:

$$ReLU(x) = \max(0, x). \quad (4)$$

It speeds up the learning process by preventing gradient vanishing. The output layer uses the sigmoid function that normalizes the output data.

The model is compiled using the Adam optimizer that implements the following formula for updating weights:

$$\omega_{i+1} = \omega_t - \frac{\alpha}{\sqrt{\hat{v}_t + \varepsilon}} \widehat{m}_t , \quad (5)$$

where $\widehat{m}_t$ and $\hat{v}_t$ are the estimates of the first and second moments, α is the learning rate, and ε is a small value to prevent division by zero.

The mean square error is used as the loss function, since our goal is to minimize the difference between the original image and the reconstructed one.

The architecture of the autoencoder is shown in Fig. 1.

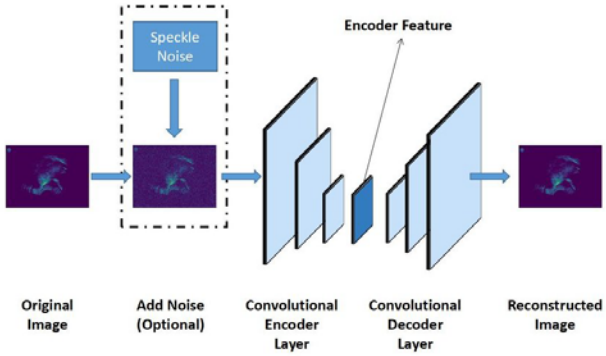

Fig. 1. Basic autoencoder [8]

Advantages of autoencoders for noise removal:

1) Noise Removal: Autoencoders are effectively trained to distinguish noise from key image features, making them ideal for filtering tasks.

2) Adaptability: They can be trained on real data, taking into account specific types of noise present in images (e.g. speckle noise in ultrasound).

3) Preserving Structures: Unlike simple filtering methods (such as the median filter), autoencoders can remove noise while preserving important image details.

Thus, our architecture uses four pooling levels to reduce the image size from 1024×1024 to 64×64, and then restores it to its original dimensions through four upsampling stages, making the autoencoder an effective tool for image processing with filtering and restoration tasks.

Fig. 2 shows an architectural diagram describing the work process.

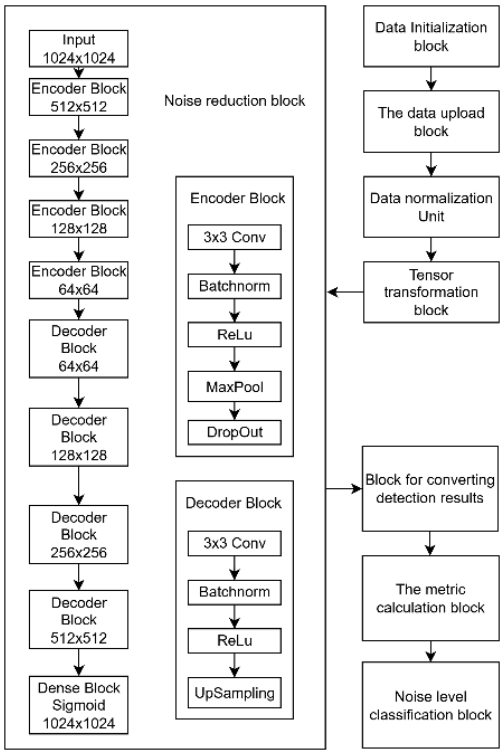

Fig. 2. Structural diagram of the algorithm

B. Dataset

An ultrasound dataset, including data from [9], was used to train and test the model. The dataset contains images divided into three categories: normal, benign, and malignant. In total, approximately 7800 ultrasound images were used in the study.

C. Threshold classification

Threshold classification of noise levels. Metrics are needed to objectively evaluate the effectiveness of noise removal and image restoration after its processing [10]. Image quality assessment using metrics allows quantitative comparison of the restored image with the original one and determine how successfully the noise was removed without losing important information.

In the present paper, noise level classification is performed based on several metrics, each focusing on different aspects of image quality [11-13]. Among them are PSNR, MSE, SSIM, ERGAS, and UQI. Each noise level is defined by a threshold filter that classifies the values of each metric into three categories: low noise, medium noise, or high noise. The metrics used are described below:

PSNR measures the ratio between the maximum signal power and the noise present in an image, according to the formula:

$$PNSR = 10 * \log_{10}\left(\frac{MAX^2}{MSE}\right), \quad (6)$$

where MAX is the maximum pixel value (e.g. 255 for 8-bit images), and MSE is the mean square error.

MSE measures the standard deviation between the original and reconstructed images, according to the formula:

$$MSE = \frac{1}{N}\sum_{i=1}^{N}\left(I_{original}(i) - I_{predicted}(i)\right)^2, \quad (7)$$

where $I_{original}(i)$ and $I_{predicted}(i)$ are the pixel intensities of the original and reconstructed images, respectively, and N is the total number of pixels.

SSIM evaluates the structural similarity between two images, making it more sensitive to changes in texture and structure than PSNR or MSE, according to the formula:

$$SSIM = \frac{(2\mu_x\mu_y + C_1)(2\sigma_{xy} + C_2)}{(\mu_x^2+\mu_y^2 + C_1)(\sigma_x^2 + \sigma_y^2 + C_2)}, \quad (8)$$

where μ_x and μ_y are the mean values of the intensities of the two images, σ_x^2 and σ_y^2 are the variances, and σ_{xy} is the covariance.

ERGAS estimates the global image restoration error according to the formula:

$$ERGAS = 100 * \frac{h}{l}\sqrt{\frac{1}{N}\sum_{i=1}^{N}\left(\frac{RMSE(b_i)}{\mu(b_i)}\right)^2}, \quad (9)$$

where h is image resolution, l is scale, RMSE(bi) is root mean square error for each channel, a $\mu(b_i)$ average value of channel intensity.

UQI measures the image quality by considering the brightness, contrast and structural similarity between the original and predicted images, according to the formula:

$$UQI = \frac{4 * \bar{x} * \bar{y} * \sigma_{xy}}{(\bar{x}^2 + \bar{y}^2)(\sigma_x^2 + \sigma_y^2)}, \quad (10)$$

where $\bar{x}$ and $\bar{y}$ are the mean values, σ_x^2 and σ_y^2 is the variance, σ_{xy} is the covariance between the original and predicted images.

These metrics characterize different aspects of image quality, and their values will vary depending on the level of noise in the image.

To assess the noise level in images, a complex method is proposed based on the analysis of several quality metrics. Each of the metrics has established threshold values that are used to classify noise into weak, medium and strong levels. Tabl. I shows the thresholds for each metric.

After calculating the values of all the specified metrics for each image, they are compared with the set thresholds, which allows determining the noise level for each metric. Then, based on the calculation of the

number of metrics that fall into one category or another, the final classification of the noise level is carried out. If most metrics indicate a weak noise level, the image is classified as weakly noisy; if the medium level dominates, the image has a medium degree of noise; the classification for strong noise occurs in a similar manner.

The proposed method provides a comprehensive approach to assessing noise in images, taking into account various aspects of image quality allowing for a more accurate and objective analysis of the noise level based on multiple criteria.

TABLE I. CATEGORIES OF NOISE LEVELS BY DIFFERENT METRICS

Metrics	**Noise levels**		
	Weak noise	***Medium noise***	***Strong noise***
PSNR	PSNR ≥ 32	20 ≤ PSNR < 32	PSNR < 20
MSE	MSE < 50	50 ≤ MSE < 120	MSE ≥ 120
SSIM	SSIM ≥ 0.7	0.4 ≤ SSIM < 0.7	SSIM < 0.4
ERGAS	ERGAS < 2	2 ≤ ERGAS < 5	ERGAS ≥ 5
UQI	UQI ≥ 0.98	0.94 ≤ UQI <0.98	UQI < 0.94

III. RESULTS

This section presents the results of using an autoencoder to remove speckle noise from an ultrasound image.

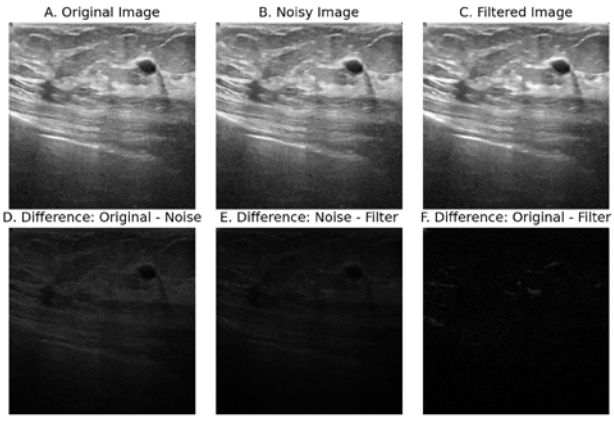

Fig. 3. Visual comparison of speckle noise removal in ultrasound images

Fig. 3 shows the original image (A), the noisy image (B), the result of autoencoder processing (C), and difference maps showing the changes between the images (D–F). Image (D. Original – Noise) visualizes the distribution of the added noise. The highest intensity is observed in areas with high texture activity, which corresponds to the nature of speckle noise [14, 15]. Image (E. Noise-Filter) displays the components removed by the autoencoder. The predominance of noise patterns confirms the effectiveness of the model. Image (F. Original-Filter) reveals minimal differences, which confirms the preservation of diagnostically significant information.

Comparative analysis of image quality metrics before and after noise reduction

Tabl. II shows a comparative analysis of the image quality before and after denoising. The "Predicted" column presents the metric values for the images after processing by the autoencoder, and the "Noisy" column presents the metrics for the original noisy images. The classification data reflects the degree of noise: Low, Medium, and High noise levels. High PSNR and low MSE in the "Predicted" column indicate successful image restoration, while a significant deterioration in the "Noisy" column confirms the presence of strong noise in the original data.

TABLE II. COMPARATIVE ANALYSIS OF IMAGE QUALITY METRICS BEFORE AND AFTER NOISE REDUCTION

Metrics	**Metrics and classification results**			
	Predicted	***Noisy***	***Classification (Predicted)***	***Classification (Noisy)***
PSNR	34.618	26.542	Низкий	Средний
MSE	22.450	144.153	Низкий	Высокий
SSIM	0.910	0.560	Низкий	Средний
UQI	0.998	0.994	Низкий	Низкий
ERGAS	1.083	2.744	Низкий	Средний

IV. CONCLUSIONS

Based on the results of testing the proposed noise reduction system on ultrasound images, it can be concluded that the system of algorithms using a convolutional autoencoder is applicable for removing speckle noise from ultrasound images. For testing, 20 % of the images from the original dataset were used. The average processing time per image was 63 milliseconds. The experiments were conducted on a personal computer with the following specifications: Intel Core i9-9920X, 64 GB RAM, 2× NVIDIA Quadro RTX 6000 GPUs, 3×4 TB SATA HDDs, and a 1 TB SSD.

The proposed method provides a comprehensive approach to assessing noise in images, taking into account various aspects of image quality, which allows for a more accurate and objective analysis of the noise level based on multiple criteria.

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Theoretical Study and Experimental Verification of Recognition Algorithms Based on The Measure of Precedence

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Abstract. **This study investigates metric algorithms based on the measure of precedence. The main purpose is to implement these algorithms and to compare their performance to other classification algorithms. As a result of this work, three classification problems were solved using different algorithms. Accuracy and time efficiency of the applied algorithms were compared. To automate the process of testing, a project of the corresponding system is proposed.**

Keywords: **measure of precedence, comparison function, decision rule, classification, one-hot encoding, automated testing**

I. Introduction

The problem of object recognition is highly relevant nowadays. And there is a range of algorithms based on measures of similarity, precedence, and resemblance which can help to solve it. This study will examine in detail algorithms based on the measure of precedence, which relies on analyzing the previous examples (precedents) to make decisions in new situations. Additionally, theoretical aspects of this measure will be considered, and experimental studies will be conducted to evaluate effectiveness of algorithms based on it.

It is important to note that algorithms based on the measure of precedence can only operate with data represented in binary form (all object features must take on values of either 0 or 1). However, using different encoding methods, any feature can be represented as several features with values of 0 or 1. Therefore, the class of problems solvable by these algorithms remains quite broad.

To apply recognition algorithms to practical tasks, experimental verification of their functionality and determination of their scope of application are required. Hence, the problem of developing the corresponding system capable of conducting comprehensive experiments is of undeniable interest, both from a theoretical and practical standpoint. The concept of building such a system will also be proposed in this work.

II. General algorithm

The object recognition problem is stated as follows:

Suppose we have a set of objects X, divided into subsets (classes) $X_1, \dots, X_l$ ($l \in \mathbb{N}$). The classes do not overlap, meaning $X_i \cap X_j = \emptyset \ \forall i \neq j \ (i, j \in \{1, \dots, l\})$. We choose a sample $X^0 \subset X$, satisfying $X^0 \bigcap X_i \neq \neq \emptyset \ (\forall i \in \{1, \dots, l\})$. Additionally, for every object $x \in X^0$ information about its membership in classes $X_1, \dots, X_l$ is known. This information is represented as an informational vector $P(x) = (P_1(x), \dots, P_l(x))$, where the components are determined as:

$$P_i(x) = \begin{cases} 1, & if\ x \in X_i \\ 0, & otherwise \end{cases}.$$

There is a general algorithm for solving this problem, based on the measure of precedence [5, p. 286]. It includes the following steps.

Step 0. Split sample X^0. This step can be repeated a certain number of times. Each time, sample X^0 is divided into two parts X^0_{train} and X^0_{test} referred to as the training and testing samples, respectively;

Step 1. Determine the pairwise comparison function for objects in X, whose general view is

$$s: X \times X \to \mathbb{R}\ . \qquad (1)$$

Each object $x \in X$ is compared to objects from training sample X^0_{train}. As a result, object x can be associated with vector $(s(x, x_1), \dots, s(x, x_m))$ where the first m_1 components are the results of comparisons of x with objects from $X^0_{1(train)}$, the next m_2 components correspond to comparisons with objects from $X^0_{2(train)}$ and so on;

Step 2. Determine the comparison function between objects from set X and objects from training set $X^0_{i\ (train)}$, whose general view is

$$f_i: \mathbb{R}^m \to \mathbb{R},\ i \in \{1, \dots, l\}\ . \qquad (2)$$

Using these functions, each vector $(s(x,x_1),\dots, s(x,x_m)) \in \mathbb{R}^m$ can be mapped to vector $(f_1(x),\dots,f_l(x)) \in \mathbb{R}^l$.

Step 3. Determine decision rule P^A, whose general view is

$$P^A: \mathbb{R}^l \to \mathbb{B}_2^l,\ \mathbb{B}_2 = \{0,1\}. \quad (3)$$

Vector $P^A(x) = (P_1^A(x),\dots,P_l^A(x))$ is typically referred to as the classification vector, as its values are interpreted as follows: object $x \in X$ is classified (or not) by algorithm A into class X_i, if $P_i^A(x) = 1\ (=0)$.

Therefore, to construct a specific algorithm, it is necessary to select functions (1) and (2), as well as decision rule (3).

To determine functions required for the algorithm, it is necessary to calculate the algorithm parameters [5, p. 304].

For all classes $i \in \{1,\dots,l\}$ and all features $j \in \{1,\dots,n\}$ calculate

$$b_{ij} = (m_i)^{-1}\left(\sum_{x_t \in X_i^{0,train}} x_{tj}\right),$$
$$b_j = (l)^{-1}\left(\sum_{i=1}^{l} b_{ij}\right), \quad (4)$$
$$a_{ij} = \left|b_{ij} - b_j\right|,$$

where x_{tj} is the value of feature j in vector $x_t \in X_{i\,(train)}^0$ $(t \in \{1,\dots,m_i\})$.

Using parameters (4), functions (1) – (3) can be determined as it is described below.

A. Algorithm 1 (A_1)

Assuming that x_1 is an arbitrary object from X, $x_2 \in X_{i\,(train)}^0$ and for all such x_2 function (1) can be calculated as follows

$$s_1(x_1,x_2) = \left(\sum_{j=1}^{n} a_{ij}\right)^{-1} \times \left(\sum_{j=1}^{n} (-1)^u \times a_{ij}\right),$$

where

$$u = \begin{cases} 1, if\ x_{1j} \neq x_{2j} \\ 2, otherwise \end{cases}.$$

For each $i \in \{1,\dots,l\}$, function (2) is determined as follows

$$f_i(x) = \max_{x_t \in X_{i\,(train)}^0} \{s_1(x,x_t)\}$$

and decision rule (3) is chosen based on the maximum distance to class evaluation

$$P_i^A(x) = \begin{cases} 1, if\ f_i(x) = \max\limits_{i\in\{1,\dots,l\}} \{f_1(x),\dots,f_l(x)\} \\ 0, \qquad otherwise \end{cases}.$$

B. Algorithm 2 (A_2)

The second way to determine functions (1) – (3) is to invert corresponding functions described in algorithm A_1. Thus, the following formulas are obtained

$$s_2(x_1,x_2) = 1 - s_1(x_1,x_2),$$
$$f_i(x) = \min_{x_j \in X_{i\,(train)}^0} s_2(x,x_j),$$
$$P_i^A(x) = \begin{cases} 1, if\ f_i(x) = \min\limits_{i\in\{1,\dots,l\}} \{f_1(x),\dots,f_l(x)\} \\ 0, \qquad otherwise \end{cases},$$

where $s_1(x_1,x_2)$ is a pairwise comparison function used in algorithm A_1.

C. Algorithm 3 (A_3)

In the third algorithm, function (1) is determined using the diameter of the set. For each subset $X_i^0 = X^0 \cap X_i$ $(|X_i^0| = m_i)$, using function $s_2(x_1,x_2)$ selected during the construction of algorithm A_2 the diameter of set X_i^0 is calculated using the following formula

$$d_i = \max_{(x_u,x_v) \in X_i^0 \times X_i^0} s_2(x_u,x_v).$$

As a result, set $(d_1, d_2, \dots, d_l)$ is obtained, for which calculate

$$d = max(d_1, d_2, \dots, d_l).$$

Now, using diameter d, function (1) can be determined as

$$s_3(x_1,x_2) = max\{0, 1 - \tfrac{s_2(x_1,x_2)}{d}\}.$$

Functions (2) and (3) are determined in a similar way as in algorithm A_1

$$f_i(x) = \max_{x_j \in X_{i\,(train)}^0} s(x,x_j),$$

$$P_i^A(x) = \begin{cases} 1, if\ f_i(x) = \max\limits_{i\in\{1,\dots,l\}} \{f_1(x),\dots,f_l(x)\} \\ 0, \qquad otherwise \end{cases}.$$

III. VARIABLES ENCODING

Algorithms described above can only operate with data represented in binary form (all object features must take on values of either 0 or 1). However, using different encoding methods, any variable can be represented as several variables with values of 0 or 1.

Applying one or another encoding method depends on a type of variable. To encode a categorical variable the one-hot encoding method can be used. As for quantitative variables, the binary encoding method can be used.

One-hot encoding is a method for converting categorical variables into a binary format [4]. It creates new columns for each category where 1 means that the category is present and 0 means that it is not present. The primary purpose of one-hot encoding is to ensure that categorical data can be effectively used in machine learning models.

There are 2 main reasons for using this method.

Firstly, one-hot encoding eliminates ordinality. Many categorical variables have no inherent order (e.g.,

"Male" and "Female"). If we were to assign numerical values (e.g., Male = 0, Female = 1) the model might mistakenly interpret this as a ranking and lead to biased predictions. One-hot encoding eliminates this risk by treating each category independently.

Secondly, it improves model performance by providing a more detailed representation of categorical variables. It allows models to capture complex relationships within the data that might be missed if categorical variables were treated as single entities.

To encode a quantitative variable, the binary encoding method can be used. To encode an integer variable, represent it in binary form. For each bit of this form, create a new variable. Assigning every created variable a value of the corresponding bit will perform binary encoding.

To encode a floating-point variable, multiply it by 10 to the power of the number of decimal places. This will convert the floating-point number into an integer while preserving its scale. Next, encode this new integer variable as described above.

Unlike the one-hot encoding method, binary encoding preserves ordinality and scale. For example, value 186 will still be treated greater than 19, which is essential for quantitative variables.

IV. Experiments and results

A. Datasets

To perform experimental testing of the algorithms described, several datasets with different features were chosen.

The employee dataset [1] contains information about employees of an unknown company. The information includes education, place of birth, age, gender and other variables. The goal of this dataset is to predict if an employee was fired or not, which means that this is a problem of binary classification. All the variables are categorical in the dataset. The dataset is also imbalanced, which means that the number of employees that were fired differs from the number of employees that were not fired.

The heart disease prediction dataset [2] contains medical information about some patients. The goal is to predict if they have any heart disease or not, which means that this is a problem of binary classification. The variables are mostly quantitative in the dataset. The dataset is slightly imbalanced. There is a bit more patients with heart diseases than healthy ones.

The mobile price dataset [3] contains technical specifications of mobile phones produced in a company. The goal is to predict the price category of a phone. There are 4 possible categories: low cost, medium cost, high cost and very high cost. It means that this is a problem of multiclass classification. There are some quantitative and categorical variables in the dataset. The dataset is perfectly balanced. The number of mobile phones of every cost category is equal.

B. Experiments

The experiments were conducted on the Intel(R) Core(TM) i9-14900HX 2.20 GHz CPU. The results of the experiments are shown in Tabl. I – III. The best results for every dataset are highlighted in bold. Hyperparameters of the algorithms were chosen using the grid search method and can be seen in Tabl. IV.

TABLE I. Results of applying different machine learning algorithms to the employee dataset

Algorithm	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)	Fit time (s)	Evaluation time (s)
A_1	69.62	57.49	59.80	58.62	0.0002	5.3051
A_2	69.62	57.49	59.80	58.62	0.0002	5.5125
A_3	69.98	58.13	59.30	58.71	5.1424	5.4723
Logistic Regression	70.52	69.71	67.29	67.68	0.0052	0.0008
SVM	77.40	78.58	74.00	74.85	0.5556	0.1573
Decision Tree	**79.75**	**81.42**	**76.48**	**77.49**	0.0038	0.0010
Random Forest	77.58	79.84	73.70	74.61	0.0192	0.0021

TABLE II. Results of applying different machine learning algorithms to the heart disease prediction dataset

Algorithm	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)	Fit time (s)	Evaluation time (s)
A_1	59.00	62.30	67.86	64.96	0.0002	0.2006
A_2	59.00	62.30	67.86	64.96	0.0002	0.2337
A_3	59.00	62.30	67.86	64.96	0.2010	0.2338
Logistic Regression	73.00	72.13	72.28	72.20	0.0019	0.0006
SVM	**74.00**	73.19	73.50	73.32	0.0050	0.0010
Decision Tree	**74.00**	**75.15**	**75.73**	**73.96**	0.0017	0.0006
Random Forest	71.00	71.67	67.24	67.46	0.0180	0.0025

TABLE III. RESULTS OF APPLYING DIFFERENT MACHINE LEARNING ALGORITHMS TO THE MOBILE PRICE DATASET

Algorithm	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)	Fit time (s)	Evaluation time (s)
A_1	63.75	60.80	63.75	59.93	0.0003	3.8911
A_2	63.75	60.80	63.75	59.93	0.0004	3.7052
A_3	63.75	60.80	63.75	59.93	1.8284	3.9671
Logistic Regression	84.00	84.41	84.43	84.39	0.5888	0.0057
SVM	**88.00**	**88.39**	**88.27**	**88.31**	0.4701	0.0207
Decision Tree	80.00	80.08	80.92	80.05	0.0078	0.0012
Random Forest	77.25	77.40	78.00	77.38	0.0298	0.0128

TABLE IV. HYPERPARAMETERS CHOSEN USING THE GRID SEARCH METHOD

Algorithm	Employee dataset	Heart disease dataset	Mobile price dataset
SVM	*Kernel=RBF*	*Kernel=Linear*	*Kernel=Linear*
Decision Tree	*Max tree depth=8*	*Max tree depth=3*	*Max tree depth=5*
Random Forest	*Criterion=LogLoss* *Number of trees=13* *Max tree depth=8*	*Criterion=LogLoss* *Number of trees=18* *Max tree depth=5*	*Criterion=Entropy* *Number of trees=19* *Max tree depth=5*

C. Results

It is easy to see that the decision tree algorithm was the best at solving 2 out of 3 problems. This algorithm is not only the most accurate but the most time efficient too. However, the mobile price problem was better solved with the SVM algorithm, which means that this data is highly linearly separable.

Speaking about the metric algorithms, it can be easily seen that A_1 and A_2 performed the same. It could be foreseen because they do not differ greatly. As for A_3, its performance differs a bit for the employee dataset. But this accuracy raise is not significant relative to the time it spends to fit.

V. CONCLUSION AND FURTHER RESEARCH

In conclusion, it should be said that at this stage of the research the metric algorithms do not perform well relative to other machine learning algorithms. More experiments with other different combinations of comparison functions and decision rules should be conducted. It can increase accuracy of the algorithms for a certain set of problems.

To conduct these experiments, it will be efficient to implement an automated testing system. This system must meet several requirements. Firstly, it needs to work with any tabular data. Therefore, it needs to automatically adapt to different data sizes and perform exploratory data analysis, at least the simplest steps: remove duplicates, handle missed data, detect possible outliers and etc. Secondly, the system needs to automatically encode all the non-binary variables. Otherwise, metric algorithms would not be able to work with these data. Thirdly, this software needs to allow its user to choose a set of algorithms he wants to test. Ideally, it should support metric algorithms, classic machine learning algorithms and neural network models made in Keras or PyTorch Python libraries as these libraries are the most popular. Finally, after the software completed evaluation, it needs to create a tabular report, showing algorithms performance, highlight and save best models. From this report the user will understand what algorithm is the best at solving the particular problem.

The system described above will make algorithm testing very easy. It can significantly lower requirements for machine learning engineers as they will not need to learn any programming language to solve object recognition problems. In the future, it is planned to implement such a system. Of course, similar software can be developed to solve other machine learning problems like regression, clusterization and etc.

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Comparative Evaluation of the Performance of Scoring Functions in Docking-Based Virtual Screening and Drug Design

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***Abstract*. In this study, we evaluated the commonly used virtual screening pipeline applying a customized CASF-2016 benchmark to assess the impact of different scoring functions (SFs) on the prediction accuracy of binding affinity between ligands and protein targets. To this end, traditional SFs AutoDock Vina, NNScore2, and RF-Score-4 were compared with the five new scoring tools CENsible, HGScore, OnionNet-2, PIGNet2, and PLANET via two scenarios. In the first scenario applied to the crystallographic ligand poses, SFs HGScore and OnionNet-2 showed strong correlations. In the second scenario, which mimicked real screening conditions with the docked ligand poses and RDKit-generated conformers, NNScore2, CENsible, and PIGNet2 demonstrated significant accuracy drop, while OnionNet-2 and PLANET maintained the robust results. These findings highlight the promise of the use of OnionNet-2 and PLANET for reliable docking-based virtual screening, with HGScore and RF-Score-4 also showing competitive potential pending further evaluation.**

***Keywords:* scoring function, CASF-2016, docking-based virtual screening, protein-ligand interactions, binding affinity prediction, machine learning, drug design**

I. INTRODUCTION

Structure-based drug discovery methods, such as molecular docking and virtual screening, have become invaluable tools in developing novel drugs. One of the critical components of successful docking programs is the assessment of binding affinity between ligands and protein targets. Therefore, a lot of attention is currently devoted to the analysis and validation of the accuracy of current docking scoring functions (SFs). In recent years, many new SFs have been proposed based on the deep learning models offering alternatives to using explicit empirical or mathematical functions for scoring ligand-protein complexes. In this regard, the goal of this study was to provide a practical comparison of different state-of-the-art scoring tools using a customized CASF-2016 benchmark.

The traditional approach to compare SFs evaluating the crystallographic poses gives a general idea of their accuracy. However, there are several obstacles that prevent us from assessing the accuracy of these SFs in the context of the docking-based virtual screening problems:

1) The first and most obvious point is that crystal structures are not evaluated in molecular docking. Instead, the docked ligand-protein complexes are assessed.

2) In molecular docking, protein structures do not have a ligand-adapted binding site, as observed in crystal structures.

3) In molecular docking, ligand structures are not X-ray ones adapted to the protein crystal structures. Instead, they are generated using cheminformatics packages, such as RDKit (https://www.rdkit.org).

To avoid these obstacles and determine the accuracy of the SFs under conditions as close as possible to the realities of docking-based virtual screening, a customized CASF-2016 benchmark comparison scenario was developed.

II. MATERIALS AND METHODS

A. Scoring Functions

1) Traditional tools

AutoDock Vina uses an empirical SF that sums weighted Gaussian steric interactions, repulsion,

hydrophobic effects and hydrogen-bonding to estimate binding free energy. Its smooth, differentiable form enables multithreaded gradient optimization for fast, accurate docking and widespread use in drug discovery [1].

NNScore2 uses an ensemble of neural networks to regress continuous binding affinity (pKd) for protein–ligand complexes. It extracts interaction features – like close-contact counts and electrostatics – from docked poses and outputs a single affinity score. This regression-based approach improves pose ranking and virtual screening performance over its classification-based predecessor [2].

RF-Score-v4 (referred to as RF::VinaElem in the original publication) uses a random forest trained on element-pair count features from docked complexes to predict binding affinities, capturing nonlinear interaction patterns [3]. This gives more accurate ranking and scoring than traditional empirical functions, boosting virtual screening and structure-based drug design [3].

2) Novel tools

CENsible is a novel SF for predicting protein–ligand binding affinities that leverages Context Explanation Networks to offer interpretable insights. Rather than providing just a binding score, it also highlights which molecular interactions contribute to the affinity prediction. By integrating structural and energetic features from protein–ligand complexes, CENsible not only ranks binding poses effectively but also helps users understand the key determinants of binding, making it especially useful for structure-based drug design [4].

HGScore also presents a new SF that uses a heterogeneous graph convolutional neural network to predict protein–ligand binding affinities. In HGScore, both the protein and the ligand are represented as separate graphs, and their interactions are captured by distinguishing intra- and inter-molecular edges. The model processes these heterogeneous graphs through dedicated graph convolutional layers tailored for each edge type to produce atomic embeddings, which are then aggregated into molecular fingerprints. Finally, the concatenated fingerprints are fed into a multi-layer perceptron to generate an affinity score, showing competitive performance on standard benchmarks compared to classical and other AI-based scoring methods [5].

OnionNet-2 is a 2D convolutional neural network–based SF designed to predict protein–ligand binding affinities (ΔG) using residue–atom contacting shells as its key descriptor. In this model, the protein is represented at the residue level and the ligand at the atomic level, and their interactions are quantified by counting the number of specific residue–atom contacts within multiple concentric distance shells. These contact counts are arranged into a 2D matrix (akin to an image), which serves as the input to a CNN architecture consisting of several convolutional layers followed by fully connected layers. The simplicity and efficiency of OnionNet-2 allow it to achieve high predictive accuracy on benchmark datasets such as CASF-2016 and CASF-2013, outperforming several earlier machine learning–based SFs [6].

PIGNet2 is an advanced graph-neural-network-based SF designed to predict protein–ligand binding affinities with improved interpretability and accuracy. This SF is based on its predecessor by integrating physics-inspired features with data-driven learning, using graph representations to capture the complex interactions between protein and ligand atoms. By incorporating both structural and energetic information into its network architecture, PIGNet2 not only achieves competitive performance on benchmark datasets but also offers insights into which intermolecular interactions are most influential for binding. This makes it a promising tool for structure-based drug discovery and rational ligand design [7].

PLANET utilizes graph neural networks within a multi-task learning framework to predict protein–ligand binding affinities. In PLANET, both the protein and the ligand are represented as graphs, enabling the model to capture detailed atomic interactions and spatial relationships. Its multi-task design not only forecasts binding affinities but also learns auxiliary properties, which improves overall predictive performance and interpretability. By integrating physics-inspired descriptors with advanced deep learning techniques, PLANET has demonstrated high accuracy on benchmark datasets, making it a promising tool for structure-based drug discovery [8].

B. Customized CASF-2016 benchmark

The CASF-2016 benchmark is a well-established dataset for evaluating the performance of SFs in structure-based drug design and discovery [9]. It comprises a carefully curated core set of high-quality protein–ligand complexes along with their experimentally determined binding affinities. Researchers use CASF-2016 to assess various aspects of SFs, including scoring power (how well SF can predict binding affinities), ranking power (the ability to correctly rank ligands for the same target), docking power (the capacity to identify the correct binding pose), and screening power (how effectively SF can distinguish true binders from decoys). By providing standardized metrics and a diverse set of complexes, CASF-2016 serves as an essential tool for benchmarking and comparing the accuracy and

reliability of different computational scoring methods in virtual screening.

The CASF-2016 core set includes 57 distinct protein targets, each represented by 5 protein–ligand crystal structures, resulting in a total of 285 protein–ligand complexes, with the protein provided in .pdb format and the ligand in .sdf and .mol2 formats. For each protein–ligand complex, CASF-2016 provides binding data in the form of $logK_a$ (K_a is an association constant), which corresponds to *-logKd* (if dissociation constant data are available) or *-logKi* (if inhibition constant data are provided). The *logKa* values in the dataset range from 2 to 12 corresponding to concentrations from 10 mM to 1 pM, with a mean value of 6.5 (or 350 nM) and a standard deviation of 2.2.

The choice of CASF-2016 as a benchmark is due to this benchmark is one of the most popular for comparing SFs, which in turn encourages developers of scoring tools to exclude this benchmark from the training set.

C. Comparison Scenarios

1) The scoring functions evaluate the crystallographic poses from CASF-2016

The protein in the .pdbqt format was prepared using the MGLTools 1.5.6 software package (https://ccsb.scripps.edu/mgltools/). Due to the lack of support for Zn, Mg, Ca, and Na ions in the prepare_receptor4.py script provided by MGLTools for protein preparation, seven complexes (PDB IDs: 5c2h, 3twp, 1z9g, 1oyt, 3utu, 3ryj, 1lpg) were excluded from the test dataset. The .mol2 format was chosen as the initial ligand format, which was then converted to .sdf using PyMOL, followed by conversion from .sdf to .pdb using the RDKit library (https://www.rdkit.org) in Python, and finally from .pdb to .pdbqt using the MGLTools 1.5.6 software package. Because of reading errors in three ligand .sdf files, three complexes were excluded from the dataset (pdb id: 3arp, 3ge7, 4dli). Due to the high sensitivity to the .sdf format data leading to the frequent errors during scoring, the SF PLANET was not included in the first comparison.

2) The scoring functions evaluate the docked poses

The first point that needed to be addressed was that the protein binding site is adapted to its ligand, which is not the case in the realities of docking-based virtual screening. Since CASF-2016 provides 5 different protein-ligand structures for each target, it was decided to "shuffle" the proteins for each target class. This means that for each ligand, docking was performed not into its own protein from the complex, but into a protein from another complex with a different ligand. To achieve this, each protein with a given PDB ID was randomly paired with another protein from the same target class but with a different PDB ID. Then, this second protein was aligned to the first protein using PyMol align (protein chains that form contacts with the ligand at a distance of 10 Å were selected as the target for alignment). The alignment was considered successful if the RMSD value between the structures was < 1 Å. If the RMSD value was $\geqslant$ 1 Å, an attempt of alignment was made again using PyMol super and cealign. As a result, 279 out of 285 proteins were aligned. Visual analysis of the six aligned structures with the RMSD value >1 Å revealed that the proteins exhibit moderate differences in the conformation of the entire protein.

Secondly, there was a need to generate three-dimensional (3D) representations for the ligands using RDKit. However, the ligand structures in the .sdf format provided by CASF-2016 were unsuitable for this purpose due to inaccuracies in bond multiplicities, which can be a critical factor when generating 3D representations. To solve this problem, the ligand structures were identified in the .pdb files of their complexes obtained from the RCSB PDB, and then they were downloaded in the .sdf format from the RCSB PDB, which provides high-quality .sdf structures for small molecules. The ligand structures from complexes 5tmn, 4tmn, and 3bv9 could not be identified automatically, as the ligands shifted positions during the preparation of the complexes by the CASF-2016 authors. The ligand structures for 3uri and 1a30 could not be obtained because they are peptides, and the RCSB PDB does not provide the .sdf files for peptides. The generation of a new 3D conformer using RDKit followed the standard protocol: first, a conformer was generated using the ETKDGv3 method [10], then it was optimized in the MMFF force field [11] until convergence to a local energy minimum. If unsuccessful, an attempt was made to generate a conformer using the ETKDGv3 method with random coordinates. For the ligand structures from the 2yge and 2x00 complexes, it was not possible to generate a 3D conformer due to changing their stereochemistry during the generation process.

To complete the final scenario, it was necessary to dock the generated 3D conformers into an aligned protein from another complex. For creating a grid box for docking, the X-ray ligand structure was used as a reference by taking its maximum and minimum x, y, and z coordinates with a 6 Å margin. The aligned protein and the generated 3D conformer of the ligand were converted into PDBQT format using MGLTools 1.5.6 (the protein structures 5c2h, 1z9g, and 3ryj which we intended to use for evaluating the affinity of ligands from the structures 5c28, 4tmn, and 2weg

could not be converted for the reasons described above). Molecular docking of the prepared structures was performed using AutoDock Vina 1.2.5 with the exhaustiveness parameter set to 100. The docked ligand was converted into the .sdf and .pdb formats using RDKit, and .sdf was then transformed into .mol2 by PyMol.

III. Results

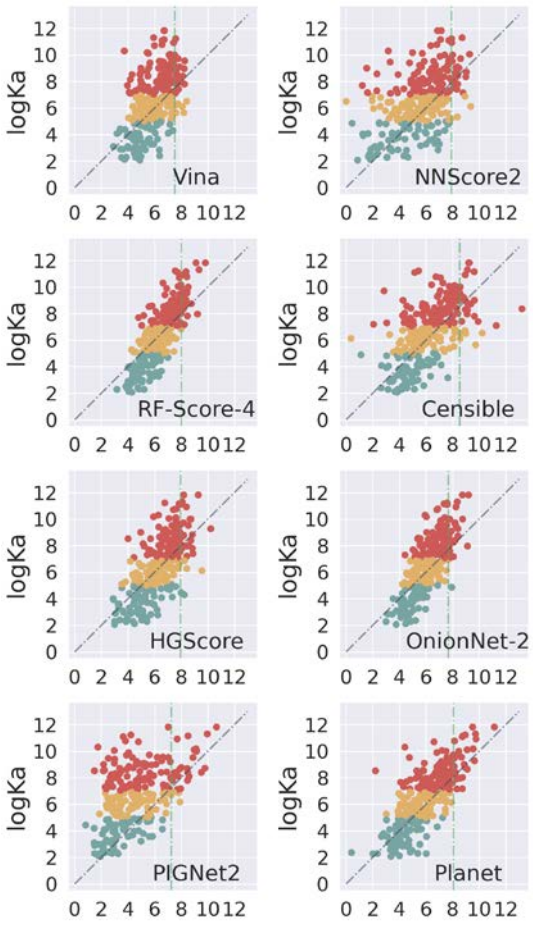
Table I presents the Pearson correlation coefficient and RMSE (Root Mean Squared Error) values for the compared SFs calculated between the experimental logKa values and their predicted values for the first comparison scenario. The SFs RF-Score-4, OnionNet-2, and HGScore exhibit relatively high correlation values (>0.8) and relatively low RMSE values (<1.5). However, at the time of the RF-Score-4's release, the CASF-2016 benchmark did not yet exist, so a custom dataset was used for testing. As a result, 241 out of the 275 complexes used in the comparison were included in the RF-Score-4 training set, which explains its high performance. When these complexes are excluded from the evaluation, the Pearson correlation coefficient drops to 0.75, and the RMSE value increases to 1.64 (sample size n = 34). It is observed that Vina, RF-Score-4, HGScore, and OnionNet-2 tend to make conservative predictions, overestimating logKa for the low activity compounds and underestimating logKa for the highly active ones.

In total, 270 out of 285 complexes were evaluated for the second scenario. The SFs NNScore2, CENsible, and PIGNet2 showed a significant drop in prediction accuracy of binding affinity and demonstrated a moderate correlation with the experimental logKa data (Table). AutoDock Vina exhibited a moderate decline in prediction accuracy; however, given for the low predictive ability in the first comparison scenario, these general indicators place this SF on par with the three SFs mentioned above. OnionNet-2 showed only a slight decline in prediction accuracy while maintaining a high correlation. PLANET indicated high predictive power, on par with OnionNet-2. HGScore revealed a moderate decrease in prediction accuracy and had comparable performance to PLANET and OnionNet-2. Meanwhile, RF-Score-4 demonstrated the best accuracy (r = 0.8 and RMSE = 1.38), which can still be attributed to the presence of test samples in the training dataset. Excluding these samples from the test set leads to a drop in the RF-Score-4 accuracy to r = 0.79 and RMSE = 1.73, which remains comparable to the best SFs; however, the sample size in this case (n = 34) is insufficient to reliably assess its true accuracy.

When inactive compounds vastly outnumber active ones, it is crucial that the SF is robust to outliers that could result in a large number of false-positive hits at the top. From the parity plot (Figure), it is evident that the SF Planet effectively separates active compounds from inactive ones. At the same time, OnionNet-2 and PIGNet2 also do it well.

Pearson correlation coefficients and RMSE values between the predicted scores of the SFs and experimental $\log K_A$ values

Scoring function	Crystal poses		Docking poses	
	Pearson, r	**RMSE**	**Pearson, r**	**RMSE**
AutoDock Vina	0.61	1.86	0.50	1.97
NNScore2	0.68	1.65	0.50	2.25
RF-Score-4	*0.89 (~0.75)*	*1.15 (~1.64)*	*0.83 (~0.79)*	*1.33 (~1.73)*
CENsible	0.71	1.54	0.56	1.91
HGScore	**0.81**	**1.31**	0.70	1.57
OnionNet-2	**0.83**	**1.27**	**0.77**	**1.48**
PIGNet2	0.75	1.68	0.49	2.87
PLANET	-	-	**0.76**	**1.51**



Parity plot of predicted logKa values (x-axis) vs. experimental logKa values (y-axis) for the scoring functions (docked structures). Points with low experimental activity (logKa ⩽ 5, not less than 10 μM) are highlighted in turquoise, those with moderate activity (5 < logKa ⩽ 7, less than 10 μM and not less than 0.1 μM) in orange, and those with high activity (logKa > 7, less than 100 nM) in red. For each SF, a dashed vertical line is drawn representing the 10th percentile of the predicted values, which corresponds to the predicted value of the 27th best compound

IV. Conclusion

Thus, comparative analysis of the commonly used SFs AutoDock Vina, NNScore2, and RF-Score-4 with the five new scoring tools CENsible, HGScore, OnionNet-2, PIGNet2, and PLANET, carried out with a customized CASF-2016 benchmark, showed that the SFs OnionNet-2 and PLANET demonstrate the high prediction accuracy under docking-based virtual screening conditions and may be promising for discovering new active compounds. At the same time, HGScore and RF-Score-4 operate similarly and can also be used in docking-based virtual screening; however, a new testing dataset is needed to more accurately assess the accuracy of RF-Score-4.

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MIVAR Decision-Making System for Cargo Distribution and Transportation by Groups of Warehouse Robots

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Abstract. **In this article we propose an intelligent mivar decision-making and information processing system (DMIPS) designed for the distribution and transportation of cargo by groups of warehouse robots. This mivar DMIPS integrates three distinct groups of warehouse robots: the Loader Robot, the Transporter Robot, and the Unloader Robot. The selection and determination of the state of each robot (Loader Robot, Transporter Robot, and Unloader Robot) are based on corresponding calculations performed using specially developed algorithms. The system of equations takes into account the robot's state, operational capability, ability to complete cargo transportation, cargo compatibility, and more. Additionally, the Manhattan distance is considered to determine the robot's ability to complete its task. The article provides a detailed description of the system of equations and the calculation algorithm, as well as a formalized description of the domain in which the mivar logical AI system operates. The logical schematic of the DMIPS system and the decision-making rules that aid in robot selection are also presented, making the system more efficient. Experimental results demonstrate that the system functions normally according to the predefined logic and objectives, accurately completing all distribution tasks while exhibiting good stability and reliability.**

Keywords: **mivar, mivar systems, logical AI, distribution system, robotics, group of warehouse robots, loader robot, transporter robot, unloader robot**

I. INTRODUCTION

According to Statista, the annual growth rate of the marketplace in Russia reached 37 %, with the total number of orders exceeding 7 billion. With the rapid growth of global logistics and supply chain demands, intelligent warehouse systems have become a key technology for improving efficiency and reducing costs [1]. Warehouse systems of Ozon, Amazon, and JD Logistics each have their unique features in terms of automation level, system planning efficiency, and energy consumption, but they also share common shortcomings. Ozon focuses on regional layout but has a low level of automation and heavily relies on manual labor [2]; Amazon, represented by Kiva robots, has achieved a high degree of automation but faces high energy consumption and system complexity [3]; JD Logistics, with its fully automated "Asia No. 1" warehouse and green energy integration, still encounters issues with high maintenance costs and energy consumption [4]. All three systems face bottlenecks in planning efficiency during peak periods and a high dependency on manual labor. Areas for improvement include enhancing energy efficiency, optimizing planning algorithms, reducing maintenance costs, and strengthening human-machine interaction.

In recent years, the integration of mivar technologies of logical artificial intelligence, centralized management systems, and robotics has provided new ideas and solutions for the development of intelligent warehouse systems [5]. For example, the MIPRA system, based on mivar technology, has demonstrated superior performance in robot action planning [6], particularly in solving STRIPS-type problems in dynamic environments, showcasing the effectiveness of mivar systems in real-world robotics applications. In warehouse environments, mivar technologies can optimize decision-making processes through logical rules and knowledge base models, such as using expert systems for diagnosing repair issues [7, 8] and making optimal decisions [9]; they can also be used for autonomous route planning [10] and obstacle avoidance by robots [11] in two-dimensional and three-dimensional logical spaces [12]. Combined with mivar technologies of logical AI [13], centralized management systems can more accurately allocate tasks, monitor equipment status, and coordinate the interaction of multiple robots. In large warehouse centers, centralized management systems can analyze

inventory data in real-time [14], dynamically adjust robot sorting tasks [15], thereby reducing waiting times and resource losses.

This article summarizes the current state of the application of these technologies in intelligent warehouse systems and proposes a mivar intelligent distribution decision-making and information processing system (DMIPS) for warehouse logistics, integrating the Loader Robot (LR), Transporter Robot (TR), and Unloader Robot (UR). This system utilizes mivar technologies of logical artificial intelligence, achieving dynamic optimization of task allocation and planning through real-time information processing within the system, thereby reducing transportation time and energy consumption, as well as exploring mechanisms for collaborative work among multiple robots to enhance overall system efficiency.

II. Proposed Approach

In this section we explain how the three robot combinations work and how the mivar system works.

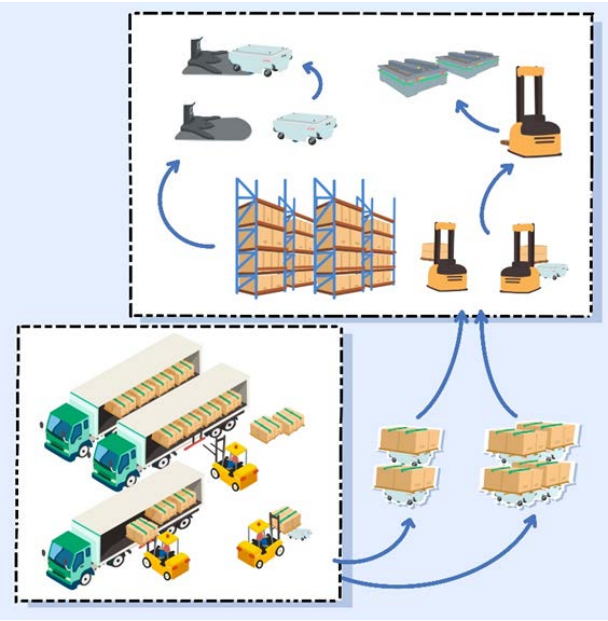

Fig. 1. Illustration of the Workflow of Warehouse Robots

Fig. 1 illustrates the workflow of warehouse robots: at the loading dock, cargo arrives, and a group of LRs operates; in the warehouse, a group of URs operates; and a group of TRs receives cargo with the help of LRs, transports the cargo to the warehouse, and stores it with the help of URs. The warehouse contains shelves and charging stations for TRs and URs.

Fig. 2 shows the working principle of the DMIPS system. Based on current parameters, the system determines the compatibility of robots with cargo and assigns cargo to the appropriate robots, issuing commands in the form of state variables

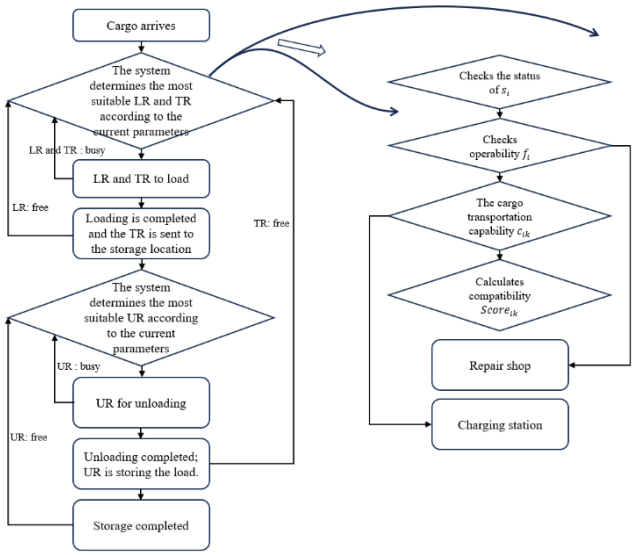

Fig. 2. Schematic Diagram of the DMIPS System

Fig. 2 shows the working principle of the DMIPS system. Based on current parameters, the system determines the compatibility of robots with cargo and assigns cargo to the appropriate robots, issuing commands in the form of state variables.

III. Mathematical Model

The mathematical model of DMIPS is defined. Since the intelligent mivar system manages three groups of robots considering the list of current cargo, the proposed mathematical model of DMIPS consists of four main components: the system of equations for the Transporter Robot, the system of equations for the Loader Robot, the system of equations for the Unloader Robot, and the system of command variables. Each subsystem is carefully designed to ensure seamless coordination and dynamic optimization of the entire warehouse workflow. Next, we will detail the mathematical formulations, algorithmic implementations, and experimental validations of this model.

The capacity of TR_i to carry a load k:

$$c_{ik}(t) = \begin{cases} 1, & if\ E_i(t) > \dfrac{D_{ik}}{200} + 20, \\ 0, & if\ TR_i\ needs\ to\ be\ charged. \end{cases} \quad (1)$$

Dynamic compatibility function of TR_i and load k:

$$Score_{ik}(t) = c_{ik}(t)\left(\frac{\alpha}{1+\sqrt{d_{ik}}} + \beta\frac{E_i(t)}{50}\right). \quad (2)$$

Decision Variable:

$$x_{ik}(t) = \begin{cases} 1, & if\ i^*, k^* = argmax_k Score_{ik}(t), \\ 0, & otherwise, \end{cases} \quad (3)$$

where $E_i \in [0,100]$– TR battery charge; $\alpha + \beta = 1$ – weights; d_{ik} – Manhattan distance TR_i to loading point; D_{ik} – the total Manhattan distance TR_i for cargo transportation.

The capacity of UR_p to carry a load k:

$$c_{pk}(t) = \begin{cases} 1, & if\ E_p(t) > \frac{D_{pk}}{100} + 20, \\ 0, & if\ UP_p\ needs\ to\ be\ charged. \end{cases} \quad (4)$$

Dynamic compatibility function of UR_p and load k:

$$Score_{pk}(t) = c_{pk}(t)\left(\frac{\alpha}{1+\sqrt{d_{pk}}} + \beta\frac{E_p(t)}{50}\right). \quad (5)$$

Decision Variable:

$$x_{pk}(t) = \begin{cases} 1, & if\ p^*, k^* = argmax_k Score_{pk}(t), \\ 0, & otherwise, \end{cases} \quad (6)$$

where $E_p \in [0,100]$– UR battery charge; $\alpha + \beta = 1$ – weights; d_{pk} – Manhattan distance UR_P to loading point; D_{pk} – the total Manhattan distance UR_P for cargo transportation.

Dynamic compatibility function of LR_p and load k:

$$Score_{jk}(t) = \frac{1}{1+\sqrt{d_{jk}}}. \quad (7)$$

Decision Variable:

$$x_{jk}(t) = \begin{cases} 1, & if\ j^*, k^* = argmax_k Score_{jk}(t), \\ 0, & otherwise, \end{cases} \quad (8)$$

where d_{pk} – Manhattan distance LR_i to loading point.

Part of the command variables:

$$s_{fixed\_i}(t) = \begin{cases} 1, & if\ cargo\ is\ fixed\ in\ RP, \\ 0, & otherwise, \end{cases} \quad (9)$$

$$s_{delivery\_i}(t) = \begin{cases} 1, & if\ cargo\ was\ delivered\ by\ RT, \\ 0, & otherwise, \end{cases} \quad (10)$$

$$s_{unload}(t) = \begin{cases} 1, & if\ unloading\ is\ completed, \\ 0, & otherwise. \end{cases} \quad (11)$$

IV. Experiments and Results

We input these parameters into our model in the KESMI system and obtained the results presented in Fig. 3 and 4.

We specifically set up different scenarios: a busy LR 2; a TR 1 with insufficient battery charge; and a broken UR 2 in need of repair. The results show that the system can not only select the most suitable robots from the robot groups based on the algorithm but also determine the operational capability and cargo transportation ability of the robots based on current parameters and inform the user through on-screen prompts.

Fig. 3. Results of Robot Selection and Cargo Transportation

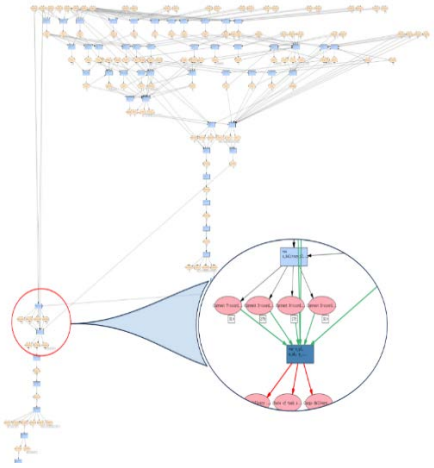

Fig. 4. Decision Graph

The scenario is described as follows:

1. Task Assignment: For each cargo item in sequence, the system performs calculations based on current parameters and assigns the most suitable Transporter Robot (TR) and Loader Robot (LR).

2. Robot Movement: Upon receiving the system's command, the TR and LR move to the loading location. Their status changes from "idle" to "busy."

3. Loading Process: When the TR and LR arrive at the loading location, the system issues a loading command. The LR loads the cargo onto the TR. Once the TR's securing device locks the cargo and the LR releases it, the TR sends feedback to the system: loading is complete. Subsequently, the LR's status changes from "busy" to "idle," and the TR proceeds to the storage location.

4. Storage Robot Assignment: As the TR heads to the storage location, the system immediately performs calculations and selects the most suitable Unloader Robot (UR). The UR is commanded to move to the storage location, and its status changes from "idle" to "busy."

5. Unloading Process: When both the TR and UR arrive at the storage location, the system issues an unloading command. The TR's securing device releases the cargo, and the UR secures and unloads it. The TR then sends feedback to the system: unloading is complete, and its status changes to "idle."

6. Storage Completion: The UR places the cargo in the designated location on the shelf. After completing the storage task, the UR sends feedback to the system: storage is complete, and its status changes to “idle.”

V. Discussion

This article demonstrates the effectiveness of the mivar-based decision-making system in optimizing warehouse operations through intelligent task allocation and real-time coordination among robots. By dynamically assigning tasks to the most suitable robots based on current parameters, the system minimizes delays and maximizes efficiency. The seamless transition between loading, transporting, and unloading processes, coupled with real-time status updates, ensures smooth workflow execution. Additionally, the system’s ability to handle feedback and adapt to changing conditions highlights its robustness and reliability. However, further testing in real-world environments with unpredictable variables, such as sudden cargo volume changes or robot malfunctions, is necessary to validate its scalability and adaptability. Future enhancements could include integrating machine learning algorithms to improve decision-making in complex scenarios.

VI. Conclusion

This paper proposes an intelligent system designed for a scenario where three groups of robots – Transporter Robots (TR), Loader Robots (LR), and Unloader Robots (UR) – collaborate to transport cargo from the loading area to the storage location. The mathematical model and detailed description of the mivar approach are presented, based on which the system was implemented in the KESMI environment and experiments were conducted. The experimental validation confirmed that the system operates in strict accordance with predefined logic and objectives. It demonstrated high accuracy in task allocation, as well as excellent stability and reliability during operation.

Thus, the effectiveness of integrating an expert system based on the mivar approach with a robot management system for solving dynamic cargo distribution tasks by warehouse robots has been justified. The synergy of mivar’s logical intelligence technology and robot management systems enable dynamic optimization of task distribution and planning through real-time information processing. This, in turn, contributes to reduced transportation time, lower energy consumption, and provides insights into mechanisms for coordinating the collaborative work of multiple robots to enhance overall system efficiency.

In the future, based on this work, more complex tasks can be addressed, such as multiple robots jointly transporting a single large cargo, a single robot transporting multiple small cargos simultaneously, or even developing a system for a group of hybrid robots.

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Genomic-Based Algorithms for Identification of Mycobacterium Tuberculosis and Nontuberculous Mycobacteria

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Abstract. **The effectiveness of treatment for tuberculosis and diseases caused by nontuberculous mycobacteria depends on the speed and accuracy of detecting the relevant bacteria. Traditional methods of identification based on phenotypic characteristics, such as morphology, growth rate, pigmentation, and optimal temperature conditions, are widely employed. However, these methods are labour-intensive, relatively slow, and may lead to delays and errors in therapeutic strategies. To overcome the limitations of established methods, molecular techniques for studying organisms are being developed, including DNA sequence analysis. In this study, genomes of Mycobacterium tuberculosis and three common pathogenic types of nontuberculous mycobacteria have been investigated. The Fisher's exact test and support vector machine method have been utilized to analyze the features of DNA sequences which represent *k*-mers, resulting in classification accuracies ranging from 0.98 to 1.00 for some of the features for testing data. Additionally, sequences of two specific genes were investigated, achieving a classification accuracy of 1.00 using the *k*-nearest neighbors method.**

Keywords: **Mycobacterium tuberculosis, nontuberculous mycobacteria, Fisher's exact test, SVM, MPB64 gene, nikA gene**

I. INTRODUCTION

The research is dedicated to detecting genomic features on which algorithms for identifying different species of organisms belonging to the genus Mycobacterium can be based. The genus Mycobacterium encompasses three groups of human pathogens: Mycobacterium tuberculosis (MTB), Mycobacterium leprae, and nontuberculous mycobacteria (NTM). Mycobacterium tuberculosis is responsible for a widespread infectious disease affecting humans and animals – tuberculosis – which is one of the infectious diseases with the highest mortality rates. According to the World Health Organization (WHO), approximately 1.5 million individuals die from this disease each year. However, tuberculosis is treatable and preventable. It is estimated that global efforts to combat tuberculosis have saved 79 million lives since the year 2000. The effectiveness of therapy relies on the speed and accuracy of detecting Mycobacterium tuberculosis in humans; therefore, methods based on genomic data analysis of mycobacteria can significantly improve treatment outcomes. Another group of mycobacteria – nontuberculous mycobacteria – also presents interest regarding the application of genomic data analysis methods. Nontuberculous species include Mycobacterium avium, Mycobacterium intracellulare, Mycobacterium abscessus, Mycobacterium kansasii, Mycobacterium chelonae, Mycobacterium ulcerans, among others. Similar to Mycobacterium tuberculosis, many nontuberculous species are pathogenic to humans. Research efforts are made by scientific community to address the identification of various species of nontuberculous mycobacteria based on genomic analysis [1, 2].

In addition to methods, based on whole-genome analysis, algorithms that rely solely on a small portion of the genome – such as a specific gene or insertion sequence – are of significant interest. Sequencing the complete genome is a laborious and resource-intensive task compared to obtaining the sequence of a specific gene. Consequently, there arises a need to identify genes that are significant for organism classification and to develop algorithms based on the analysis of DNA sequences of those genes. In the current study it has been shown that two genes – MPB64 and nikA – give promising results in the problem of mycobacteria discrimination.

The dataset for the study comprises 157 DNA sequences of mycobacteria, including genomes of Mycobacterium tuberculosis (49 samples) and three species of nontuberculous mycobacteria – Mycobacterium abscessus (45 samples), Mycobacterium avium (34 samples), and Mycobacterium intracellulare (29 samples).

II. K-MERS IN GENOMIC SEQUENCES

The features of DNA sequences examined in this study represent *k*-mers – ordered pairs of nucleotides

(A-A, A-C, A-G, A-T, C-A, etc.) such that the nucleotides forming the pair are separated by *k* nucleotides in the genomic sequence. The experiments were conducted for all values of *k* in the range of 0 to 10. The value of a feature for a DNA sequence is defined as the number of corresponding *k*-mers occurring in that sequence, normalized by the maximum possible value of that feature for the given sequence. We will use the notation XkY to represent a feature, where X and Y are nucleotide symbols (A, C, G, or T), and *k* is the distance between them in the sequence. In total, 4*11 * 4 = 176 features are under consideration. For the genomes included in the study, the values of all features lie within the range of 0.01 to 0.15.

A. Analysis of features using Fisher's exact test

The most promising features are those for which the samples are separable on the numerical line, i.e., those for which there exists a threshold value *t* of the given feature such that for all genomes of tuberculous mycobacteria, the value of the feature is less (or greater) than *t*, while for all genomes of nontuberculous mycobacteria, the value is greater (or less) than *t*. For our dataset, two such features were identified: C1A (Fig. 1) and G1T. For the remaining 174 features, the samples partially or completely overlap.

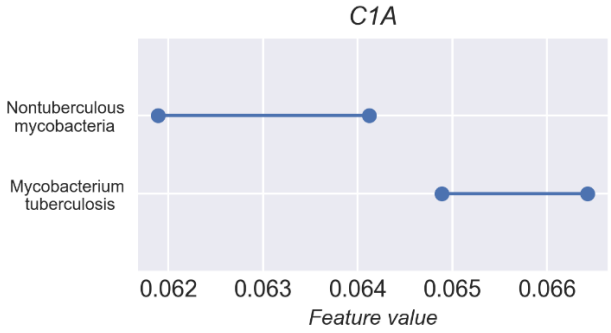

Fig. 1. A feature that separates the types of mycobacteria

Among the features by which the samples of tuberculous and nontuberculous mycobacteria overlap, those with a smaller length of the overlap interval are considered more promising. Based on this assumption, in addition to the separating features C1A and G1T, 28 non-separating features with the smallest overlap intervals were selected for further analysis.

TABLE I. CONTINGENCY TABLE STRUCTURE

	Mycobacterium tuberculosis	**Nontuberculous mycobacteria**
Feature is present	n_{00}	n_{01}
Feature is absent	n_{10}	n_{11}

To investigate the selected features, a two-tailed Fisher's exact test – a statistical significance test used in the analysis of contingency tables for small sample sizes – was applied. The Fisher's test operates with a contingency table constructed for a single feature, assessing the independence of its rows and columns. The structure of the contingency table for this case is presented in Tabl. I , where n_{ij} represents the number of sequences belonging to the corresponding group of mycobacteria that possess or do not possess the feature.

It remains to define the meaning of "feature is present" and "feature is absent" for our case. To do this, it is necessary to introduce a threshold value *t* for this feature and subsequently consider, that for a DNA sequence with a feature value less than *t*, this feature is absent, while for a sequence with a value greater than *t*, it is present. For features that are separable on the numerical line, the midpoint of the separating interval was taken for the value of *t*. For the other selected features, the midpoint of the interval on the numerical line where the samples overlap was taken the value of *t*.

The result of the test is represented by the *p*-value, which reflects the probability that there is no association between the values of the feature and the type of mycobacterium. The smaller the *p*-value, the more significant the feature is considered. In this study, *p*-value less than 5×10^{-5} was deemed sufficiently small. Among 176 features, 20 were identified for which the *p*-value does not exceed 5×10^{-5}, which provides grounds to consider these features significant in the problem of mycobacteria identification. The best five features along with corresponding threshold values *t*, and the *p*-values are presented in Tabl. II in ascending order of the latter.

TABLE II. BEST FEATURES ACCORDING TO FISHER'S TEST

Feature	**Value of threshold *t***	**Mycobacterium type which possesses the feature**	***p*-value**
C1A	0.0645031	Mycobacterium tuberculosis	$6.87 \cdot 10^{-42}$
G1T	0.0683023	Mycobacterium tuberculosis	$6.87 \cdot 10^{-42}$
T1G	0.0646523	Mycobacterium tuberculosis	$9.01 \cdot 10^{-37}$
A1C	0.0684262	Mycobacterium tuberculosis	$9.01 \cdot 10^{-37}$
G0T	0.0585834	Mycobacterium tuberculosis	$3.56 \cdot 10^{-29}$

Thus, through the analysis of contingency tables using Fisher's test, it was possible to identify 20 features for which the *p*-value does not exceed 5×10^{-5}, providing justification to consider these features significant in the problem of classifying mycobacteria.

B. Analysis of Features Using Support Vector Machine

The Support Vector Machine (SVM) method is a widely utilized algorithm for addressing classification

tasks. It involves constructing a hyperplane that optimally separates the objects in the dataset. The algorithm operates under the assumption that the greater the distance between the separating hyperplane and the objects of the distinct classes, the lower the average classification error of the classifier. The pure form of SVM performs well only on linearly separable samples. For linearly inseparable samples, a transition from the original feature space to a new space is achieved through a variety of functions called kernels. If the new feature space has sufficiently high dimensionality, then the dataset may become linearly separable within it. The most commonly used kernels include linear, polynomial, radial basis function, and sigmoid.

In this study, an implementation of the Support Vector Machine method without kernel application and with each of the types of kernels mentioned above was used. The SVM was applied to the same features of the form XkY as used in the Fisher's test – pairs of nucleotides separated by a distance k in the range of 0 to 10. The accuracy of the classifier's predictions was assessed using 3-fold cross-validation. Because it is not always possible to achieve high prediction accuracy when relying solely on a single feature of the objects, features can be combined into pairs, triplets, etc., allowing each object to be analyzed as a point in an n-dimensional space. The Support Vector Machine method is designed for high-dimensional spaces; therefore, it can be applied to the current problem by replacing individual features with pairs of features. From the 176 features discussed above, $C_{176}^{2} = 15400$ pairs of the form $X_1k_1Y_1$ - $X_2k_2Y_2$ were formed. The SVM method was applied to each of these pairs of features, both without a kernel and with the four types of kernels mentioned above. In all cases, it was possible to identify between 2000 and 14000 pairs of features on which classification accuracy reached 0.98, with approximately half of them achieving a classification accuracy of 1.00 on our dataset. Fig. 2 illustrates as an example the feature space for the pair of *k*-mers A8G – C1T and the positioning of sample instances within it.

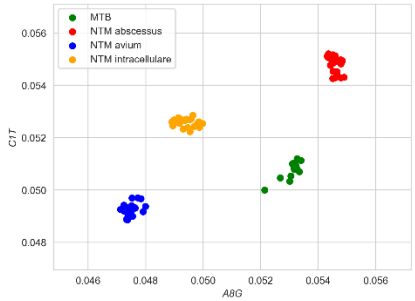

Fig. 2. An example of feature space and the position of dataset elements within it

From Fig. 2, it is evident that samples from different species of mycobacteria are linearly separable based on these features, which explains the high classification accuracy achieved using the Support Vector Machine method.

III. Analysis of Specific Genes

For the identification of features in genomic data, both entire genome and specific regions – such as genes and insertion sequences – can be analyzed. Although the genome appears homogeneous in structure, different regions exert varying influences on the phenotypic traits of the organism. The objective is to identify such regions (often they represent specific genes), locate them within the DNA sequence, and conduct a search for significant features in these areas, disregarding the remaining parts of the genome.

In this study we investigated the DNA regions of mycobacteria corresponding to the MPB64 gene (also known as MPT64) and the nikA gene. The MPB64 gene plays a role in discriminating tuberculous and nontuberculous mycobacteria in "Anyplex MTB/NTM Real-time Detection" test system developed by Seegene (Korea) [3, 4]. It encodes an immunogenic protein of mycobacteria. The nikA gene encodes a substrate-binding protein and is also referenced in studies addressing the problem of mycobacteria identification [1]. The lengths of these two genes range from 660 to 1630 base pairs, while the total genome length is approximately 4 to 6 million base pairs, making the analysis of these genes convenient and allowing for the application of a wide range of algorithms.

A. *Comparing gene sequences*

As a measure of similarity between two sequences, this study employs the BLAST [5] score of their optimal alignment with each other. To compare the sequences of the MPB64 (nikA) gene between two species of mycobacteria, the scores of alignment of all sequences of one species against the reference sequence of this gene from the other species were calculated, and vice versa. Based on the results of these alignments, a 4×4 matrix was constructed (corresponding to the number of species), where each element represents the average alignment score of the associated sequences. The visualization of the obtained matrices is presented in Fig. 3.

As illustrated in Fig. 3, alignments of two sequences of the same species of mycobacteria receive significantly higher scores compared to alignments of sequences of different species. This result supports the hypothesis regarding the significance of the MPB64 and nikA genes in differentiating between tuberculous and nontuberculous mycobacteria, including discriminating of various species of nontuberculous mycobacteria from one another. To assess the feasibility of classifying mycobacteria based on these characteristics, an experiment utilizing the *k*-nearest neighbors method was conducted.

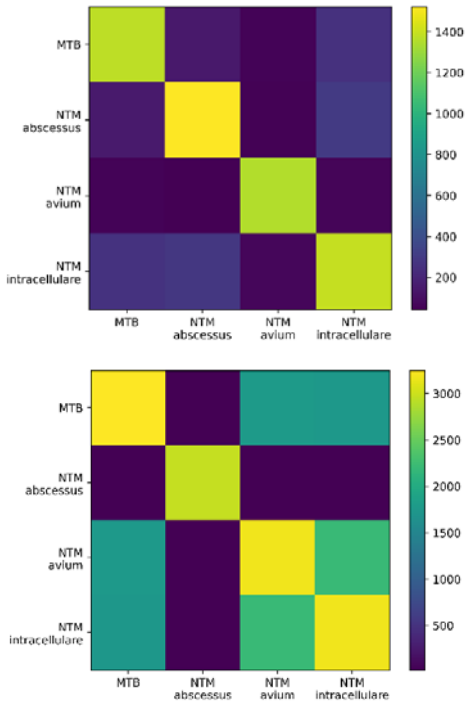

Fig. 3. The matrices of similarity scores between different mycobacterium species by MPB64 gene (above) and nikA gene (below)

B. *Application of the k-Nearest Neighbors Method*

The *k*-nearest neighbors method is an algorithm which relies on the assumption that objects belonging to the same class are located close to one another in the feature space, while objects from different classes are situated further apart. To apply this algorithm for the classification of mycobacteria based on the sequences of the MPB64 and nikA genes, it is essential to define a distance function within the genomic sequence space. In this study, the distance between two gene sequences was defined as the inverse of the BLAST alignment score for these sequences. The greater the similarity between two sequences, the higher their alignment score, and consequently, the smaller the distance between them.

For the experiment, the dataset was divided into training and testing subsets in a 4:1 ratio, ensuring that the balance among the numbers of samples of different species was maintained. The parameter *k* (the number of nearest neighbors considered) was set to 5. The experiment was conducted separately for both the MPB64 and nikA genes. In both cases, the classification accuracy reached 1.00. The results obtained affirm the potential of these two genes for addressing the task of mycobacterial identification and indicate the feasibility of utilizing their sequences for rapid and accurate diagnostics of diseases caused by these four species of mycobacteria.

IV. Conclusion

In this study several methods of identifying Mycobacterium tuberculosis and three common pathogenic species of nontuberculous mycobacteria were investigated. The analysis of *k*-mers from the genomic sequences of the bacteria was conducted using the Fisher's exact test and the Support Vector Machine method, which revealed features with classification accuracy reaching 0.98 to 1.00 on our dataset. Additionally, genomic regions corresponding to the MPB64 and nikA genes were examined, and samples were classified based on these regions using *k*-nearest neighbors algorithm, achieving a classification accuracy of 1.00 for each of the two genes.

Acknowledgment

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Computational Identification of Novel Potential Inhibitors Against the InhA Enzyme of Mycobacterium tuberculosis Using a Drug Repurposing Strategy

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Abstract. **The enoyl-acyl carrier protein reductase (InhA) of *Mycobacterium tuberculosis* (*Mtb*) plays a critical role in the biosynthesis of mycolic acids, essential components of the bacterial cell wall. In this study, a drug repurposing strategy was applied to identify novel small-molecule inhibitors of the InhA enzyme by virtual screening of the library of the FDA-approved drugs and experimental drug candidates. High-throughput molecular docking and molecular dynamics simulations were performed to predict the power of the ligand binding to the InhA-NAD^+ structure, evaluate stability of the ligand/InhA-NAD^+ complexes, and identify the most probable drug candidates. Experimental validation of the five identified molecules carried out in terms of the minimum inhibitory concentration MIC_{90} revealed the lead compound with the MIC_{90} value of 62.5 μM against Mycobacterium bovis BCG and *Mtb*. The data obtained suggest that this compound present a promising scaffold for the lead optimization and development of novel antitubercular agents inhibiting the catalytic activity of the InhA enzyme.**

Keywords: ***Mycobacterium tuberculosis*****, drug-resistant tuberculosis, enoyl acyl carrier protein reductase (InhA), drug repurposing, molecular docking, molecular dynamics, binding free energy calculations, antitubercular agents**

I. INTRODUCTION

After many years of intensive research, science community has made progress in developing effective drugs for Tuberculosis (TB) treatment, but the statistics are still alarming. About 10.1 million people fell ill with TB and over 1.5 million patients died in 2020 [1]. The treatment and eradication of TB are hindered by the emergence and spread of multidrug (MDR) and extensively drug-resistant strains of *Mycobacterium tuberculosis* (*Mtb*). Therefore, there is a pressing need for new therapeutics that can effectively treat both drug-susceptible and drug-resistant strains.

Analysis of the current clinical TB-drug pipeline and target/inhibitor preclinical development shows that the modern therapeutic strategies are generally focused on the designing drug candidates that target the DNA replication, protein synthesis, cell wall biosynthesis, energy metabolism, and proteolysis of *Mtb* [2]. Among the *Mtb* drug targets playing an important role in the cell wall biosynthesis, special attention should be paid to the InhA protein which is one of the key enzymes within the FAS-II pathway [3-5]. Enoyl Acyl Carrier Protein (ACP) Reductase (InhA) is an enzyme involved in fatty acid synthesis, mainly mycolic acid biosynthesis [6]. InhA catalyses trans-double bond reduction which is linked to a carbonyl group of an intermediate covalently linked to an acyl carrier protein in the FAS-II pathway [7]. The first-line therapy drug isoniazid (INH) is the most known InhA inhibitor [8]. INH is a prodrug able to overcome activation by the catalase-peroxidase KatG before forming INH-NAD adduct and binding the active site of the InhA [9]. Inhibition of InhA by INH–NAD results in impaired synthesis of mycolic acids [10].

Due to INH is a prodrug, not only mutations in InhA gene but also in KatG can cause resistance to it. Therefore, numerous attempts to identify direct inhibitors of InhA that do not need an activation phase have been currently made [11].

In this study, the structure-based virtual screening of the library of the FDA-approved drugs and experimental drug candidates was used to identify novel potential inhibitors of *Mtb* that can directly inhibit the catalytic activity of the InhA enzyme. To do this, the following studies were carried out:

1) High-throughput molecular docking of the InhA enzyme with the biologically active molecules from the chemical databases DrugBank [12], ZINC15 [13], and Selleck Chemicals (https://www.selleckchem.com/);

2) Evaluation of the binding affinity of the docked ligand/InhA-NAD^+ complexes using classical and machine learning scoring functions (SFs);

3) Calculations of the exponential consensus rank (ECR) for each compound and ranking the ligands according to their ECR values;

4) Molecular dynamics (MD) simulations of the ligand/InhA-NAD^+ complexes with the highest ECR values, binding free energy calculations, and selection of the best-scored compounds as potential inhibitors of the *Mtb* InhA enzyme;

5) Experimental determination of the minimum inhibitory concentration MIC_{90} for these compounds.

II. Materials and Methods

A. Molecular docking and calculations of the ECR values

28,260 molecules, including the FDA approved drugs and experimental drug candidates, were assembled into the virtual molecular library from the above chemical databases and prepared for molecular docking using the MGLTools software (https://ccsb.scripps.edu/mgltools/). Molecular docking of these compounds with the active site of the *Mtb* InhA enzyme was carried out by the AutoDock Vina program [14] in the approximation of rigid receptor and flexible ligands.

The InhA structure was isolated from the enzyme complex with the InhA inhibitor Inh_468 (N-(3-chloro-2-methylphenyl)-1-cyclohexyl-5-oxopyrrolidine-3-carboxamide) (PDB ID: 4TZT) [15]. The grid box for docking included the substrate-binding pocket of InhA with the NAD^+ coenzyme and had the following parameters: ΔX = 22.92 Å, ΔY = 15.74 Å, ΔZ = 15.94 Å centered at X = 40.62 Å, Y = 51.97 Å, Z = 59.73 Å. The value of exhaustiveness parameter defining number of individual sample runs was set to 100 [14].

The values of binding free energy were estimated in terms of classical SF AutoDock Vina [14], as well as machine learning-based SFs RF-Score-4 [16] and NNScore 2.0 [17]. According to the values of each SF, the ranks of compounds were then calculated and the ECR value was obtained from these data for each ligand by the following formula [18]:

$$ECR = \sum_{sf} \frac{1}{\sigma_{sf}} * \exp\{-\frac{rank_{sf}}{\sigma_{sf}}\}$$

Where $rank_{sf}$ is the rank of the compound according to the scoring function *sf*, σ_{sf} is the parameter that controls the influence of the scoring function *sf* on the results of consensus selection (ECR was calculated using σ_{sf} = 10 for all considered *sf*, since the contributions of the individual scoring functions were taken to be equal).

Based on the ECR values, 23 top-ranked compounds were selected for analysis of their complexes with InhA-NAD^+ by MD simulations to identify the most promising drug candidates able to block the catalytic activity of the enzyme.

B. Molecular dynamics

a) Preparation of InhA-NAD+ and ligands for MD simulations

Preparation of the ligand/InhA-NAD^+ structure for MD simulations was carried out using the AmberTools18 program [19]. The Antechamber module was employed to set the AM1-BCC atomic partial charges on the ligands and NAD^+ [19]. To prepare the force field parameters for the ligands and NAD^+, the general Amber force field (GAFF) was used [19]. Initially, the ligand/InhA-NAD^+ complexes were each placed in a regular truncated octahedral box with periodic boundary conditions. In addition to the ligand/InhA-NAD^+ complex, the box included the TIP3P water [20] as an explicit solvent, as well as Na^+ and Cl^- ions providing the overall salt concentration of 0.15 M.

b) Molecular dynamics simulations

The classical molecular dynamics of the ligand/InhA-NAD^+ was made with the Amber18 software using the Amber ff14SB force field [19]. After setting up the system, the backbone atoms of the protein were fixed by an additional harmonic potential with the force constant of 2.0 kcal/mol/Å^2 and the system was subject to the equilibration phase performed using the sander module of Amber18 [19]. The system equilibration was carried out in four consecutive stages: (1) energy minimization was performed using 500 steps of the steepest descent algorithm followed by 500 steps of the conjugate-gradient method, (2) the system was gradually heated

from 0 K to 300 K for 50 ps in NVT ensemble using Langevin thermostat with a collision frequency of 2.0 ps^{-1}, (3) pressure equilibration was made for 50 ps at 1.0 bar in NPT ensemble using Berendsen barostat with a 2.0 ps characteristic time, (4) the constraints on the complex assembly were removed and the system was equilibrated again at 300 K over 0.5 ns under constant pressure conditions. After equilibration was achieved, the MD simulations were carried out for 200 ns in the NPT ensemble at temperature T = 300 K and P = 1.0 bar. Bonds involving hydrogen atoms were constrained using the SHAKE algorithm [21] to achieve the integration time-step of 2 ps. Long-range electrostatic interactions were calculated using the Particle Mesh Ewald (PME) algorithm [22]. Coulomb interactions and van der Waals interactions were truncated at 8 Å.

Two potent InhA inhibitors of direct action, Genz10850 [23] and Inh_468 [15], with the values of inhibition constants IC_{50} of 0.16 μM and 23.12 μM, respectively, were used in the calculations as a positive control.

c) Binding free energy calculations

The values of enthalpy component of the binding free energy were calculated with AmberTools18 [19] using the MM/GBSA method [24]. The polar solvation energies were computed in continuum solvent using the generalized Born continuum-solvation model with ionic strength of 0.15 M. The non-polar terms were estimated using solvent accessible surface area [19]. The values of the entropic term of the binding free energy were calculated using the Nmode module of AmberTools18 [19]. The calculations were made for 150 snapshots extracted from the last 150 ns of the MD trajectories, by keeping the snapshots every 1 ns. Analysis of the MD trajectories was performed for the last 150 ns time domain by the CPPTRAJ module of AmberTools18 [19].

C. Determination of the minimum inhibitory concentration (MIC) for the best-scored compounds

To determine the MIC, the vaccine strain Mycobacterium bovis BCG and *Mtb* were grown in 7H9 broth (supplemented with OADC) (BD Difco) to exponential phase, respectively, then the cultures were diluted to an OD600 of 0.001 in 200 μL 7H9 broth containing the appropriate concentration of inhibitor. All concentrations were tested in triplicate. After cultivation at 37 °C for 10 days, cell growth was measured by OD600. The lowest concentrations that inhibit 90 % of bacterial growth were determined as MIC_{90}.

III. RESULTS

Analysis of the data from the MD simulations revealed eight compounds (Figure) that exhibited strong attachment to the catalytic site of InhA, in line with the low averages of binding free energies and standard deviations (Table). Given the MM/GBSA standard error of about 2.9 kcal/mol [24], these data suggest that the binding affinity of the identified compounds to InhA is comparable or significantly higher compared to the potent InhA inhibitors Genz10850 [23] and Inh_468 [15] (Table). Calculations of the root-mean square deviations (RMSD) of the atomic positions between all of the dynamic ligand/InhA-NAD^+ models and their starting structures indicate that these complexes do not subject to significant structural reorganizations throughout the calculations. This is confirmed by the low mean values of RMSD calculated for the identified molecules bound to InhA which are close to those predicted for the reference compounds. At the same time, the RMSD average obtained for InhA in the unliganded state is comparable with the corresponding values calculated for the identified compounds bound to the enzyme.

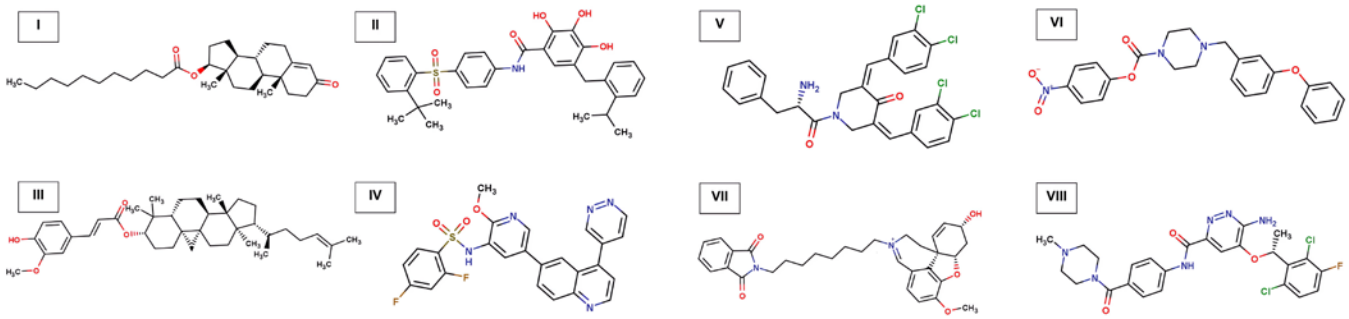
Thus, the data on the binding affinity of the ligand/InhA-NAD^+ complexes predicted using molecular modeling methods indicate a high potential of inhibitory activity of the identified compounds (Figure) against the *Mtb* InhA enzyme.

Examination of the antimycobacterial effect against the vaccine strain Mycobacterium bovis BCG and *Mtb* carried out for the five identified molecules (compounds II, III, IV, VI, VIII) which were available for purchase showed that compound VIII exhibits the MIC_{90} value of 62.5 μM both against *Mtb* and Mycobacterium bovis, and compound VI inhibits only the BCG growth with the MIC_{90} value of 31.25 μM, while the other 3 compounds did not demonstrate the acceptable MIC_{90} values. These results collectively indicate that compound VIII is the most promising basic structure for the development of novel potent drugs against drug-resistant TB.

IV. CONCLUSION

In this study, 28,260 molecules from the virtual molecular library, including the FDA approved drugs and investigational drug candidates, were screened using molecular docking, molecular dynamics simulations, and binding free energy calculations to estimate potential of their inhibitory activity against the substrate-binding site of the *Mtb* InhA enzyme. Based on the data obtained, eight top-ranking compounds that showed the high binding affinity to the enzyme were selected as the most promising InhA inhibitors, in line with the low values of binding free energy and the RMSD data. Five of these eight molecules were tested *in vitro* for inhibition of Mycobacterium bovis and *Mtb* growth, resulting in the

identification of the lead compound (compound VIII; Figure 1) which showed in both cases the MIC_{90} value of 62.5 μM. In light of the data obtained, this compound may be considered as a promising scaffold for the development of new antitubercular molecules of clinical significance with potent inhibitory activity towards an attractive target of *Mtb*.



Chemical structures of the identified compounds. The systematic names of these molecules are given

AVERAGE VALUES OF BINDING FREE ENERGY ΔG, ENTHALPY AND ENTROPY CALCULATED FOR DYNAMIC MODELS OF THE LIGAND/PROTEIN COMPLEXES.

Ligand	<ΔH> kcal/mol	ΔH_{STD}, kcal/mol	<TΔS>, kcal/mol	$(T\Delta S)_{STD}$, kcal/mol	<ΔG>, kcal/mol	ΔG_{STD}, kcal/mol
I	-54.6	3.1	-24	5.2	-30.5	5.8
II	-53.7	3.3	-24.8	4.1	-28.9	5.1
III	-54.3	3.5	-26.2	4.6	-28.1	5.8
IV	-51.5	3.5	-23.9	6.1	-27.6	7.1
V	-52.5	5.8	-26.5	5.4	-26.0	7.1
VI	-48.2	7.1	-25.2	4.6	-23.0	8.7
VII	-46.2	4.5	-24.7	4.8	-21.5	6.6
VIII	-47.1	4.3	-25.8	6.9	-21.3	8.2
Genz10850	-42.9	4.3	-22.3	4.9	-20.6	6
Inh_468	-38.2	3.2	-21.6	4	-16.6	5.1

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Design and Implementation of a Lightweight UGS System Using Dual Geophones

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***Abstract*. Unattended Ground Sensor (UGS) systems have garnered significant attention as a critical technological solution for regional intelligent monitoring since their inception. This study proposes a novel lightweight UGS solution based on seismic wave detection, which incorporates a dual LGT-2 geophone complex, a high-performance data acquisition card and a remote host with a wireless data transmission via WiFi module. The system demonstrates real-time detection of personnel and vehicle targets, azimuth measurement, and multi-feature fusion classification. These research provides a valuable technical reference for critical applications such as intrusion monitoring of personnel and vehicles in restricted areas.**

***Keywords:* UGS, seismic wave detection, regional monitoring, real-time surveillance**

I. INTRODUCTION

Unattended Ground Sensor (UGS) systems have emerged as a pivotal autonomous monitoring technology with significant applications in critical infrastructure protection, ecological environment monitoring, and border security [4–6]. However, conventional optical-based UGS systems exhibit notable limitations, as their monitoring effectiveness is susceptible to environmental occlusion effects, leading to surveillance blind spots in areas with restricted fields of view. To address the urgent demands for security in key areas, there is a pressing need to develop next-generation UGS solutions featuring low power consumption, environmental robustness, and high sensitivity.

To this end, this study proposes a novel solution based on seismic sensing technology. By capturing surface vibration signals induced by target movement and combining them with advanced signal processing algorithms for feature extraction and target classification/ identification, the system significantly enhances monitoring performance in complex environments.

II. RELATED WORK

In the research field of target detection and identification using Unattended Ground Sensors (UGS), numerous scholars have conducted systematic investigations and achieved significant results. Researchers such as Altmann et al. [1] analyzed acoustic-seismic signals generated by different ground targets, extracting harmonic line relative power from power spectra as feature vectors, and employed Learning Vector Quantization (LVQ) algorithm for target classification. The research team led by Ahmad [2] performed Short-Time Fourier Transform (STFT) and power spectrum energy analysis on acoustic and seismic signals respectively, constructing feature spaces before utilizing Support Vector Machine (SVM) classifiers to accomplish target recognition. Saulnier et al. innovatively adopted wavelet transform for feature extraction based on time-frequency characteristics of vehicle targets' acoustic-seismic signals, combined with neural network classifiers for target discrimination. Luo Xianglong [9] made breakthroughs in acoustic-seismic signal fusion, proposing a block-based cepstrum summation feature extraction algorithm that effectively distinguished different vehicle types using SVM classifiers.

Building upon previous work, this study proposes an innovative seismic monitoring technological solution that effectively captures surface vibration signals induced by target movement through the adoption of a high-sensitivity geophone array ($200 \pm 10\ \%\ \mathrm{V}/(\mathrm{m}/\mathrm{s})$).

By integrating an adaptive STA/LTA detection algorithm, the system achieves a target detection probability exceeding 90 % within a 20-meter range. The support vector machine classification model constructed based on a multi-feature fusion strategy further enhances system identification performance. Field test results in campus environments demonstrate that the system exhibits outstanding environmental adaptability and real-time data processing capabilities, providing valuable references for technological advancements in the target detection domain.

III. System Architecture Design

This study employs the LGT-2 geophone as the core sensing unit, integrated with a high-precision data acquisition system and a self-developed host computer software platform, to establish a comprehensive seismic wave signal collection and analysis system for ground target detection.

The system operates through the following workflow as shown in Fig. 1: the dynamic sensor detects surface vibration signals (induced by target movement) and converts them into analog electrical signals, which are then transmitted via shielded cables to the data acquisition terminal. The data acquisition card performs preliminary processing including amplification and filtering before wirelessly transmitting the digitized signals in real-time to the host computer through a Wi-Fi module. The MATLAB-based data processing program on the host computer conducts time-frequency domain analysis of the received seismic signals, ultimately achieving visual representation of target directional information. The system's innovation lies in its fully automated processing chain encompassing signal perception, data transmission, and information interpretation.

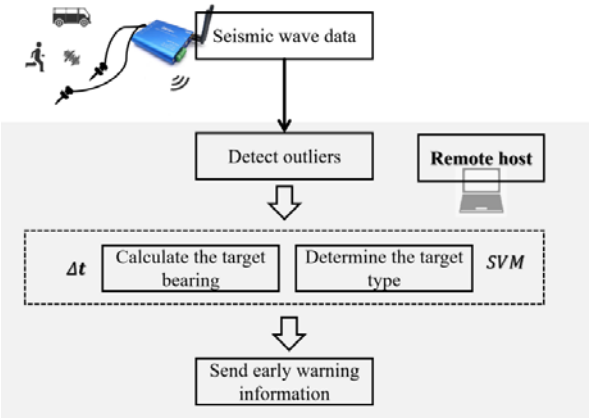


Fig. 1. System Block Diagram

A. Seismic Wave Sensors

This research adopts a dual LGT-2 geophone complex as the core sensing unit. The physical picture is shown in Fig. 2.

Fig. 2. LGT-2 geophones arrays

TABLE I. Technical specifications of the LGT-2 geophone

Parameter Name	Value
Natural Frequency (Hz)	2 ±15%
Coil Resistance (Ω)	5800 ±5%
Case to Coil Motion P-P (mm)	3
Moving Mass (g)	60
Operating Temperature (℃)	-40 to +80
Work Range (Hz)	2 to 300

The sensors feature a passive design that significantly reduces overall system power consumption. These sensors demonstrate the following notable technical advantages:

- Wide operating temperature range capability, enabling stable monitoring performance under extreme environmental conditions.
- High-sensitivity design that effectively captures weak vibration signals, substantially improving the system's detection capability for low-energy targets.
- Optimized dynamic response mechanism ensuring low-latency and high-fidelity signal transmission, providing reliable data support for real-time monitoring and early warning.
- Compact and lightweight design that facilitates rapid deployment while maintaining excellent concealment characteristics, fully meeting the stringent requirements for equipment portability and stealth in monitoring missions.

B. Data Acquisition Card

This study employs the VK701W-SD high-precision data acquisition card (Shenzhen Vkinging Electronic Co., Ltd) as the core data acquisition unit. The physical picture is shown in Fig. 3.

Fig. 3. VK701W-SD high-precision data acquisition card

This study employs the VK701W-SD high-precision data acquisition card as the core data collection unit. The device utilizes 24-bit $\Sigma-\Delta$ analog-to-digital conversion technology, supporting four-channel synchronous sampling at up to 102.4 ksps with wide input dynamic range. Its programmable gain design enables acquisition of both strong vibration signals and amplified weak seismic signals. The acquisition card incorporates a digital anti-aliasing filter to suppress high-frequency interference and provides multiple communication interfaces for distributed networking. Additionally, the device features local storage capability for data security and supports simplified power supply solutions.

TABLE II. TECHNICAL SPECIFICATIONS OF THE ACQUISITION CARD

Parameter Name	Value
Resolution (bits)	24
Max Sampling Rate (ksps)	102.4 ksps per channel
Input Range (V)	-10 to +10
Analog Input Bandwidth (kHz)	0 to 20
Operating Temperature (℃)	-40 to +85

C. Target Detection Algorithms

The data processing algorithm in this study mainly consists of two parts: target detection and feature extraction. The target detection is performed using the STA/LTA algorithm to achieve endpoint detection for dual-channel audio signals. The STA/LTA algorithm [3] is a seismic wave signal detection method based on an energy ratio approach. This signal detection method calculates the short-term characteristics of the signal to determine whether there is an abrupt change in the features being monitored, thereby identifying the presence of a target signal. The method computes the ratio R between the signal's characteristics within a short-time window and those within a long-time window, using this ratio to reflect the variations in the signal within the short-time window. If the calculated ratio exceeds a predefined threshold T, the presence of a target signal is detected. The calculation of the ratio R is shown in Equations (1) – (3):

$$LTA(i) = \frac{1}{l}\sum_{n_1=i}^{i+l} C\,F(n_1), \tag{1}$$

$$STA(i) = \frac{1}{s}\sum_{n_2=i+l}^{i+l+s} C\,F(n_2), \tag{2}$$

$$R = \frac{STA(i)}{LTA(i)}. \tag{3}$$

As STA/LTA algorithm aims at assessing the abrupt changes in the time-domain waveform of signals, this study selects $CF(i) = x(i)^2$ as the characteristic function, where $x(i)$ represents the value at each data point of the signal's time-domain waveform. This calculation method not only characterizes the energy of a segment of the signal in the time domain but also amplifies the variation of data points, making it suitable for detecting abrupt changes in signals. The dynamic computation strategy adopted for the energy ratio threshold effectively avoids the sensitivity issue of fixed thresholds towards environmental noise. The dual-channel energy feature extraction method, while simplifying computational complexity, retains the information about amplitude jumps in signals intact, thereby enhancing the robustness of seismic wave signal detection under complex noisy environments.

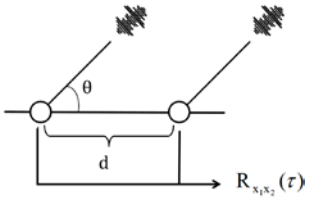


Fig. 4. Schematic Diagram of Angle Measurement

This study employs a dual-sensor array to detect target-induced seismic wave signals. Based on the Time Difference of Arrival principle [7], precise azimuth calculation is achieved. The Δt is obtained through cross-correlation analysis of dual-sensor signals, while the acoustic wave velocity is determined by (7):

$$\theta = \arcsin\left(\frac{v\cdot\Delta t}{d}\right). \tag{4}$$

D. Feature Selection and Extraction

Based on previous research [8], this study selects the following features to construct the feature matrix: zero-crossing number (ZCN), spectral energy distribution, root mean square (RMS) in the time domain, and peak-to-peak amplitude.

The ZCN detection algorithm was employed to count the number of times the signal crosses the zero line within a unit of time, reflecting the frequency characteristics of the signal. The ZCN of pedestrian vibration signals predominantly fall within the range of 10–100, while vehicle vibration signals typically exhibit zero-crossing counts between 1–60. In contrast, environmental noise demonstrates zero-crossing counts mainly distributed between 60–110. The formula for calculating the Zero Crossing Number (ZCN) is as follows:

$$ZCN = \sum_{n=2}^{N} I\left[\, sign(x(n)) \cdot sign(x(n-1)) < 0 \,\right]. \tag{5}$$

Here, sign(x) denotes the sign function, and I(x) represents the indicator function, as defined below:

$$sign(x) = \begin{cases} 1\,, & x > 0, \\ 0\,, & x = 0, \\ -1\,, & x < 0, \end{cases} \tag{6}$$

$$I(x) = \begin{cases} 1\,, & x = -1, \\ 0\,, & \text{else}. \end{cases} \tag{7}$$

The energy of a frequency-domain energy signal is calculated using all or selected frequency points of the signal, representing the total energy across the entire frequency band or within a specific frequency range.

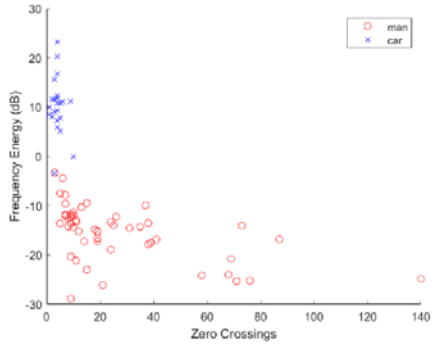


Fig. 5. Correlation Analysis Between ZCN and Spectral Energy

As shown in Fig. 5, the experimental data demonstrate distinct distributions in zero-crossing rate and spectral energy between pedestrian and vehicle targets, with vehicles exhibiting significantly higher spectral energy content. The SVM classifier effectively utilizes these discriminative features, along with other extracted parameters, to achieve reliable target classification.

IV. Experimental Methodology

To validate the proposed system, the following experimental methodology was designed. This study employs a dual sensor array configuration to acquire target azimuth information through phase difference analysis, while utilizing SVM algorithms for target classification. The experimental protocol comprises two distinct phases: preliminary experiments and formal experiments. The preliminary phase primarily establishes fundamental seismic wave parameters through systematic measurements, thereby providing essential parametric references for subsequent experimental procedures.

A. Seismic Wave Velocity Measurement

The time difference method is employed to determine the propagation characteristics of seismic waves in the experimental area. The specific methodology involves: positioning a standard seismic source (lead block free fall) at 5m along the extension line of the sensor array baseline, precisely measuring the time delay Δt of direct wave arrival between two sensors, and calculating the seismic wave propagation velocity by (8)

$$v = d/\Delta t. \tag{8}$$

Using the known sensor spacing d. The experiment is repeated 10 times with averaged results to reduce random errors.

B. Target Detection Threshold Determination

Based on measured data analysis, statistical characteristic models are established for background noise and target signals. The following data sets are collected separately:

1) Environmental background noise under target-free conditions (10 datasets).

2) Signals from standard test personnel (60 kg body weight) walking at 3m/s.

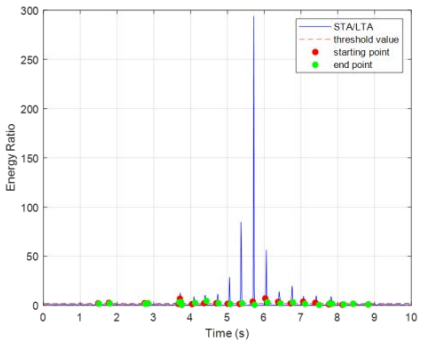
3) Signals from typical vehicles (2.4-ton SUV) moving at 20km/h.

C. Experimental Validation

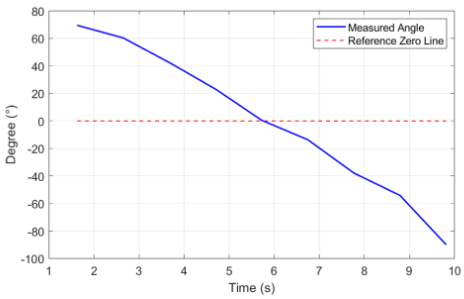
The experimental site was located adjacent to a roadway, utilizing a dual-geophone array configuration with 3-meter sensor spacing. The specific experimental environment is shown in Fig. 6.

Fig. 6. Field Deployment Layout

The test target moved along the road direction parallel to the sensor baseline. Real-time signal waveforms were monitored via the host computer, and target detection was performed using the STA/LTA algorithm.



a



b

Fig. 7. Target Detection Results (a), Bearing Angle Diagram(b)

As shown in Fig. 7, key experimental results include: successful detection of target signals at 20-meter range, with target azimuth angles calculated through phase-difference analysis demonstrating strong correlation with actual movement trajectories. Furthermore, the pre-trained SVM classification model achieved 91.3 % accuracy in distinguishing between personnel and vehicle targets within 20-meter detection range.

V. Conclusion

This paper presents a UGS system based on dual LGT-2 geophones and VK701W-SD data acquisition cards, which enables personnel and vehicle monitoring in remote areas through WiFi modules and host computer control. The system overcomes the limitations of traditional optical sensor-dependent UGS systems, expands applicable environments, and significantly enhances environmental adaptability. Furthermore, we developed host computer software that allows selection of seismic wave sampling rates and visualization of channel waveforms.

In field tests, this study established a comprehensive target feature dataset and significantly enhanced real-time processing performance through the implementation of a low-complexity STA/LTA algorithm. Experimental results demonstrate that the system achieved 100 % target detection rate within a 20-meter range, along with over 90 % target classification accuracy, thereby fully validating the feasibility of the proposed technical solution.

In summary, we have constructed an easy-to-deploy, highly adaptable, and low-power UGS system for personnel or vehicle detection and angle measurement, demonstrating substantial practical value and promising potential for future research.

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Open-World Person Re-Identification Based on Face and Appearance Features

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***Abstract*. The algorithm for open-world person re-identification that uses a descriptor to describe human features based on neural network features of their face and figure is presented. If a person in image is looking at the camera, a feature vector is formed for him that characterizes the face. One global and two local neural network descriptors are used to describe the appearance features of a person. The person figure is represented by 1536 features extracted using DenseNet-121. The proposed approach ensures high accuracy of re-identification when it is possible to identify a person by face and allows re-identification in the case of hidden faces and parts of a person's figure. The results of the experiments are presented. Software implementation of the open-world person re-identification prototype is described.**

***Keywords:* person re-identification, convolution neural network, hyperparameter tuning, face identification, compound descriptor**

I. INTRODUCTION

Re-identification is defined as the determination of the person presence previously identified by a video surveillance system on the same scene at different times or in various video surveillance locations upon query. Persons images are usually used as a query. Therefore, their distinctive features must be identified during practical implementation. Comparison of the query features with the images set descriptors of a gallery of person allows re-identification to be performed. Moreover, the composition of the features set largely determines the re-identification effectiveness.

The wide range of person re-identification systems applications determines the existence of a large number of algorithms and approaches for solving this problem. A distinction is made between close-world re-identification systems, which use ready-made data sets for training and testing, and open-world, in which the image gallery is constantly supplemented with new frames [1]. Close-world systems are usually used for research purposes. Dataset consists of a limited number of video sequences or images obtained from several surveillance cameras. The data in such sets is annotated and prepared in advance, the query is present in the gallery. Open-world systems use a dataset that changes over time as new recordings from surveillance came ras are received, bounding boxes must be generated in real time, and training data must be annotated. Such systems are closest to real conditions and are accompanied by a number of complicating factors. Thus, in [2], modern approaches to open-world re-identification are studied. It is noted that such systems combine two tasks of computer vision, such as person detection and re-identification. This means that for an effective solution it is necessary to combine algorithms for person detection and re-identification. In [3], the main problem of open-world systems is called the problem of the other people similarity to the query, and for its solution it is proposed to use adversarial learning. To display the query, synthetic images of very similar person are generated, which allows the system to become more resistant to such examples. In [4, 5], a significant problem is called the appearance variability over time, and the solution is seen as the analysis of actions, such as gait [6], or three-dimensional modeling of the shape and texture of the person body without taking into account clothing [5]. In [4], long-term re-identification is considered, which is typical for open-world systems. The authors consider illumination variations to be the main problem, and present an algorithm that allows restoring the illumination level of images obtained under different video surveillance conditions to the level of test images.

In this work, we highlight several problems at once. Among which are the presence of persons overlaps by other people and background objects; similar appearance of different people and the likelihood of changing the appearance of the same person over time is a necessity; the need to form a dataset for training a convolutional neural network (CNN) in conditions similar to the conditions for deploying a re-identification system [7]. The paper describes ways to solve the above-mentioned problems and provides a software implementation of an open-world person re-identification prototype.

II. Person re-identification algorithm by face and appearance features

To solve the overlapping persons problems, the variability of the appearance of one person and the same clothes in different people, the paper proposes a re-identification algorithm that involves the formation of a person's face features and a compound features vector to describe a persons' figure. To form a human face descriptor, a trained CNN model ResNet50@WebFace600K from Insightface is used, which forms 512 distinctive features.

At the first stage, a person and their figure keypoints are detected in frames of video sequences and described by a bounding box. Any image with fewer than 3 detected keypoints is considered invalid and excluded from further processing. For all correct images, a compound neural network descriptor is formed that describes the entire a person figure, its upper and lower parts. The upper part of the figure will be considered visible if at least one keypoint is detected on any four parts of the body from the following: face, shoulder, elbow, wrist, thigh. The lower area of the human figure is visible when at least one keypoint is detected on two parts of the body, such as hips, knees or ankles. If a person in image is looking at the camera, a feature vector is formed for him that characterizes the face.

Thus, the algorithm performs the following steps for each frame of video sequence:

1) Bounding box A_p and keypoints (A_1–A_{17}) are created for each person in the frame using YOLOv7 convolutional neural network. Steps 2–10 are performed for each detected person.

2) Keypoints are used to calculate bounding box of the upper and lower half of a person's body, and to form advising masks for them (M_T, M_B). If an area is obscured, typically by another object, and cannot be localized, the corresponding mask is filled with zeros and the feature vector of such area is not used in further analysis. The possibility of using localized areas is stored in boolean variables (E_T, E_B). Then, the following expression is used to determine the possibility of using global feature vector:

$$E_p = E_T \wedge E_B. \quad (1)$$

3) Convolutional neural network based on DenseNet-121 is used for feature extraction, the input of which is a part of the image contained within the bounding box (A_p) and masks(M_T, M_B). The output is combined into a «feature set» F with the following elements: F_p (global descriptor), F_T (top part descriptor), F_B (bottom part descriptor). Some of these can be missing in case their corresponding E is false.

4) Face detection is attempted in the localized area. A face is considered to be found only when all the following conditions are successfully met.

4.1) Based on the keypoints A_1 (nose), A_2 (left eye), A_3 (right eye), A_4 (left ear), A_5 (right ear), an approximate face region is calculated. This step does not provide an exact localized region, but results in a reduction in computational cost in subsequent processing. Detection confidence for the points (A_1 – A_3) should not be lower than 0.5, and for A_4 or A_5 it should be not lower than 0.2.

4.2) If the detection confidence of A_4 is greater than A_5, then $A_{ear} = A_4$, $A_{eye} = A_2$, otherwise $A_{ear} = A_5$, $A_{eye} = A_3$.

4.3) Person's gaze direction is checked. For this purpose, we calculate the distance D_{ear} between points A_{ear} and A_{eye} and the distance D_{nose} between points A_1 and A_2, then the following condition is checked:

$$(D_{nose} / D_{ear}) = 0.9. \quad (2)$$

Facial features can only be used in reidentification if this condition is met.

5) The buffalo_l CNN from InsightFace is used to obtain a more accurate bounding box of the face and to extract a vector L of 512 facial features.

6) The images group ID is assigned to the feature vector as follows:

6.1) We compose an array S of entries corresponding to feature vectors by querying all feature vector from R-Tree T at a given distance from F_p. Each entry contains a group ID that was assigned to this entry, as well as the corresponding feature set. Similar operation is done with local features F_T and F_B to get S_T and S_B, however a shorter distance is used, as local features aren't as reliable as F_p due to sampling from a smaller part of an image.

6.2) An array of entries S_{free} is composed from the vectors of S, S_T and S_B that are not assigned to a group ID.

6.3) The number of entries in S, S_T, S_B belonging to each group ID is counted.

6.4) The group S_{group} , to which the largest number of entries belongs, is selected.

6.5) If the number of entries belonging to the array S_{free} is greater than those belonging to the group S_{group}, then:

6.5.1) The following condition is checked: the number of entries not belonging to any group is greater than or equal to the specified threshold value.

6.5.2) If condition 6.5.1 is met, a new group S_{group} is created. Current entry, as well as each entry from S_{free}, are assigned to S_{group}.

6.5.3) If condition 6.5.1 is not met, the entry has no assigned group.

6.6) If the number of entries in S_{free} is less than in S_{group}, then:

6.6.1) The entry is added to the group S_{group}.

6.6.2) The vectors corresponding to entries in S_{free} are removed from the R-Tree *T*, to avoid creating new ID groups next to the existing one

6.7) The new vector is added to *T*.

7) The same algorithm is used to group face features *L* in case they were extracted in step 5.

8) A unique identifier based on facial features for the current person is returned.

9) If person face features were extracted in step 5 and a group is assigned to them in step 7, the group number to which they were added is returned.

10) Otherwise, if a group was assigned in step 6 and at least one image in this group has a unique identifier, this identifier is returned.

11) Group splitting can be done when it's known that a single group contains several people to improve accuracy. Currently this is done when multiple images were assigned to a single group while processing a single set of frames, as we can assume that the same person can't be seen on multiple cameras at once, or multiple times on a single camera.

The splitting algorithm is defined as follows: given a pair of feature sets of two persons that were assigned to a single group *G*, feature vector (one of F_P, F_T, F_B) is selected that exists in both feature sets. Splitting cannot be done with given pair of feature sets if such feature vector does not exist. Two new groups are created, each corresponding to a person. Then, for each entry that belongs to the group *G*, distance is measured from entry's feature set to each person's feature vector, and feature set gets assigned to the group of the closest person's feature vector.

III. Hyperparameters Adjustment of the Neural Network Training for Person Re-Identification by Appearance

Approaches to improve the person re-identification accuracy can be divided into two groups: those used at the stage of CNN training and at the stage of post-processing of extracted features. At the training stage, the re-identification accuracy can be improved by choosing the CNN architecture, using the most effective values of hyperparameters, increasing the size and diversity of training data [8], and selecting the most effective loss functions. At the stage of post-processing of extracted features, the re-identification accuracy will be influenced by the algorithm that determines the type of features.

To increase the system's resistance to occlusions, image resolution, lighting variability and detector errors, when individual fragments of human parts are detected, an augmentation algorithm is used. This algorithm uses color exclusion and vertical and horizontal pixel shifting, replacing the fragment with a reduced copy of another image from the batch [9]. Images obtained with this augmentation method are not plausible, and to increase accuracy and reduce the values of the loss function, a two-stage learning technology is used, in which at the first stage learning is carried out on augmented data, and fine tuning on the original images.

During training, the batch size should increase. From the 1st to the 60th epoch, the batch size is 8 images. From the 60th to the 90th epoch, a batch of 16 images is used. After the 90th epoch, the batch size is 32 images. The learning rate changes from $\eta_0 = 0.05$ to η_i according to the formula:

$$\eta_i = 0.98\ \eta_{i-1}. \quad (3)$$

where *i* is the epoch number.

The DenseNet-121 [10] is used as a feature extractor, and is trained on the PolReID1077 training set [11] generated under video surveillance conditions similar to the testing conditions of the developed re-identification system. To improve robustness to domain changes and increase the size and diversity of training examples, PolReID1077 is combined with existing datasets: Market-1501 [12], DukeMTMC-ReID [13], MSMT17 [14], CUHK02 [15] and CUHK03 [16]. The training was carried out on a personal computer: Intel Core i5 3.11 GHz, 16 Gb RAM, Nvidia GeForce RTX-3060 6 Gb. The loss function is calculated and weight coefficients are adjusted as described in [17].

The accuracy results are given when training neural networks with a fixed batch size and a learning rate that changes after 40 epochs and the proposed adjustment of hyperparameters during training is applied: on different datasets of the basic re-identification algorithm [18]; on an extended training set; on an extended training set using two-stage learning and data augmentation technology; on an extended training set using local feature analysis, two-stage learning and data augmentation technology. Determination of CNN accuracy is proposed to be performed using Rank1, mAP and mINP metrics. Rank1 determines the ranking quality of the feature table and shows the percentage of correctly given results for a query among the first answers. The mAP metric allows us to evaluate the accuracy of the re-identification algorithm. Computation of mINP metric requires the introduction of additional metrics: Negative Penalty is a negative penalty imposed for incorrect predictions for the *i*-th query and decreasing the probability of correct re-identification in the case of incorrect finding of the most complicated coincidence; Inverse Negative Penalty is an inverse of metric NP whose growth indicates an improvement of system performance. mINP characterizes the mean value of inverse Negative Penalty for all queries. In Table, the values of the

increase in re-identification accuracy relative to the basic algorithm are given in brackets.

PARAMETERS FOR TRAINING

Joint train sample	Augmentation and two-stage train	Analyses local features	Hyperparameter tuning	Metrics		
				Rank1	**mAP**	**mINP**
Market-1501						
baseline				84.02	64.29	28.15
			+	85.48(+1.5)	65.43(+1.1)	29.75(+1.6)
+				92.13	79.48	48.92
+			+	93.44(+9.4)	82.28(+17.9)	54.43(+26.28)
+	+			92.75	82.03	53.40
+	+		+	93.59(+9.6)	83.40(+19.1)	56.29(+28.14)
+	+	+		94.12	85.73	61.41
+	+	+	+	94.89(+10.9)	86.47(+22.2)	62.12**(+33.9)**
DukeMTMC-ReID						
baseline				72.80	53.16	15.88
			+	75.00(+2.2)	55.14(+1.9)	17.27(+1.4)
+				83.84	70.30	31.66
+			+	85.86(+13.1)	73.03(+19.9)	36.13(+20.3)
+	+			85.50	72.75	35.26
+	+		+	86.71(+13.9)	74.05(+20.9)	37.23(+21.4)
+	+	+		87.79	76.68	38.70
+	+	+	+	87.93(+15.1)	77.12(+23.9)	38.82(+22.9)
PolReID1077						
baseline				90.33	68.39	23.43
			+	92.35(+2.0)	70.60(+2.2)	26.04(+2.6)
+				96.25	82.90	43.14
+			+	96.84(+6.5)	85.13(+16.7)	47.33(+23.9)
+	+			96.94	85.25	47.53
+	+		+	97.14(+6.8)	86.78(+18.4)	50.80(+27.4)
+	+	+		97.19	89.32	56.53
+	+	+	+	97.29(+6.9)	90.14(+21.8)	56.74**(+33.3)**
MSMT17						
baseline				54.98	26.67	02.61
			+	57.11(+2.1)	27.88(+1.2)	03.55(+0.9)
+				73.51	46.76	08.18
+			+	76.32(+21.3)	50.20(+23.5)	09.66(+7.1)
+	+			75.10	50.13	10.24
+	+		+	77.11(+22.1)	52.28(+25.6)	11.09(+8.5)
+	+	+		80.32	57.55	13.05
+	+	+	+	80.83**(+25.9)**	57.68(+31.0)	13.94(+11.3)
Occluded-Duke						
baseline				32.31	21.50	04.67
			+	35.06(+2.8)	23.63(+2.1)	05.45(+0.9)
+				54.47	41.78	15.25
+			+	55.92(+21.9)	42.37(+20.9)	15.74(+11.1)
+	+			57.47	45.70	18.41
+	+		+	61.44(+29.3)	47.44(+25.9)	19.42(+14.8)
+	+	+		69.55	58.17	27.86
+	+	+	+	71.47**(+39.2)**	59.98**(+38.5)**	28.23(+23.6)

The presented re-identification assessment values by different metrics show that the use of hyperparameter adjustment during training allows to increase the re-identification accuracy both relative to the baseline model for different datasets, and when using an extended training set, two-stage training technology on augmented data and using an algorithm with a compound neural network descriptor. The largest increase in the Rank1 metric relative to the baseline algorithm was 39.16 for the Occluded-DukeMTMC dataset. According to the mAP metric, the maximum accuracy improvement was also noted for Occluded-Duke and amounted to 38.48. The largest increase in mINP was achieved for the Market-1501 and PolReID1077 datasets and amounted to 33.97 and 33.31.

IV. SOFTWARE PROTOTYPE FOR OPEN-WORLD PERSON RE-IDENTIFICATION

Fig. 1 shows the main screen of the implemented open-world person re-identification systems. The bottom part of the screen shows all the videos available to the system. The selection of videos for display on the left side of the screen is done by pressing the left mouse button. The detected human images are sorted into groups according to the identifiers assigned to them and are displayed on the right half of the screen.

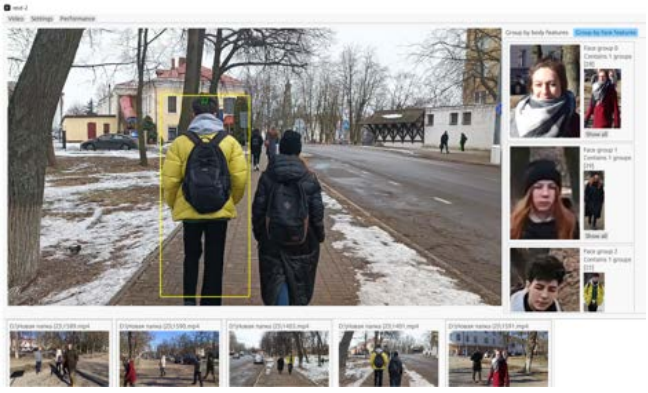

Fig. 1. The main screen of the user interface of open-world person re-identification systems

The initial distribution of detected person images is carried out by appearance, and may allow for inaccuracies due to different viewing angles or illumination variations. But after a person's face is detected in one of the images, the groups are redistributed and a unique identifier is assigned to the person. An example of displaying images of people grouped according to assigned identifiers is shown in Fig. 2.

For the person of interest, it is possible to display all received images, as well as information about the place and time of receiving the frame from which this image was received.

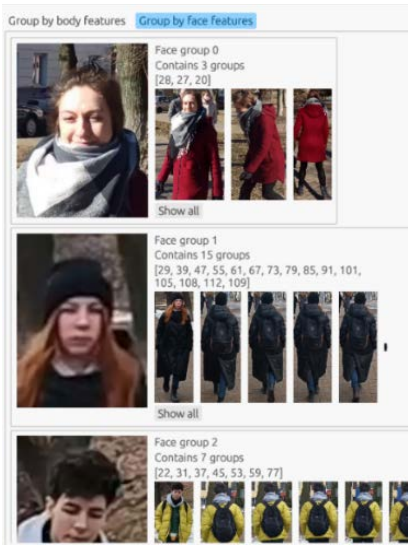

Fig. 2. Person re-identification example by face and appearance features

V. CONCLUSION

The paper presents a software implementation of a system that detects and person re-identification in CCTV images by combining facial features and the appearance of a human figure using a compound neural network descriptor. To form a human face descriptor, a trained CNN model ResNet50@WebFace600K from Insightface is used. The human figure is described by a compound descriptor that includes 1536 features for the entire image, its upper and lower parts, which is formed using DenseNet-121. This approach allows for person re-identification in the presence of hidden faces due to the features of the entire human figure visible part, increases accuracy in the presence of background objects overlapping people, and refines the result if a human face is detected.

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Unclonable Identification and True Random Number Generation Based on CRO PUF

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Abstract. **The problem of generating true random numbers and unique identifiers is more relevant than ever in the modern digital world. This paper analyzes the bits of a binary counter acting as a number's recorder of impulses generated by the physically unclonable functions (PUF) based on a configurable ring oscillator (CRO). The results of the conducted experiments using FPGA chips and an analytical study of the PUF CRO model show the possibility of generating unique stable identifiers and true random numbers at the same time.**

Keywords: **physical unclonable functions, configurable ring oscillator, identification, true random numbers, mathematical model, binary counter**

I. INTRODUCTION

Security is paramount in nowadays interconnected world, innovative solutions are constantly evolving. Robust methods of protection are highly desirable for sensitive data and systems. Physical Unclonable Functions (PUFs) offer a unique approach to security. PUFs based on extracting and measuring unique physical characteristics of semiconductor crystals of digital devices are the basic elements of physical cryptography [1]. Their unpredictable nature makes them incredibly difficult to clone or replicate, cause fake and manipulated PUFs are not able to generate the true IDs. This technology has great potential for improving security in various applications, as it has a simple structure and is capable of solving two problems at the same time. According to various rattling sounds (jitters), caused by various factors, which include instability of the supply voltage, thermal noise of the environment and the semiconductor devices, imperfection of the measuring equipment, etc. PUF-circuits can also, in addition to identification, solve the problem of generating true random numbers.

PUF generates an output bit sequence as response to an input (challenge): $R_n = \mathrm{PUF}(CH_n)$, where $n \in [0, 2^L - 1]$. The response of a PUF to a given challenge should show uniqueness, reliability, and unpredictability [2]. The PUF scheme is represented in Fig. 1.

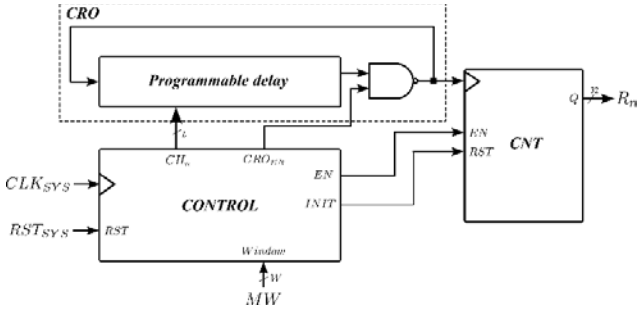


Fig. 1. Scheme of the CRO PUF

This is a reduced circuit scheme of the CRO PUF for the counter, full scheme is in [4]. The general scheme of the CRO can be represented as a programmable delay circuit and a controlled inverter, implemented, as a rule, using a NAND2 gate, which are united by a feedback loop [3, 4]. To build a PUF circuit based on the CRO, it is necessary to have a counter CNT (Measure phase) and a control unit CONTROL, which generates the necessary sequence of signals. In addition, CONTROL generates the response value of the CRO based on the supplied request value CH_n (Select/Switch phase) in the determined measuring window.

II. EXPERIMENT DESCRIPTION

A. Time parameters of ring oscillator

The frequencies of CRO circuits are inherently unpredictable and random. To measure the frequency (or period) of signals generated by the CRO, the sampling frequency must, according to the Kotelnikov theorem, exceed at least twice the frequency of the signal under investigation. Measurements were carried out on FPGA rapid prototyping boards with a system frequency of 50 MHz. Accordingly, CRO frequencies up to 25 MHz can be measured with confidence. If the signal period (the time interval between two rising edges of a periodic digital signal) must be determined, the signal can be applied to the synchronization input of a binary counter implemented on the FPGA. On the selected FPGA family, a 32-bit counter can reliably

operate at up to 180 MHz; therefore, CRO frequencies up to 180 MHz can be measured using such devices.

The width of the measurement window (multiplier k_{factor}) and the bit depth of the registering counter affect the accuracy of measuring the frequency of the CRO signal. With repeated M measurements on the same window MW, different values of the registering counter are observed, caused by various factors, which can include instability of the voltage supply, temperature noise of the environment and the FPGA crystal, imperfection of the measuring equipment, etc.

To increase the resolution of the measurement circuit, let us estimate the period (frequency) of the CRO signal by feeding it to the synchronization input of the binary synchronous counter in the measurement time window $MW = k_{factor} \cdot P_{sys}$, $k_{factor} = 2^i$, $i \in \mathbb{Z}$, which is a factor of the stationary period P_{sys} of the system synchronization signal. Such a measurement method will allow us to estimate the frequencies of $F_{cro} \leq 180$ MHz. The measurement accuracy of P_{cro} depends on the window size: $P_{cro\_i} = MW / R_n^m = 2^i \cdot P_{sys} / R_n^m$, or value $\lambda_i = P_{sys} \cdot P_{cro}^{-1} = R_n^m \cdot 2^{-i}$, where R_n^m is value registered by the counter in m-th measurement with $k_{factor} = 2^i$, $m \in [0, M - 1]$.

The number of clock signals in a certain time window is used as a quantitative measure. When converting the values R_n^m into binary form, the division between the stable (signal) and unstable (noise) parts is visible. The registered values in repeated measurements can be represented by the probabilities of the appearance of a single symbol in each digit of the counter. $P_j^1 = M^{-1} \cdot \sum_{m=0}^{M-1} B_j^m$, $P_j^0 = 1 - P_j^1$, where B_j^m is the value of the j-th digit of the counter in the m-th measurement in a fixed window. The counter length affects the group size, also let us denote $P_j = \max(P_j^0, P_j^1)$.

As can be seen in Fig. 2, the values of all significant digits can be divided into three groups (subsets):

- The group of stable digits G_0, which includes digits for which $P_j = 1$.
- The group of conditionally stable digits G_1, which includes all B_j, for which either $1 > P_j > 0{,}5+\varepsilon$, where ε is a small value characterizing the deviation from the value of 0,5.
- The group of highly unstable digits G_2, for which $P_j < 0{,}5 + \varepsilon$.

Due to the 32-bit counter (see Fig. 1) the values of $i \in [0,30]$ and $M = 1000$ were used in all experiments. The maximum value of $i = 30$ is used because next equation:

$$|G_0| + |G_1| + |G_2| = \lceil \log_2 R_n^m \rceil = \lceil \log_2 (\lambda_i \cdot 2^i) \rceil = \lceil \log_2 \lambda_i \rceil + i = N_i,$$

where $\lceil \log_2 \lambda_{30} \rceil + 30 = 32$.

B. Tests for normal distribution

It was hypothesized that the data from the CRO PUF counter form a normal discrete distribution. To test the hypothesis of normality there are graphical and statistical tests. Visually, there are histograms with an overlaid normal curve and Q–Q [6] plot to see if data quantiles line up with theoretical normal quantiles.

Combining both approaches give a quantitative decision and an intuitive sense of how and where any deviations occur. All data sets under study passed visual tests. The Q-Q test shows deviations at the ends, as already mentioned in the previous study on the assessment of the unstable part. Normality also was tested using the Shapiro–Wilk [6], Anderson–Darling [6], and Pearson tests [6], which compare set's distribution with the ideal normal. In static tests there are already deviations from the normal distribution, but the aim is to show the similarity of the digit-wise probabilities with the ideal model of the normal

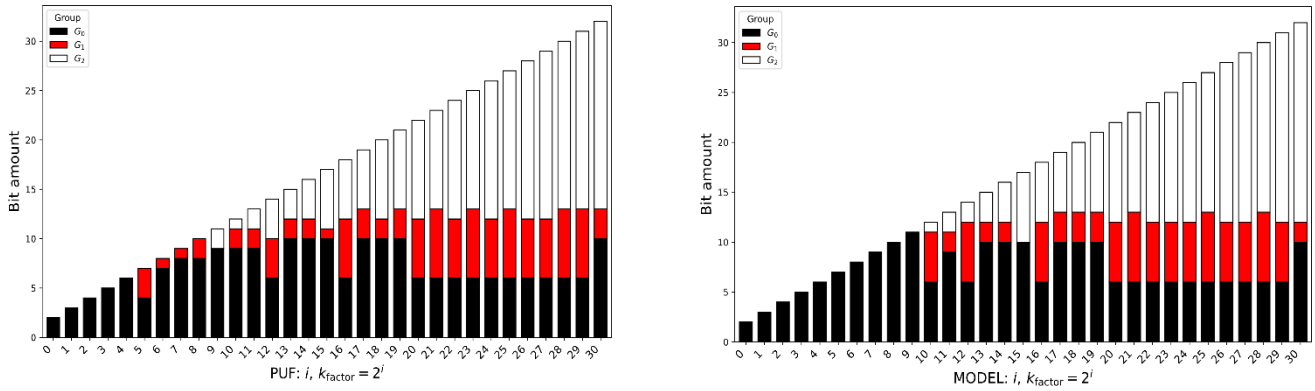
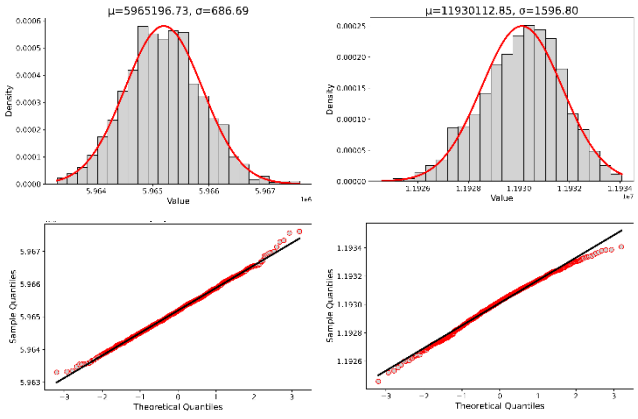


Fig. 2. Devision on groups in PUF and Model data

distribution.

In Fig. 3 there are examples of graphic tests for i = {21,22}.



a b

Fig. 3. Graphical tests for datasets, i=21 (*a*), i=22 (*b*)

III. Program Model of Normal Distribution

Since the data has similarities with a normal distribution, there is need to construct a mathematical model of the ideal normal distribution to predict theoretically the functionality of the selected CRO PUF with known mean and variance. There is need to make sure that the bitwise probabilities of model data P_j^{Model} and of experimental data P_j^{PUF} will be almost the same.

A. Software Model description

To confirm this hypothesis, a software mathematical model of the CRO PUF scheme with a counter was built based on the *numpy* library of the Python language, which generates a discrete set U_{model} of a given size with fixed values of the mean μ_{model} and variance σ^2_{model}.

Model is based on *np.random.normal* function with rounding to the nearest integer.

B. Comparison of PUF and model data

In Fig. 3 comparison with groups of U_{model} and U_{PUF} for different i (k_{factor}) is represented.

First, it is necessary to determine the deviation of model estimates from experimental ones using the Euclidean distance. Let us V_i^{PUF} to be a vector of *PUF* data, V_i^{Model} to be vector with the same size of modeled data. Each component of vector represents the value P_j, then the maximum Euclid distance between V_i^{PUF} and V_i^{Model} can be estimated as $D_{em}^{\max}(i) = \sqrt{\lceil \log_2 \lambda_i \rceil + i} = \sqrt{N_i}$.

Distance of similarity between vectors V_i^{PUF} и V_i^{Model} is estimated through their normalized Euclidean distance $D_{em}^{norm}(i)$. In Fig. 4, it shown that $D_{em}^{norm}(i)$ is close to 0,01:

$$D_{em}^{norm}(i) = \frac{1}{D_{em}^{max}(i)} \cdot \sqrt{\sum_{j=0}^{N_i-1} \left(V_i^{PUF}(j) - V_i^{Model}(j)\right)^2}.$$

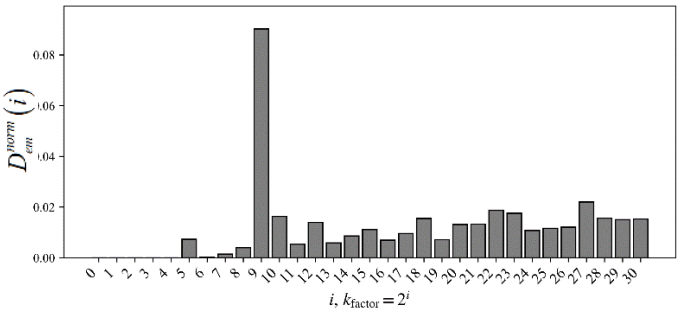


Fig. 4. The plot of $D_{em}^{norm}(i)$

The Fig. 3 shows that the groups sizes are almost the same. This proves that the mathematical model can indeed be used to replicate the work of the CRO PUF.

IV. Experiments with different CRO PUFs on different FPGAs

Experimental results are illustrated with datasets from four similar FPGAs (instances *F*0, *F*1, *F*2, *F*3) with four similar CRO PUFs (instances *C*0, *C*1, *C*2, *C*3). In each FPGA four PUFs were located in different places. In figure 6 there is heatmap of P_j values from 16 combinations.

It was shown that the counter values can indeed be divided into three groups, and the bits of the stable groups G_0 and G_1 can be used as identifiers, cutting off the highly unstable part of G_2. The hypothesis is that all identifiers will be different. For the experiment i = 21 and M = 500 were chosen.

As it is shown in Fig. 5, $|G_0|$, $|G_1|$ are different for all instances, and $|G_2|$, is almost the same.

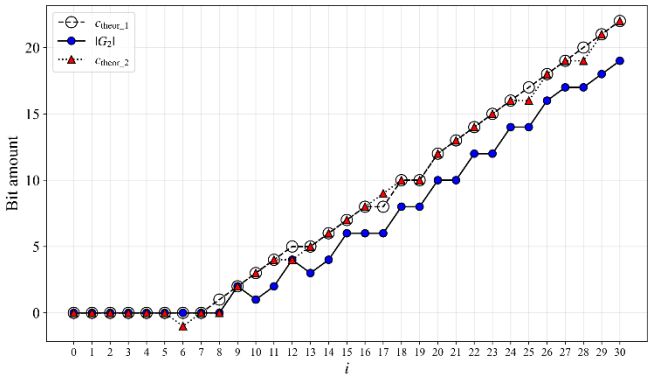


Fig. 5. $|G_2|$ estimation for data with different i

A. *Estimation of highly unstable group G_2*

The length $c = |G_2|$ of highly unstable group G_2 can be estimated with metrics, based on min/max (c^1_{theor}):

$$c^1_{theor} = \lceil \log_2(\max(U) - \min(U)) \rceil,$$

where $U = \{U_{model}, U_{PUF}\}$) values and σ ($c^2_{theor}$ = = $\lceil \log_2(6\sigma) \rceil$).

In theoretical normal distribution 99,7 % values are in range of (-3σ, 3σ), but as *PUF* distribution has deviations at the ends, as it was shown in Fig. 5, the metrics, c^2_{theor} is more accurate, than c^1_{theor}.

Size of group G_2 can be estimated in Fig. 6 with expression $c \le c^2_{theor} \le c^1_{theor}$.

B. *Identification with stable groups G_0, G_1*

Like in many articles [7], the metrics most usually employed to evaluate PUF performance are based on the average Hamming distances (*HD*) evaluated on PUF responses of different PUF instances (HD_{inter}) or different measurements of the same PUF response (HD_{intra}). $ID_{x:y}$ is identifier for each instance F_x:C_y, for the experiment x, $y \in [0,3]$. The Hamming distance between the identifiers of two instances is the number of distinct characters divided by its length.

HD_{intra} is the arithmetic (HD_a) or geometric (HD_g) mean between all pairs $\{y_1, y_2\}$ for fixed x.

HD_{inter} is the arithmetic (HD_a) or geometric (HD_g) mean between all pairs $\{x_1, x_2\}$ for fixed y.

First identifier was built with length $|ID| = \min(|G_0|) = 6$ (Fig. 7) for all observed sets. Results of HD_{intra} and HD_{inter} are in the Tabl. I.

TABLE I. INTRA- AND INTER- UNIQUENESS FOR $|ID| = 6$

HD_{intra}			HD_{inter}		
	HD_a	HD_g		HD_a	HD_g
*F*0	0,250	0,236	*C*0	0,194	0,000
*F*1	0,361	0,340	*C*1	0,389	0,340
*F*2	0,333	0,333	*C*2	0,278	0,252
*F*3	0,333	0,303	*C*3	0,252	0,236

A key advantage of the geometric mean is its immediate identification of identical values, as observed in *C*0. In this case the uniqueness is weak, since there are repeating examples. The length of fully stable group not enough for good uniqueness.

According to the maximum likelihood estimation, the length of unique identifier can be expanded up with values, where $P_j > 0{,}5 + \varepsilon$, $|ID| = \min(|G_0| + |G_1|) = 12$ (Fig. 7).

TABLE II. INTRA- AND INTER- UNIQUENESS FOR $|ID| = 12$

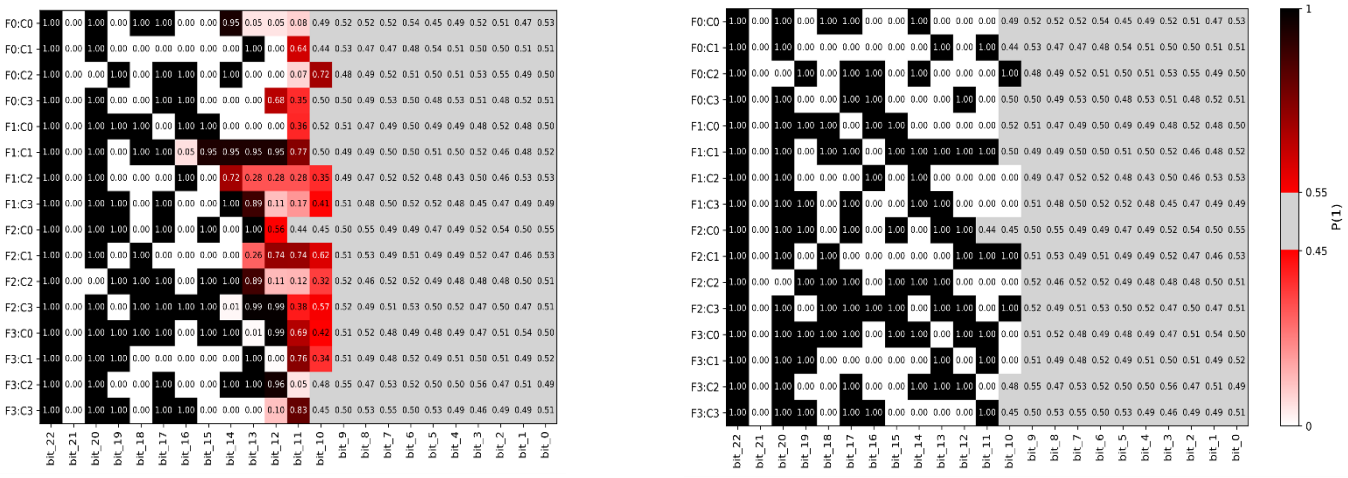
HD_{intra}			HD_{inter}		
	HD_a	HD_g		HD_a	HD_g
*F*0	0,417	0,407	*C*0	0,375	0,360
*F*1	0,431	0,411	*C*1	0,389	0,376
*F*2	0,458	0,446	*C*2	0,319	0,280
*F*3	0,403	0,394	*C*3	0,403	0,394

As can be seen in Fig. 6 red group has gone. Now there are only two groups, stable and highly unstable. It can be seen that the identifiers are different and have good intra- and inter-uniqueness.

Also, the *ID* length can be estimated with metrics c^2_{theor}:

$$|G_0| + |G_1| > N - \lceil \log_2(6\sigma) \rceil.$$

This metrics can help to draw a boundary between unstable and stable group. For example, in experiment $\log_2(6\sigma_{exp}) = \lceil 11{,}9 \rceil = 12$, $N = 23$.



a b

Fig. 6. Distribution of bit probabilities before the maximum likelihood estimation of group (G_2 (a), gray zone is $P_j < 0{,}55$) and after (b)

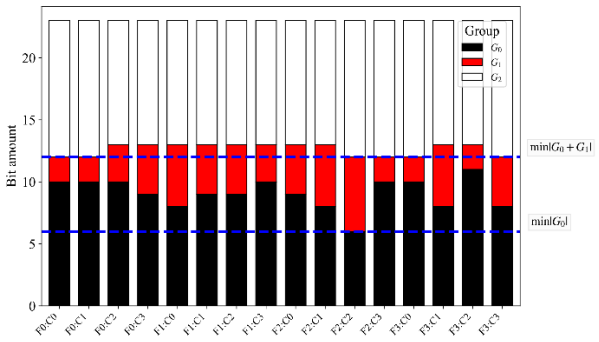


Fig. 7. Group's sizes distribution for experimental data

Without any checking of length groups, only with σ the *ID* length can be chosen. For experimental data the *ID* length is $|ID| = 23 - 12 = 11$.

TABLE III. INTRA- AND INTER- UNIQUENESS FOR $|ID| = 11$

HD_{intra}			HD_{inter}		
	HD_a	HD_g		HD_a	HD_g
*F*0	0,409	0,399	*C*0	0,364	0,339
*F*1	0,424	0,410	*C*1	0,424	0,410
*F*2	0,455	0,445	*C*2	0,303	0,272
*F*3	0,394	0,389	*C*3	0,394	0,381

The scores are slightly lower than those for $|ID| = 12$, but still satisfy the conditions of uniqueness and difference.

CONCLUSUON

CRO PUF is a simple design that exploits the same hardware to generate TRNG response and unique identifier without the need of changing it.

An estimation of a highly unstable group was given, suggesting that so many channels could be used as a source of randomness. To ensure greater randomness, various manipulations can be made with these data. Ways to expand the unique identifier were also provided. It was shown that identifiers from CRO PUF are indeed distinct and unique, and have good intra- and inter-uniqueness.

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Semantic Space: between Continuity and Infinity

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***Abstract*. The paper describes approaches to unified knowledge representation, providing the formation of semantic space models. On the basis of previously proposed models for the representation of non-numeric structures with denotational and operational semantics, quantitative attributes and approaches to their calculation are proposed. They allow to reveal additional topological and metric properties of semantic space structures. A model of multiversal (protomultiversal) numbers is proposed. This model is a formal basis for clarifying the meaning and revealing semantic properties of network structures and models such as artificial neural networks, Kolmogorov-Arnold networks and other models with operational semantics and using numerical features to solve problems within the semantic space.**

***Keywords:* semantic space, denotational semantics, operational semantics, topological space, metric space, pseudo metrics, canonical form, finite structure, countability, graph entropy, graph tensor multiplication, temporal models**

I. Introduction

One of the attributes of knowledge is the presence of a semantic metric [1]. Thus, if "metric" is understood in the mathematical sense then knowledge-based systems are closely related to the concepts of metric space [2, 3] and topological space [4]. The presence of an additional spatial signature on the knowledge set of an intelligent system is closely related to such another feature of knowledge as scaling [1].

Generalized formal languages [5] are used to represent knowledge in knowledge-based systems.

When representing knowledge, (formal) concepts [6] are formed, which form the basis of ontologies [5, 6]. Each concept can have a communicative designation (name) and a meaning (value) [5].

The approach to modeling the semantic space [7] can be referred to theoretical-synthetic (interior) approaches based on unification [5]. Unification assumes that for a set of designations $N = C \cup I$ (signs $S \subseteq C$, concepts C and names (terms) I), there is a set of meanings (senses) E (Fig. 1). Correspondence between designations and their meanings are defined:

$$v_N \subseteq N \times E . \quad (1)$$

Tolerance of meanings (values) is similarity relation t_N:

$$t_N \overset{def}{=} v_N \circ \left(v_N^{-1}\right). \quad (2)$$

Projection t_N onto the set of concepts C is a relation of equivalence of meanings (values):

$$\sim_C \overset{def}{=} t_N \cap (C \times C). \quad (3)$$

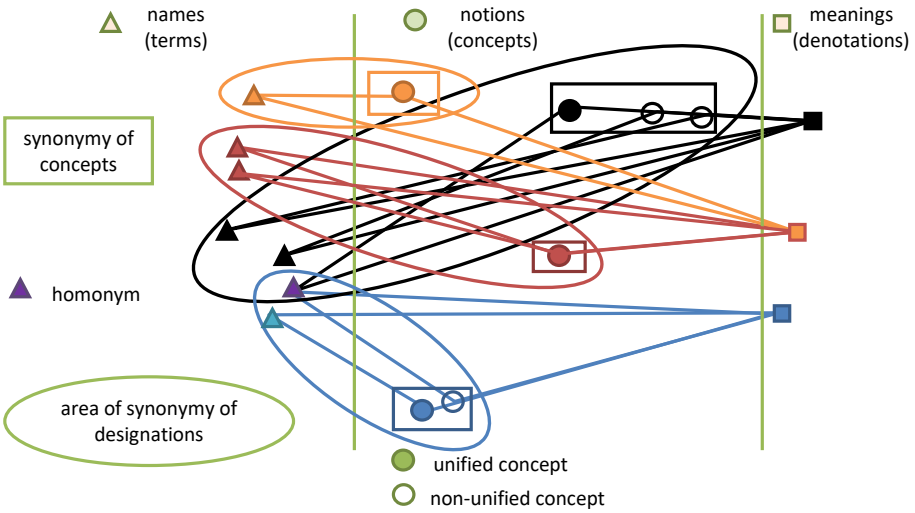

Fig. 1. Unification in the semantic space

The equivalence relation $\sim_C$ forms equivalence classes. There is a bijection between them and signs $S : C_{\sim_C} |\leftrightarrow| S$ with (denotation) $d_N \overset{def}{=} v_N \circ (C \times E)$ being an injection $S |\leftrightarrow E$.

Unification consists in the transition in the relation of similarity $t_N \circ (\sim_C \cap (C \times S))$ from designations N to signs S. Semantic normalization in the languages of the knowledge representation model used assumes that primary meanings $F \subseteq E$ are distinguished among the meanings $E \subseteq 2^{N \cup F}$.

II. Semantic Space Features and Models

A. Static ontological structures

For ontological structures of knowledge bases with denotational semantics, the set-theoretic representation (using the membership relation as a basic one) and its generalization [5] are used to represent various (finite) classical and non-classical mathematical substructures [5] and to investigate their spatial properties including topology discrete structures (Fig. 2–4).

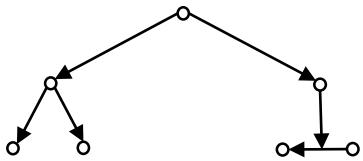

Fig. 2. Ontological structure

In this case, when modeling the semantic space, canonical representations of ontological structures are used. These allow us to identify their canonical spatial features and talk about canonical models of the meaning space. This works in cases when the structures are represented completely.

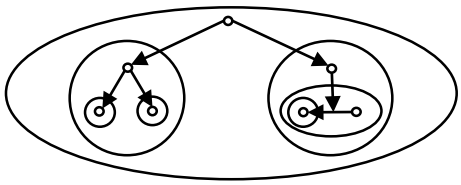

Fig. 3. Ontological structure and extensional closures of its elements

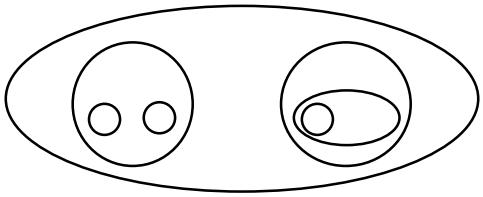

Fig. 4. Closed non-empty sets of the corresponding topological space

The algorithm consists of the following steps:

1. Form closed sets of ontology structure elements based on extensional closure.

2. Order the closures and their elements according to the order relation of the closed subsets, constructing a (topologically sorted) canonical form of the orgraph of this relation, obtaining a directed acyclic metagraph.

3. Starting from the lower vertices (from which there are no paths to other vertices) of the metagraph and up to the upper ones, in the order given by its canonical form, construct and complete the canonical forms of ontological structures included in the corresponding vertices of the metagraph.

In accordance with the canonical forms of ontological structures, canonical matrices and their embeddings can be constructed: adjacency, semantic distances, semantically bounded stable distances (due to the property of knowledge connectivity, the values cannot exceed 8), distance matrices of ontological structure elements in the minimum dimensionality basis.

The embedding of canonical adjacency matrices:

$$\left(\begin{pmatrix}\begin{pmatrix}(0)&0&0&0&0\\0&(0)&0&0&0\\1&0&0&0&3\\0&1&0&0&3\\0&0&3&3&0\end{pmatrix} & \begin{matrix}0&0&0&0&0\\0&0&0&0&0\\0&0&0&0&0\\0&0&0&0&0\\0&0&0&0&0\end{matrix} & \begin{matrix}0&0&0\\0&0&0\\0&0&0\\0&0&0\\0&0&0\end{matrix}\\ \begin{matrix}0&0&0&0&0\\0&0&0&0&0\\0&0&0&0&0\\0&0&0&0&0\\0&0&0&0&0\end{matrix} & \begin{pmatrix}\begin{pmatrix}(0)&0&0\\1&0&3\\0&3&0\end{pmatrix} & \begin{matrix}0&0\\0&0\\0&0\end{matrix}\\ \begin{matrix}0&1&0\\0&0&0\end{matrix} & \begin{matrix}0&3\\3&0\end{matrix}\end{pmatrix} & \begin{matrix}0&0&0\\0&0&0\\0&0&0\\0&0&0\end{matrix}\\ \begin{matrix}0&0&0&0&1\\0&0&0&0&0\\0&0&0&0&0\end{matrix} & \begin{matrix}0&0&0&0&0\\0&0&0&0&1\\0&0&0&0&0\end{matrix} & \begin{matrix}0&0&3\\0&0&3\\3&3&0\end{matrix}\end{pmatrix}$$

The embedding of canonical distance matrices:

$$\left(\begin{pmatrix}\begin{pmatrix}(0)&8&1&7&4\\8&(0)&7&1&4\\1&7&0&6&3\\7&1&6&0&3\\4&4&3&3&0\end{pmatrix} & \begin{matrix}17&16&19&15&12\\17&16&19&15&12\\16&15&18&14&11\\16&15&18&14&11\\13&12&15&11&8\end{matrix} & \begin{matrix}5&11&8\\5&11&8\\4&10&7\\4&10&7\\1&7&4\end{matrix}\\ \begin{matrix}17&17&16&16&13\\16&16&15&15&12\\19&19&18&18&15\\15&15&14&14&11\\12&12&11&11&8\end{matrix} & \begin{pmatrix}\begin{pmatrix}(0)&1&4\\1&0&3\\4&3&0\end{pmatrix} & \begin{matrix}2&5\\1&4\\4&7\end{matrix}\\ \begin{matrix}2&1&4\\5&4&7\end{matrix} & \begin{matrix}0&3\\3&0\end{matrix}\end{pmatrix} & \begin{matrix}12&6&9\\11&5&8\\14&8&11\\10&4&7\\7&1&4\end{matrix}\\ \begin{matrix}5&5&4&4&1\\11&11&10&10&7\\8&8&7&7&4\end{matrix} & \begin{matrix}12&11&14&10&7\\6&5&8&4&1\\9&8&11&7&4\end{matrix} & \begin{matrix}0&6&3\\6&0&3\\3&3&0\end{matrix}\end{pmatrix}$$

The embedding of distance matrices of ontological structure elements in the basis (bold on the diagonal) of minimal dimensionality:

$$\left(\begin{array}{ccccc}
(0) & 6 & 1 & 7 & 8 \\
6 & (0) & 7 & 1 & 2 \\
1 & 7 & 0 & 6 & 7 \\
7 & 1 & 6 & \mathbf{0} & 4 \\
8 & 2 & 7 & 4 & 0
\end{array}\right)
\left(\begin{array}{ccccc}
3 & 4 & 1 & 5 & 8 \\
9 & 10 & 7 & 11 & 14 \\
4 & 5 & 2 & 6 & 9 \\
10 & 11 & 8 & 12 & 15 \\
6 & 7 & 6 & 8 & 11
\end{array}\right)
\left(\begin{array}{ccc}
9 & 9 & 5 \\
3 & 15 & 11 \\
10 & 10 & 6 \\
4 & 16 & 12 \\
6 & 12 & 8
\end{array}\right)$$

$$\left(\begin{array}{ccccc}
3 & 9 & 4 & 10 & 6 \\
4 & 10 & 5 & 11 & 7 \\
1 & 7 & 2 & 8 & 6 \\
5 & 11 & 6 & 12 & 8 \\
8 & 14 & 9 & 15 & 11
\end{array}\right)
\left(\begin{array}{ccccc}
(0) & 1 & 2 & 2 & 5 \\
1 & 0 & 3 & 1 & 4 \\
2 & 3 & 0 & 4 & 7 \\
2 & 1 & 4 & \mathbf{0} & 3 \\
5 & 4 & 7 & 3 & 0
\end{array}\right)
\left(\begin{array}{ccc}
4 & 6 & 4 \\
5 & 5 & 3 \\
6 & 8 & 6 \\
6 & 4 & 2 \\
9 & 1 & 3
\end{array}\right)$$

$$\left(\begin{array}{ccccc}
9 & 3 & 10 & 4 & 6 \\
9 & 15 & 10 & 16 & 12 \\
5 & 11 & 6 & 12 & 8
\end{array}\right)
\left(\begin{array}{ccccc}
4 & 5 & 6 & 6 & 9 \\
6 & 5 & 8 & 4 & 1 \\
4 & 3 & 6 & 2 & 3
\end{array}\right)
\left(\begin{array}{ccc}
0 & 10 & 6 \\
10 & \mathbf{0} & 4 \\
6 & 4 & 0
\end{array}\right)$$

The previously formulated theorem [5] allows us to pass from an existing metric space to a new metric space by taking into account pseudometrics that can specify a dimension.

This is not enough to analyze topological properties of reflexive ontological structures. In order to highlight the topology of these structures, we propose to consider additional numerical features for a sign σ of the tuple μ:

$$incidensity(\sigma) \overset{def}{=} \frac{|\iota(\sigma)|+1}{|\upsilon(\sigma)|};\ weight_{\lambda}(\mu) \overset{def}{=} \frac{\sum_{\varepsilon \in_{\lambda} \mu} |C(\varepsilon)|}{\left|\bigcup_{\varepsilon \in_{\lambda} \mu} C(\varepsilon)\right|}, \quad (4)$$

where $\upsilon(\sigma)$ is a set of signs in the proximity of σ, $\iota(\sigma)$ is a set of their incidences, $C(\varepsilon)$ is a proximity of λ-type ε.

On the basis of the introduced features and similar ones, it is possible to specify the weight of connectives which can be the basis of metric properties of the semantic space. These properties allow us to form a system of closed sets of the topological subspace which is formed by means of ascending hierarchical clustering.

B. Dynamic ontological structures

For ontological structures of knowledge bases with operational semantics, we use models of transition-state diagrams (graphs) (using the becoming relation as a basic one), as well as the proposed model of operational-information space [5] which allow us to represent different (finite) formal submodels (pseudo-orgraphs) of knowledge processing and investigate their spatial properties including topology of discrete structures.

Previously [5, 8], we considered the time-averaged entropy of wavefronts of the equilibrium state of a knowledge processing model (system) with a pseudo-orgraph structure of returnable operations. Returnability are one of the three key features for constructing a general classification of operations and problems solved with their help [5].

If a pseudo-orgraph is not strongly connected or does not correspond to non-redundant operations, i.e. it contains some features, vertices in which the total flow is not conserved (final or initial) then we can apply to it some meta-operation (surgery) which completes it to a connected one. The simplest of the operations augments such a pseudo-orgraph with a bipartite complete orgraph, the first partition of which is the set of all final vertices and the second partition is the set of all initial vertices. After that, one can compute the flows for such augmented pseudo-orgraph and the corresponding flows for the original pseudo-orgraph. As for the calculation of wave fronts, lengths and periods of such a pseudo-orgraph, it is more complicated. A theorem was formulated earlier that this entropy is a monotone measure [5] for the separability relation on equivalence classes of isomorphic strongly connected pseudoormultigraphs. In addition to this, the following theorem holds true.

Theorem 1: The entropy is an additive measure with respect to the tensor product operation of equivalence classes of isomorphic strongly connected pseudoormultigraphs.

The introduced entropy is an invariant of knowledge processing operations and it is also the basis for the formation of pseudometrics on elements of ontological structures and in accordance with the mentioned theorem is the basis for the transition from one metric space to another.

C. Network problem solving models

Due to the prevalence of neural network models that compute numerical feature values of input image data in linear vector space, the question arises about the relationship between input data, object images, and their secondary image features. To what extent the computed feature values correspond to some formal context and ontological structure of the corresponding formal concepts. Whether the corresponding images and concepts have an extensional, what are their denotates and designates. A separate difficulty is that the description of features uses models of continuous mathematics (including real numbers, the power of the set of which is uncountable), and the program implementation is discrete. However, only a countable subset of real numbers is computable. To overcome computational difficulties, such models as interval arithmetic [9], quasivector spaces [10] and others have been proposed, but they do not remove all the issues [9, 11].

III. PROTOMULTIVERSAL NUMBERS

A model of protomultiversal numbers is proposed to decide the above inconsistencies and provide answers to the questions posed.

The model of protomultiversal numbers is given by:

$$\langle N, L, R, F, M, A\rangle, \tag{5}$$

where N is the set of (canonical forms of) computable numbers, L is the set of places, R and F are the sets of measurement and re-generalization steps ($`s$ is the next step after s), M is the set of protomultiversal numbers, A is the set of conjugacy constraints that is satisfied:

$$A \subseteq \left(\left(\left(\left(\left(N^2\right)^*\right)_+^{\left(2^M\right)}\right)^L\right)^R\right)^F. \tag{6}$$

Each constraint $\langle \underline{a}_t, \overline{a}_t\rangle \in N^2$ for x has the form:

$$\sum_{i=0}^{n}\sum_{j=0}^{q^i-1} \overline{a}_{\frac{q^i-1}{q-1}+j} * \prod_{k=1}^{i} x_{1+\left(\left\lfloor \frac{j}{q^{k-1}}\right\rfloor \bmod q\right)} \le 0,$$

$$\sum_{i=0}^{n}\sum_{j=0}^{q^i-1} \underline{a}_{\frac{q^i-1}{q-1}+j} * \prod_{k=1}^{i} x_{1+\left(\left\lfloor \frac{j}{q^{k-1}}\right\rfloor \bmod q\right)} \ge 0. \tag{7}$$

Each number m ($m.bottom \le \langle \top, x\rangle \le m.top$) of M:

$$m = \langle locations, low, hi, down, up, bottom, top\rangle, \tag{8}$$

where
$$\{low\}\cup\{hi\} \subseteq \left(\left(\left(\{\bot,\top\}\times N\right)^L\right)^R\right)^F$$
$$\{down\}\cup\{up\} \subseteq \left(\left(\{\bot,\top\}\times N\right)^R\right)^F \tag{9}$$
$$\{bottom\}\cup\{top\} \subseteq \left(\{\bot,\top\}\times N\right).$$

Other properties are also performed:

$$\begin{gathered}
\forall p \exists q\left(lo(f)(r)(p) \ge lo(`f)(r)(q)\right)\wedge \\
\wedge\left(hi(f)(r)(p) \le hi(`f)(r)(q)\right); \\
\forall x\left(lo(f)(r)(p) \le \langle \top, x\rangle \le hi(f)(r)(p)\right)\to \\
\to \exists q\left(lo(`f)(r)(q) \le \langle \top, x\rangle \le hi(`f)(r)(q)\right); \\
\forall x\left(lo(`f)(r)(p) \le \langle \top, x\rangle \le hi(`f)(r)(p)\right)\to \\
\to \exists q\left(lo(f)(r)(q) \le \langle \top, x\rangle \le hi(f)(r)(q)\right); \\
\forall p \exists q\left(lo(f)(`r)(p) \ge lo(f)(r)(q)\right)\wedge \\
\wedge\left(hi(f)(`r)(p) \le hi(f)(r)(q)\right); \\
lo(h)(r)(p) = lo(f)(s)(p) = lo(f)(r)(p); \\
hi(h)(r)(p) = hi(f)(s)(p) = hi(f)(r)(p); \\
bottom \le down(f)(r) \le low(f)(r)(p) \le hi(f)(r)(p) \\
\left(low(f)(r)(p) \ge hi(f)(r)(p)\right)\to\left(low(f)(r)(p)\right)_1 \\
hi(f)(r)(p) \le up(f)(r) \le top,
\end{gathered} \tag{10}$$

where

$$\begin{gathered}
\left(\langle \alpha,\chi\rangle \ge \langle \beta,\gamma\rangle\right) \Leftrightarrow \left(\langle \beta,\gamma\rangle \le \langle \alpha,\chi\rangle\right) \\
\left(\langle \alpha,\chi\rangle > \langle \beta,\gamma\rangle\right) \Leftrightarrow \left(\langle \beta,\gamma\rangle < \langle \alpha,\chi\rangle\right) \\
\left(\langle \alpha,\chi\rangle < \langle \beta,\gamma\rangle\right) \Leftrightarrow \left((\chi<\gamma)\vee\left((\chi=\gamma)\wedge\left((\neg\alpha)\wedge\beta\right)\right)\right) \\
\left(\langle \alpha,\chi\rangle \le \langle \beta,\gamma\rangle\right) \Leftrightarrow \left((\chi<\gamma)\vee\left((\chi=\gamma)\wedge(\alpha\to\beta)\right)\right) \\
\left(\langle \alpha,\chi\rangle = \langle \beta,\gamma\rangle\right) \Leftrightarrow \left(\left(\langle \alpha,\chi\rangle \le \langle \beta,\gamma\rangle\right)\wedge\left(\langle \alpha,\chi\rangle \ge \langle \beta,\gamma\rangle\right)\right).
\end{gathered} \tag{11}$$

The operation max (and similarly min) is defined:

$$\begin{gathered}
\max\left(\{\langle \alpha,\chi\rangle\}\cup\{\langle \beta,\gamma\rangle\}\right) \overset{def}{=} \\
= \left\langle\left((\alpha\wedge(\chi\ge\gamma))\vee(\beta\wedge(\chi\le\gamma))\right), \max\left(\{\chi\}\cup\{\gamma\}\right)\right\rangle.
\end{gathered} \tag{12}$$

Also:

$$expanse(m) \overset{def}{=} m.top - m.bottom; \tag{13}$$
$$latitude(m)(f)(r)(p) \overset{def}{=} m.hi(f)(r)(p) - m.low(f)(r)(p).$$

The regular protomultiversal numbers are satisfied:

$$\begin{gathered}
m.bottom \overset{def}{=} \min\left(\left\{m.down(f)(r)\middle|\langle f,r\rangle \in F\times R\right\}\right) \\
m.top \overset{def}{=} \max\left(\left\{m.up(f)(r)\middle|\langle f,r\rangle \in F\times R\right\}\right) \\
m.down \overset{def}{=} \min\left(\left\{m.low(f)(r)(p)\middle|p \in m.locations(f)(r)\right\}\right) \\
m.up \overset{def}{=} \max\left(\left\{m.hi(f)(r)(p)\middle|p \in m.locations(f)(r)\right\}\right) \\
m.locations(f)(`r) \subseteq m.locations(f)(r).
\end{gathered} \tag{14}$$

There exist three cases to define relations *expand*, *extend*, *lapse* and operations on the numbers from *M*: partially defined ($Q=O=\exists$), an unary completely defined ($\langle Q,O\rangle = \langle \forall,\exists\rangle$) and a completely defined ($Q=O=\forall$) operations. For example, for the sum operations:

$$\begin{gathered}
\forall g \forall t \forall oQhQsQqOfOrOp\left\langle l.low(g)(t)(o), l.hi(g)(t)(o)\right\rangle \overset{def}{=} \\
\left\langle m.low(h)(s)(q), m.hi(h)(s)(p)\right\rangle + \\
+\left\langle n.low(f)(r)(p), n.hi(f)(r)(p)\right\rangle
\end{gathered} \tag{15}$$

where $\langle \alpha_{low}, \alpha_{hi}\rangle + \langle \beta_{low}, \beta_{hi}\rangle = \left\langle \lfloor\rfloor \alpha_{low} + \beta_{low} [\lfloor, \lceil\rceil \alpha_{hi} + \beta_{hi} [\rceil\right\rangle$;

$$\alpha+\beta = \langle \alpha_1+\beta_1, \alpha_2+\beta_2\rangle; \tag{16}$$
$$\alpha_1+\beta_1 = (\alpha_1\wedge\beta_1)\vee\left(\left(|\alpha_2| = +\infty\right)\wedge\alpha_1\right)\vee\left(\left(|\beta_2| = +\infty\right)\wedge\beta_1\right),$$

and $\lfloor\rfloor x[\lfloor$ with $\lceil\rceil x[\rceil$ are rounding down and up on N ($\{-\infty\}\cup\{+\infty\}\subseteq N$). Other operations such as multiplication, subtraction and division can be specified similarly and according to the operations of interval arithmetic [10].

Depending on *N*, the algebraic systems of protomultiversal numbers can extend fields or linear vector spaces, exhibiting properties of rings or modules.

For each operation or function expressed by their superposition, as well as for the sum operation, we can define at least three variants: partially, unary completely and completely defined functions.

Then we can treat a concept as an image (feature value) of a name (sign), i.e. an image of the initial pattern (a set of protomultiversal numbers). Denotation (referent) is the image (value of the sign) of the concept and the image of the name (set of protomultiversal numbers). Designate is the set of all protomultiversal numbers partially or completely defined by operations (functions) between them.

IV. Conclusion

On the basis of previously proposed models for representing non-numeric structures possessing denotational and operational semantics, the steps of the algorithm and examples of identifying topological and metric features of static structures of the semantic space are considered. Semantically stable features are considered. These features allow analyzing topological and metric properties of strongly connected ontological structures. The measure of information entropy additive on the set of strongly connected pseudo-orgraphs of operations is considered for dynamic structures of the semantic space. The theorem on its additivity is formulated. On the basis of this measure as an invariant, an approach to the construction of pseudometrics specifying the metric properties of the semantic space is proposed. The model of protomultiversal numbers, which is a formal basis for the specification of meaning and revealing semantic properties of network structures and models, such as artificial neural networks, etc., is proposed. This model suggests additional studies of its practical capabilities.

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Localized Bootstrap Contrastive Learning Network for Few-Shot PolSAR Image Classification

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***Abstract*. Deep learning methods for polarimetric synthetic aperture radar (PolSAR) image classification are often limited by the number of labeled samples and tend to overlook the multi-instance nature of the data during feature extraction, resulting in suboptimal classification accuracy. To address this issue, we propose a localized bootstrap contrastive learning network (LBCLN), which incorporates a feature learning module (FLM) and a projection module (PM). The FLM combines a three-branch feature fusion network and an efficient residual channel attention (ERCA) to extract multi-dimensional scattering information from PolSAR images, thereby enhancing the network's feature extraction capability in complex data scenarios. The PM employs a parallel branch structure that learns global and local features in a 70 % and 30 % ratio, respectively, overcoming the limitations of conventional contra-stive learning in dense prediction tasks. The proposed method is validated in the Flevoland datasets. Notably, LBCLN achieves an overall accuracy of 95.48% with only 0.2 % of labeled samples.**

***Keywords:* Polarimetric synthetic aperture radar (PolSAR) images classification, few-shot, contrastive learning, localized bootstrap**

I. INTRODUCTION

Polarimetric synthetic aperture radar (PolSAR) is a multi-parameter, multi-channel radar imaging system that utilizes the polarization properties of electromagnetic waves to obtain richer target information, providing more precise data support for subsequent research and interpretation [1]. Crop classifica-tion is a fundamental aspect of agricultural remote sensing monitoring, playing a vital role in guiding agricultural produc-tion, optimizing resource allocation, and ensuring national food security [2]. Remote sensing classification technology based on PolSAR images aims to achieve accurate pixel-level classification, supporting applications such as land use and change monitoring.

In recent years, deep learning (DL) methods have played a significant role in PolSAR image classification. Zhou et al. [3] applied convolutional neural network (CNN) to perform pixel-level classification of PolSAR images, achieving significant progress. GICANet [4] implemented multi-scale feature extraction through ghost convolution. Moreover, complex-valued networks [5–7] took into account the specific characteristics of PolSAR data, achieving improved classific-ation accuracy. These methods all fall under supervised learning (SL), and their classification performance depends on the availability of labeled samples. However, acquiring accurate labels for PolSAR images is a difficult task, making the limited availability of labeled samples a significant challenge in PolSAR image classification.

Self-supervised learning (SSL) is a common approach to addressing the issue of label scarcity, primarily by learning intrinsic representations from unlabeled data, thereby maxi-mizing the use of unlabeled data to guide downstream SL tasks. Contrastive learning (CL) is a powerful method in SSL, where the goal is to learn data representations by enhancing the similarity between positive samples while reducing the similarity between negative ones [8]. The introduction of BYOL [9] eliminated the dependency on negative samples in CL, and it has been successfully applied to PolSAR image classification tasks [10]. It is worth noting that PolSAR image classification can be considered a special case of semantic segmentation. However, most existing CL methods focus on global views and fail to adequately address the multi-instance problem present in dense prediction tasks. Recently, MLCN [11] adopted meta-learning techniques to achieve high-precision few-shot classification. However, this method still requires 2 % of labeled samples during the pre-training phase.

The paper focuses on a localized bootstrap contrastive learning network (LBCLN) designed for few-shot PolSAR image classification. The key contributions are as follow:

1) The feature learning module (FLM) of the three-branch feature fusion network is combined with the efficient residual channel attention (ERCA) to efficient and lightweight extract spatial, polarimetric, and spatial- polarimetric joint features.

2) The design of a projection module (PM), which learns global and local features in a specific ratio through a parallel branch, thereby constructing a contrastive learning network with local guidance capability that enhances the accuracy of multi-instance PolSAR image classification.

II. Methodology

A. Overview of the LBCLN

PolSAR image classification is a dense prediction task where the network needs to build global representations at the image level while maintaining spatial consistency at the pixel level. Inspired by the DenseCL [12] approach, we propose the LBCLN method, which improves the CL based on BYOL [9] by incorporating the FLM and the PM.

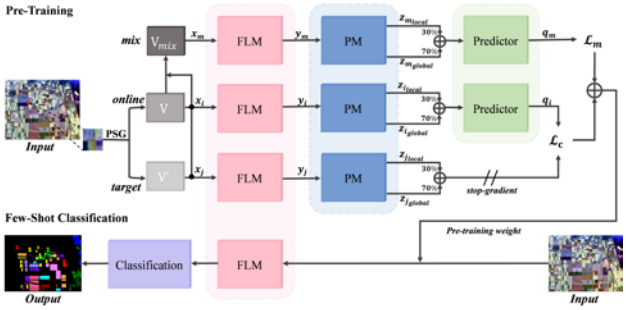

Fig. 1. Architecture of the LBCLN. The method consists of two stages: pre-training and few-shot classification. PSG is positive sample generation

As shown in Fig. 1, the LBCLN method consists of two stages: the pre-training phase and the few-shot classification phase. In the pre-training phase, the model has two branches: the contrastive branch (the online network f_θ and the target network f_ξ) and the mix branch (the mix network), where the mix network shares parameters with the online network. For the input image $x \in \mathbb{R}^{W\times H\times C}$, two augmented views, x_i and x_j, are generated through positive sample generation (PSG) and input into the online network and target network, respectively. Subsequently, x_i and x_j are linearly combined to generate the input x_m of the mix network, as expressed by the following equation:

$$x_m = \epsilon x_i + (1-\epsilon)x_j, \tag{1}$$

where the mixing coefficient ϵ is randomly sampled from a $Beta(\alpha,\alpha)$ distribution. All views undergo feature learning via their respective networks' FLM. The PM combines the learned global and local feature spaces by a predefined ratio.

The network parameters are updated and optimized following the formula:

$$\begin{cases}\theta \leftarrow O_B(\theta, \mathcal{L}_{total}, \eta)\\ \xi \leftarrow \tau\xi + (1-\tau)\theta\end{cases} \tag{2}$$

here, the target network parameters ξ are the exponential moving average (EMA) of the online network parameters θ. O represents the optimizer, B is the batch size, η is the learning rate, and τ is the EMA decay rate.

B. Feature Learning Module

CL typically generates two augmented views of the same image and inputs them into the network for feature learning. However, existing methods focus on global features and over-look the local details of multi-semantic features, which limits the accuracy of few-shot PolSAR image classification based on CL. Additionally, the complexity of PolSAR data makes it difficult for current networks to effectively learn features. To overcome these challenges, this paper constructs a three- branch feature fusion network using dynamic convolution (DyConv). The network integrates spatial feature learning (ex-tracting spatial features from a single channel), polarimetric-spatial feature learning (capturing the dependencies among the subsets of three polarization channels), and polarimetric-only feature learning (fusing spatial and polarization features). Furthermore, the ERCA module is designed to further optimi-ze information transfer, thereby enhancing the overall feature learning capability, as shown in Fig. 2.

1) Dynamic Convolution: As shown in Fig. 2, DyConv is implemented using conditionally parameterized convolutions [13], where the convolution kernel is parameterized as a linear combination of four experts, as expressed by:

$$Output(x) = \sigma(\alpha_1(W_1 * x) + \alpha_2(W_2 * x) + \\ +\alpha_3(W_3 * x) + \alpha_4(W_4 * x)), \tag{3}$$

here, σ is an activation function.

2) Efficient Residual Channel Attention: To avoid com-plex dimensionality reduction and expansion processes, and to achieve efficient and lightweight feature modeling, we des-ign an ERCA module based on ECA [14], as shown in Fig. 2. Given a channel dimension *C*, the convolution kernel size *k* is adaptively determined by the following formula:

$$k = \psi(C) = \left|\frac{log_2(C)}{\nu} + \frac{b}{\nu}\right|_{odd}, \tag{4}$$

where $|t|_{odd}$ represents the nearest odd number to t, and the parameters v and b are set to 2 and 1, respectively.

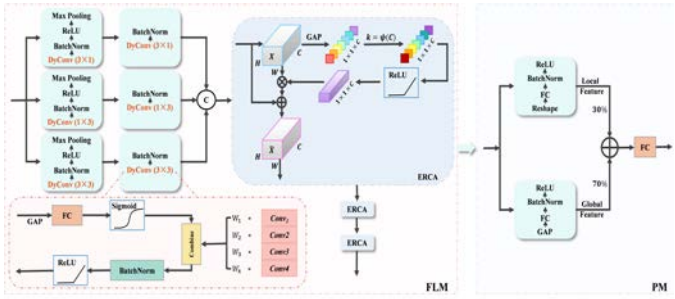

Fig. 2. Schematic of the FLM and PM

C. Projection Module

As shown in Fig. 2, the PM consists of global feature projection and local feature projection. Both projections accept the same input, with the distinction being whether the input has passed through the global average pooling (GAP) layer. CL can overcome the limitations in dense prediction tasks by considering both global representations and ensuring the spatial consistency of local representations with this module. Thus, PM combines the global and local features in a 70 % and 30 % ratio for fusion projection to enhance feature prediction ability.

D. Contrastive Loss Function

Based on the theoretical framework of BYOL, LBCLN primarily assists downstream tasks by learning feature representations. Thus, the loss function is focused on the pre-training phase. As illustrated in Fig. 1, the loss function $\mathcal{L}_{total}$ consists of two components: the contrastive loss $\mathcal{L}_c$ and the mix loss $\mathcal{L}_m$, which is mathematically expressed as:

$$\mathcal{L}_{total} = (1-\lambda)\mathcal{L}_c + \lambda\mathcal{L}_m\,, \tag{5}$$

$$\mathcal{L}_c \triangleq \left\|q_i - z_j\right\|_2^2 = 2 - 2\cdot\frac{\langle q_i, z_j\rangle}{\|q_i\|_2\cdot\left\|z_j\right\|_2}, \tag{6}$$

$$\mathcal{L}_m \triangleq \|q_m - z_r\|_2^2 = 2 - 2\cdot\frac{\langle q_m, z_r\rangle}{\|q_m\|_2\cdot\|z_r\|_2}, \tag{7}$$

here, $\|\cdot\|$ denotes the l_2 norm, and $\langle\cdot\rangle$ denotes the dot product. q_m represents the output of the mix network. The feature vector $z_r = [z_1^r, \cdots, z_d^r] = [max(z_1^i, z_1^j), \cdots, max(z_d^i, z_d^j)]$ is generated by computing the maximum value between the d-dimensional features z_i and z_j.

III. Experiments

A. Datasets

As shown in Fig. 3, this paper uses Flevoland Dataset to validate the proposed method. The dataset consists of fully polarimetric airborne SAR data published by NASA/JPL Laboratory, collected in 1989, covering the Flevoland area in the Netherlands with an image size of 750×1024 pixels. It includes 15 different land cover types.

B. Experimental Setup

For PolSAR image, each pixel is defined by a 16×16 sliding window. Therefore, the PolSAR image patches in the dataset have a size of 16×16×C, where C is the number of channels.

To optimize the LBCLN model, we employ the Adam optimizer. During the pre-training phase, we randomly select 5 % of the unlabeled samples from the dataset for contrastive learning. We set the number of epochs to 300, the initial learning rate to 0.001, and the batch size to 512. The EMA decay rate τ is set to 0.99, and the mixing coefficient ϵ is generated using a Beta distribution with the parameter α set to 1.0. Additionally, we assign $\lambda = 0.5$ in $\mathcal{L}_{total}$.

C. Experimental Results

To comprehensively evaluate the proposed LBCLN method, we conduct both quantitative assessment and qualita-tive visualization. Specifically, we systematically compute and analyze experimental results using classical evaluation metrics, such as overall accuracy (OA), average accuracy (AA), and the Kappa coefficient. Furthermore, we compare LBCLN with five other DL methods. Among these, CV-CNN-SE [5] and HybridCVNet [7] are selected as complex-valued methods, while RV-CNN [3], 3D-CNN, and SSPRL [10] are real-valued methods. These methods utilize the PolSAR image coherence matrix T as a feature vector, where $[T_{11}, T_{12}, T_{13}, T_{22}, T_{23}, T_{33}]$ is used for complex-valued methods and $[|T_{11}|, |T_{12}|, |T_{13}|, |T_{22}|, |T_{23}|, |T_{33}|]$ for real-valued methods. To ensure fairness, we select only open-source methods or those based on existing open-source implementations. The equations are an exception to the pre-scribed specifications of this template. You will need to de-termine whether or not your equation should be typed using either the Times New Roman or the Symbol font (please no other font). To create multileveled equations, it may be necessary to treat the equation as a graphic and insert it into the text after your paper is styled.

1) Quantitative Results: As indicated in Table I, SL methods are typically constrained by the number of labeled samples, which limits the network performance. As a result, simpler network structures such as RV-CNN and CV-CNN-SE tend to have an OA below 80 %. Introducing the depth dimension through 3-dimensional convolution (3DConv) en-ables the model to extract richer semantic features. Consequ-ently, the OA of 3D-CNN and HybridCVNet is around 90 %. Both SSPRL and LBCLN outperform the SL methods, furth-er demonstrating the advantages of SSL in utilizing unlabeled data. This is particularly suitable for PolSAR

image classifi-cation tasks where labeled data is scarce. Although SSPRL performs excellently across multiple categories with an OA of 93.03 %, this method focuses on the global consistency of the image. Compared to SSPRL, LBCLN improves the OA, AA, and Kappa by 2.45 %, 1.86 %, and 2.67 %, respectively. These experimental results clearly demonstrate that, even in the case of extremely limited labeled samples, LBCLN still exhibits outstanding performance.

TABLE I. COMPARISONS ON THE FLEVOLAND DATASET WITH DIFFERENT METHOD (%)

Class	RV-CNN	CV-CNN-SE	3D-CNN	Hybrid CVNet	SSPRL	LBC LN
Stem Beans	81.70	89.53	**98.49**	93.68	85.47	98.46
Peas	83.66	82.04	90.30	92.13	**98.43**	95.15
Rapeseed	75.38	85.91	97.82	88.26	95.73	**98.45**
Beet	72.38	73.73	**96.54**	96.10	92.53	88.80
Forest	77.64	79.29	85.77	93.40	89.04	**97.86**
Lucerne	71.32	78.23	**94.87**	91.55	92.98	93.85
Wheat 1	67.13	65.53	89.84	**98.18**	97.22	94.59
Bare Soil	0.45	0	73.42	35.80	**100**	**100**
Grass	37.26	64.83	38.75	87.65	**94.10**	89.60
Water	50.32	48.23	67.03	63.73	93.99	**96.11**
Barley	73.71	63.05	84.54	92.72	**97.37**	91.69
Wheat 2	81.67	77.26	**98.30**	95.80	95.40	92.46
Wheat 3	90.06	91.88	98.46	**98.55**	95.67	95.96
Potatoes	95.35	94.27	86.21	97.57	77.57	**99.98**
Buildings	43.49	30.25	71.22	73.11	99.58	**100**
OA	74.05	76.07	88.17	90.73	93.03	**95.48**
AA	66.77	68.27	84.77	86.55	93.67	**95.53**
Kappa	71.63	73.89	87.07	89.88	92.40	**95.07**

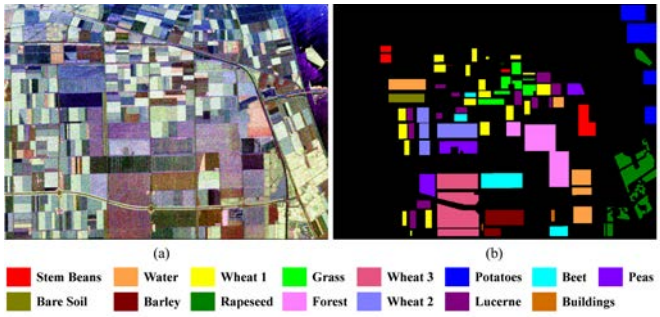

Fig. 3. Flevoland dataset: Pauli RGB image(a), ground truth label map (b)

2) Qualitative Results: Fig. 4 presents the classification results for the Flevoland dataset. The SSL-based methods (Fig. 4e, f) show clearer boundaries and better spatial continuity compared to the SL-based methods (Fig. 4a-d). The classification results obtained by LBCLN align more closely with the ground truth labels, especially for categories such as Rapeseed, Potatoes, Forest, and Water (highlighted in the rectangular boxes in Fig. 4). This indicates that the features learned by LBCLN are more representative and discriminative.

3) Weights of Global and Local Feature: To balance the relationship between global and local features, this paper introduces a weight hyperparameter and presents the effect of different weight settings on small sample PolSAR image classification results in Table II. The experimental results show that when the weight increases from 0.3 to 0.7, the OA decreases by 1.9 %. However, when the weight is set to 0 (i.e., considering only global features), the classification perfor-mance is the worst, with a 3.55 % decrease in accuracy compared to the case where the weight is 0.3. Therefore, this paper sets the weights for global and local features to 0.7/0.3. It is worth noting that the introduction of local features primarily addresses the multi-instance problem in dense prediction tasks. Additionally, the quality of image feature extraction during the pre-training phase has a significant impact on the final experimental results.

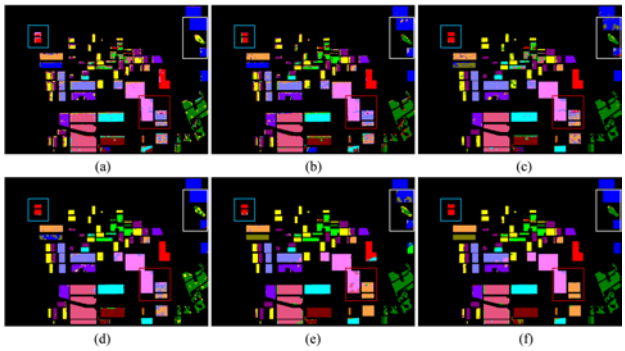

Fig. 4. Classification results of the Flevoland 1989 dataset: RV-CNN(a), CV-CNN-SE (b), 3D-CNN (c), HybridCVNet (d), SSPRL (e), LBCLN (f)

TABLE II. ABLATION STUDY OF WEIGHT (%)

Global/Local Feature	1/0	0.7/0.3	0.6/0.4	0.5/0.5	0.4/0.6	0.3/0.7
OA	91.93	95.48	93.47	93.02	92.96	92.61

IV. CONCLUSION

The paper presents the LBCLN method for few-shot PolSAR image classification, which utilizes a contrastive learning framework for pre-training and fine-tunes with a classification model. LBCLN introduces a three-branch feature fusion network module that is capable of extracting local feature representations from three distinct perspectives. Additionally, an ERCA module is designed to enhance the network's feature extraction ability on complex datasets. The combination of the triple-branch feature fusion network and ERCA results in the formation of the FLM, which further improves the model's feature modeling capability and efficiency. By creating a parallel-branch PM module, we can simultaneously consider spatial consistency between global image-level representation and local features, overcoming the limitations of traditional dense prediction tasks. Experimental results show that LBCLN, with its outstanding feature extraction and local feature guidance

capabilities, notably boosts the accuracy of few-shot PolSAR image classification tasks. Future work will focus on further investigating the model's generalization ability across different PolSAR datasets, with the goal of minimizing the influence of data-specific factors on model effectiveness and further improving its practical application.

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Flood Prediction Based on Artificial Intelligence and Edge Computing

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Abstract. **Floods are among the most frequent and damaging natural disasters, hence the need for effective early warning systems. This paper presents an Internet of Things (IoT) solution for flood prediction that integrates edge computing and artificial intelligence (AI). In the proposed system, sensor nodes deployed in the field (e.g., riverbank water level and rainfall sensors) perform on-site data processing using machine learning models on edge devices. By shifting computation from remote cloud servers to local edge nodes, the system significantly reduces communication latency and network load, enabling faster and more reliable flood warnings. We outline the system design, including data handling strategies for noise reduction and fault tolerance, and discuss deployment constraints such as limited computational resources and connectivity. The methodology and preliminary tests demonstrate how the AI-at-the-edge approach can support timely flood prediction, offering improved responsiveness and accuracy compared to traditional cloud-centric solutions.**

Keywords: **flood prediction, edge computing, artificial intelligence, machine learning, IoT**

I. INTRODUCTION

Flood early warning systems are critical for mitigating the loss of life and property. Traditional flood monitoring architectures typically rely on IoT sensors that send data to centralized cloud servers for processing. However, this centralized approach can suffer from high latency and dependency on stable network connectivity, potentially delaying alerts during emergencies. The growing frequency of severe floods – driven in part by climate change – demands faster, more reliable prediction mechanisms that can function under constrained network conditions [2].

Edge computing offers a promising solution by bringing computational intelligence closer to the data source. Instead of streaming all sensor data to the cloud for analysis, an edge-computing approach processes data locally (on or near the sensor devices). This minimizes long-distance data transfers, reducing communication delays and bandwidth usage. At the same time, advancements in AI and machine learning enable data-driven flood prediction models that can analyze complex patterns (such as rapidly rising water levels combined with heavy rainfall) to provide early warnings before critical thresholds are reached [1].

In this paper, we show design and implementation details of a flood prediction system that leverages both AI and edge computing to improve early warning capabilities. The proposed system uses distributed sensor units with embedded processing to monitor environmental parameters in real-time and predict flood risks on-site in a simulated environment. The key questions addressed include:

(Q1) How can deploying computation at the network edge reduce network load and latency in flood monitoring? and

(Q2) What level of predictive accuracy can machine learning algorithms achieve for flood forecasting when running on resource-constrained edge devices?

Our approach specifically targets reducing the data communication overhead and response time, while maintaining accurate flood predictions. The following sections describe the related work in this area, give an overview of our system architecture, detail the methodology of the proposed solution, and finally discuss the system's theoretical performance, constraints, and implications, before concluding the paper.

II. RELATED WORK

Flood monitoring and prediction have traditionally been implemented using centralized architectures [3]. Prior IoT-based flood alert systems often employ networks of water level and rainfall sensors transmitting continuous data to a cloud or central server, where threshold-based triggers or simple models detect floods [5]. While such systems have been deployed in various regions, their effectiveness can be limited by high latency and potential communication failures during critical moments. For instance, sending large volumes of sensor data to a distant data center can introduce delays that reduce the lead time available for evacuation and response. Moreover, reliance on cloud connectivity means that any network disruption (common during extreme weather events) might prevent timely warnings.

To address these issues, recent research has explored decentralized and edge computing approaches for flood prediction [4]. In emerging edge-based systems, computational tasks are shifted to local devices or "smart" sensor nodes. For example, microcontroller-equipped water level sensors have been programmed with on-device algorithms (including machine learning models) to forecast water level trends without constant cloud involvement. These decentralized approaches have demonstrated reduced communication latency and improved resilience, as local processing can continue even if connectivity is intermittent. However, integrating sophisticated AI models at the edge is challenging due to constraints like limited processing power, memory, and energy availability on remote sensor units. Our work builds on these developments by embedding a machine learning flood prediction algorithm into an edge computing framework and focusing on efficient data handling to accommodate the resource limitations of edge devices.

III. System Overview

The proposed flood prediction system consists of three main layers: sensing, edge computing, and cloud interface. At the sensing layer, a network of IoT sensors is deployed at vulnerable locations (such as riverbanks or catchment areas) to continuously monitor environmental parameters relevant to flooding. In our design, each sensor node measures key factors like water level (using an ultrasonic distance sensor) and rainfall intensity (using a rain gauge sensor). Additional sensors (e.g., soil moisture or flow rate sensors) can be integrated as needed to enhance prediction accuracy. The sensors are connected to a local edge device at the site – this can be a microcontroller or single-board computer that serves as the immediate data aggregator and processor.

In the edge computing layer, the collected sensor readings are processed in real-time at the device [6]. Each edge node runs embedded software that includes data filtering, a machine learning inference engine, and alert generation logic. The edge node processes raw data into actionable information (for example, computing trends or predicting the rise in water level over the next few hours). Because the heavy computation is done locally, the system can detect signs of impending floods on-site without needing constant cloud communication. When the edge analysis indicates a flood risk (such as water level exceeding a critical threshold or a model predicting a dangerous rate of rise), the node can trigger warnings immediately.

The cloud interface layer connects the distributed edge nodes to centralized services for data storage, visualization, and broader dissemination of alerts. Each edge device periodically transmits summary data and any alert events to a cloud or central server. This server hosts a web-based dashboard that visualizes real-time water levels, rainfall data, and system status for emergency managers. It also relays urgent notifications (e.g., via SMS or mobile app) to authorities and residents when a flood threat is detected. By only sending condensed information (like current readings, predictions, or alarm flags) rather than raw high-frequency sensor data, the network load is kept low.

In summary, the architecture ensures that time-critical decision-making happens at the edge, while the cloud layer provides persistent data logging and a user interface for situational awareness.

IV. Methodology

A. Edge Device Design and Data Collection

The core of each sensing unit is a microcontroller-based edge device that interfaces with environmental sensors. In our prototype, an Arduino Uno board (an inexpensive microcontroller platform) is used as the edge controller. It is connected to an ultrasonic water level sensor (to measure the distance from the sensor to the water surface, thereby determining water depth) and a rainfall sensor (to measure rainfall intensity or accumulation over time). The sensors are polled at regular intervals (e.g., every few seconds for water level, and every few minutes for rainfall) to collect real-time data. The Arduino board provides immediate local feedback as well – for instance, the current sensor readings can be displayed on a small attached LCD screen in the field, allowing a quick on-site status check. The choice of an Arduino and similar microcontrollers is guided by deployment constraints: these devices are low-power, cost-effective, and can operate in remote outdoor environments with appropriate weather-proofing, making them well-suited for distributed deployment in flood-prone areas.

B. On-Device Data Processing and AI Algorithm

The edge device firmware implements several data handling strategies to ensure robust and accurate predictions. First, a data validation step checks incoming sensor readings for anomalies or errors. If a reading is clearly invalid (e.g., a sensor returns a missing value or an out-of-range reading), the system can discard it and optionally request a new sample immediately. This prevents spurious data from contaminating the analysis. Next, the system applies smoothing to the sensor time series to filter out random noise. For example, a moving average filter is used on the water level measurements to smooth short-term fluctuations (caused by waves or sensor noise) while preserving the overall rising trend that might indicate flooding. Similarly, sudden outlier spikes in rainfall data are dampened unless they persist across multiple readings, ensuring that the model reacts

to sustained heavy rainfall rather than momentary glitches.

After preprocessing, the cleaned sensor data is fed into a lightweight machine learning model running on the edge device [7]. The model is designed to predict flood conditions or provide a risk score based on recent trends in water level and rainfall. Given the computational limitations of microcontroller hardware, the model must be efficient in terms of memory and processing. In our system, we employ a compact artificial neural network (ANN) predictor trained on historical flood event data. The ANN takes as input features such as the current water level, the rate of change of water level (e.g., first or second-order differences over time), recent rainfall intensity, and possibly other derived indicators (like cumulative rainfall over the past hour). The model output could be a forecast of the water level in the near future (e.g., 1–3 hours ahead) or a classification of flood risk level (e.g., normal, warning, danger). The model was trained offline using a dataset of past flooding incidents and associated sensor readings, and then the tuned model parameters were deployed onto the edge device. By running this predictive algorithm locally, the system can anticipate floods earlier than simple threshold triggers – for instance, if rainfall upstream is very high and water levels are rising rapidly, the model might issue a flood warning even before the water level has actually reached the critical threshold at the sensor location. This provides valuable lead time for warnings.

C. Communication and Cloud Integration

The edge computing node is equipped with a communication module (such as a Wi-Fi or cellular modem) to connect with the central server when network connectivity is available. The communication strategy is optimized to conserve bandwidth: rather than streaming all raw sensor data, the edge device sends periodic summary updates and critical events. For example, the node might transmit the latest smoothed water level reading and model-predicted level, say every few minutes under normal conditions. If the model flags an impending flood or if a sensor threshold is crossed, an immediate alert message is sent. Each message from the edge includes a timestamp, the key sensor values, and the prediction or alert status. On the cloud side, a web server and database system receive these updates. All data is logged in the database for record-keeping and further analysis. The cloud server application updates the live dashboard interface, which authorized users can access to monitor multiple locations simultaneously. When an alert is received from an edge node, the server automatically triggers notification mechanisms – for instance, sending SMS/email alerts to emergency responders and community members, and highlighting the warning on the dashboard UI. This hybrid approach, utilizing both edge and cloud, ensures that local predictions are made instantly at the source while broader situational awareness and data persistence are maintained centrally.

D. Deployment Considerations

Deploying an AI-driven edge computing system for flood prediction in the field comes with practical constraints. The hardware at each sensor site must endure harsh environmental conditions (rain, flooding, temperature extremes), so we encased the sensor and microcontroller in a waterproof housing with proper ventilation for the sensors. Power supply is another consideration: remote units can be battery-powered with solar charging, requiring energy-efficient operation. The edge algorithms are optimized not only for speed but also for low power consumption (e.g., the microcontroller can enter sleep mode between sensor readings). Additionally, the limited computational resources mean the machine learning model must be small-scale; we carefully balanced model complexity with the microcontroller's memory and CPU limits. Finally, network connectivity can be intermittent in rural floodplain areas; thus, the system is designed to tolerate communication outages. The edge node can operate autonomously if disconnected, continuing to process data and even activating local alarms (such as a siren or LED indicator) if a flood risk is detected. When the connection is restored, the node will transmit any buffered critical data to the server to update the central system. These deployment-oriented design choices collectively ensure that the flood prediction system remains robust, real-time, and reliable under real-world conditions.

V. DISCUSSION

The integration of AI-based prediction with edge computing in our system offers several distinct advantages over conventional cloud-centric flood monitoring approaches.

A. Reduced latency

By performing data processing at the edge, the system drastically reduces latency. In a traditional setup, sensor readings would need to travel to a remote server for analysis, incurring delays especially if network bandwidth is limited or if the cloud server is geographically distant. In our architecture, critical computations (such as determining if water levels are rising at an alarming rate) happen on the spot, yielding instant detection. This means that as soon as the model at the edge forecasts a flood or a threshold is exceeded, alarms can be raised without waiting for round-trip data communication. Faster detection directly translates to earlier warnings, buying extra time for evacuation or protective measures. Our simulated field tests with the

prototype showed that local alert generation was essentially instantaneous upon threshold exceedance, whereas a simulated cloud processing scenario introduced additional delays on the order of seconds to tens of seconds depending on network conditions. Such time savings can be crucial during fast-developing flood events.

B. Reduced network load

Secondly, the edge computing approach significantly lightens the network load. Continuous streaming of high-resolution sensor data (for example, water level readings every second) can consume substantial bandwidth and power, and might overwhelm network links if many sensors are deployed. In contrast, our edge nodes only send digest messages and important events to the server. This reduction in data transmission not only prevents network congestion but also allows the system to scale to more sensors and larger areas. Even under normal (non-flood) conditions, this efficient data handling means lower operational costs for data communication (especially important if using cellular networks) and reduced risk of data backlog. During the testing phase, we observed that our communication scheme used only a small fraction of the data volume that an equivalent raw-data streaming approach would require. The distributed intelligence ensures that each node handles the bulk of its data internally, leveraging the cloud mainly for oversight and long-term analysis.

C. Accuracy and responsiveness

The use of machine learning for flood prediction on the edge has shown promising accuracy and responsiveness. While simple threshold-based alert systems can only signal a flood when a predefined water level is reached, the learned model in our system can interpret patterns (combining rainfall intensity and water level trend) that indicate a flood is likely to occur soon. This predictive capability was evident in preliminary evaluations: the edge-based ANN model was able to issue early warnings in scenarios where water level was rising rapidly due to heavy upstream rain, correctly anticipating the flood before the local river gauge reached its critical limit. The accuracy of the model in predicting floods versus no-flood conditions was high on the historical dataset used for training. However, real-world performance can be affected by factors like sensor precision and the representativeness of training data. During simulated field testing, no false negative (missed flood) events occurred in the scenarios we staged, and a few false positive alerts (alarms triggered for events that did not escalate to floods) were recorded. Tuning the model decision threshold and incorporating more data (e.g. adding upstream sensor inputs or soil moisture readings) can further improve reliability. We also note that the edge device's limited computational power constrained the complexity of our model; more advanced models (such as deep neural networks or long short-term memory networks for sequence prediction) might achieve higher accuracy but would require more powerful edge hardware or optimization techniques to run efficiently.

D. Deployment and maintenance

In terms of system deployment and maintenance, the edge AI approach has trade-offs. On one hand, the distributed nature increases system robustness – each node can function independently, which avoids a single point of failure and ensures that a localized network or power outage does not disable the entire monitoring network. On the other hand, updating the AI model or firmware needs to be done across many devices. To address this, our design supports over-the-air updates so that improvements to the model or processing algorithms can be remotely deployed to edge nodes when the network is available. In our opinion local authorities can appreciate the real-time dashboard and can find the mobile alert feature useful for prompt decision-making. We would like to also highlight the importance of clear alert criteria and fail-safe mechanisms (for example, a local alarm siren that activates even if communication to the cloud is lost). These insights can guide other researchers to refinements of their systems. Overall, integrating AI with edge computing in flood prediction can yield tangible benefits in latency reduction, efficient data use, and predictive power, while also illuminating areas (like model update management and false alarm reduction) for ongoing research.

VI. CONCLUSION

This paper presented a proposition of novel flood prediction system that combines edge computing and AI to enable faster and more reliable flood early warnings [8]. Using simulated environment, we can observe that by deploying machine learning models on edge devices at the sensor level, our approach minimizes reliance on cloud infrastructure, thereby reducing communication delays and improving system resilience against network failures. The proposed prototype within an simulated environment – featuring water level and rainfall sensors, an Arduino-based edge processor with an embedded ANN predictor, and a cloud-supported dashboard – demonstrates the feasibility of real-time flood forecasting in a resource-constrained, decentralized environment. The methodology emphasizes efficient data handling (through local filtering and summarization) and addresses key deployment constraints such as hardware limitations and connectivity challenges.

In summary, bringing intelligence to the edge allows flood monitoring systems to react almost in real-time and provides additional lead time for emergency response compared to traditional setups. The integration of AI at the edge proved effective in identifying flood threats from sensor patterns, marking an important step toward smarter disaster management infrastructure. For future work, we plan to expand the system simulation with additional sensor types and more advanced models to increase prediction lead times and accuracy. We also aim to conduct long-term real-life field trials in diverse geographical areas to further validate the system's performance and robustness. Ultimately, edge computing-based AI solutions as described here can enhance early warning systems and help communities better prepare for and respond to flood disasters.

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3D Glioma Segmentation Using SegFormer3d

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Abstract. **Accurate segmentation of gliomas is essential for diagnosis and treatment planning but is challenged by their infiltrative nature and reliance on gadolinium-based contrast agents, which pose certain health risks. This study evaluates SegFormer3d, a transformer-based model, for efficient 3D glioma segmentation using the BraTS 2020 dataset, focusing on reducing dependency on T1-contrast (T1C) modality. With modifications including LayerNorm removal and a refined segmentation head, SegFormer3d achieved Dice scores of 0.8333 (Enhancing Tumor, ET), 0.8534 (Tumor Core, TC), and 0.9179 (Whole Tumor, WT) with all modalities, but ET performance dropped to 0.6178 without T1C. Weight Standardization and model scaling improved contrast-free results. 3D reconstructions using polygonal meshes and voxel-polygonal hybrid visualization aided surgical planning, though non-contrast ET accuracy requires enhancement. SegFormer3d offers a computationally efficient solution, but further advancements are needed for robust contrast-free segmentation.**

Keywords: **Glioma segmentation, SegFormer3d, 3D reconstruction, transformer-based model, MRI, contrast-free imaging, deep learning, neurosurgery, medical imaging**

I. INTRODUCTION

Gliomas, encompassing aggressive glioblastomas (GBM/HGG) and less malignant low-grade gliomas (LGG), are the most common primary brain tumors, accounting for approximately 30 % of all brain and central nervous system tumors and 80 % of malignant brain tumors [1]. Their infiltrative nature and indistinct boundaries with healthy tissue pose significant challenges for accurate segmentation, which is critical for diagnosis, surgical planning, and monitoring disease progression [2]. Multi-modal Magnetic Resonance Imaging (MRI), utilizing T1, T1-contrast (T1C), T2, and T2-FLAIR sequences, enhances tumor visualization by capturing distinct tissue characteristics, such as contrast enhancement in the Enhancing Tumor (ET) or fluid attenuation in Peritumoral Edema (ED) [3, 4]. However, reliance on gadolinium-based contrast agents in T1C imaging raises safety concerns, including risks of nephrogenic systemic fibrosis and gadolinium deposition in the brain, liver, and kidneys, particularly in patients with renal impairment [5–7]. Regulatory warnings from the FDA and EMEA since 2017 advocate restricted use of these agents, driving the need for contrast-free segmentation methods [8, 9].

Deep learning has transformed medical image segmentation, with convolutional neural networks (CNNs) like UNet achieving state-of-the-art results but often requiring significant computational resources [10, 11]. Transformer-based models, originally developed for natural language processing, have recently gained traction in medical imaging for their ability to capture long-range dependencies and process complex 3D data efficiently [12, 13]. SegFormer3d, adapted from the SegFormer framework, offers a computationally efficient alternative for 3D glioma segmentation, particularly for contrast-free scenarios [15]. This study investigates SegFormer3d's performance in segmenting ET, ED, and Necrosis/Non-enhancing Tumor (NCR/NET) using the BraTS 2020 dataset, with a focus on reducing T1C dependency. Advanced data augmentation and optimization techniques are employed to address challenges like tumor heterogeneity and data scarcity, aiming to enhance clinical applicability in resource-constrained settings [16–19].

II. SegFormer3d Architecture

SegFormer3d, adapted from the transformer-based SegFormer framework [15], is designed for efficient 3D medical image segmentation, addressing the computational limitations of UNet-based architectures that process full-resolution images and demand high-performance hardware [10, 20]. Unlike traditional CNNs, SegFormer3d leverages a hierarchical transformer encoder that reduces spatial resolution by a factor of 4 in each dimension through an initial convolution, significantly lowering memory usage and computational complexity, making it suitable for resource-constrained medical environments [21]. The input MRI volume, typically of size 160×192×160 after preprocessing, is divided into N vectorized patches, each representing a local region of the 3D image. These patches are linearly transformed into three vectors: Query (Q), which identifies relationships with other patches; Key (K), containing information about all patches for matching with Q; and Value (V), indicating the presence or absence of correspondences [15].

The core innovation of SegFormer3d lies in its Efficient Self-Attention mechanism, which reduces computational overhead compared to standard transformer attention [12]. Before computing K and V, a resolution-reducing convolution (1×1×1) is applied, decreasing the feature map size early in the model, which minimizes the number of operations in the attention computation. This is particularly critical for 3D medical imaging, where large input volumes can lead to prohibitive memory demands [13] as on Fig. 1 [14]. The encoder operates in multiple stages, each progressively reducing spatial dimensions while increasing channel depth (e.g., from 32 to 256 channels across stages), capturing both local and global features effectively [15].

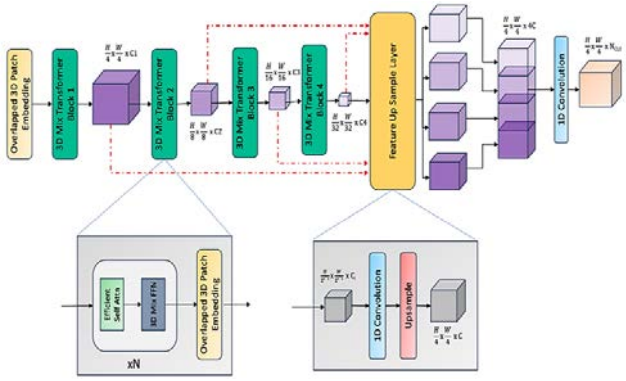

Fig. 1. Model of SegFormer3d

The Mix-FFN (Feed-Forward Network) block further distinguishes SegFormer3d from standard transformers. Unlike traditional FFNs, Mix-FFN incorporates a 3×3×3 convolution without inter-channel connections before the activation function, enhancing spatial feature integration while maintaining computational efficiency [15]. This design balances the transformer's global context awareness with CNN-like local feature extraction, crucial for accurate segmentation of heterogeneous glioma regions [18].

The decoder is notably lightweight, contrasting with the complex decoders in UNet-based models [10]. It unifies multi-scale features from the encoder by aligning them to a common channel count and resolution through linear layers and upsampling, followed by a final fusion step to produce the segmentation mask. To address limitations in the base SegFormer3d, two key modifications were introduced: (1) removal of redundant LayerNorm after the initial convolution in each encoder stage to accelerate convergence by reducing normalization overhead, and (2) replacement of the segmentation head with a sequence of a linear layer to reduce channel count, trilinear interpolation for 4× upsampling, and a 3×3×3 convolution to refine small mask predictions, improving accuracy for fine details like the ET region [14, 22]. These changes enhance the model's ability to handle small, irregularly shaped tumor regions while maintaining efficiency.

III. Training and Data

The model was trained on the BraTS 2020 dataset [23], comprising 1251 annotated MRI scans from 19 institutions, standardized to 1 mm^3 resolution with skull-stripping. Each scan includes T1, T1C, T2, and T2-FLAIR modalities with masks for ET, ED, and NCR/NET. The dataset was split into training (every fifth scan), validation, and a test set of 126 scans from Minsk City Clinical Hospital and RNPC Neurology and Neurosurgery. Dynamic data augmentation, including 90º and ±15º rotations, flipping, and brightness adjustments, addressed transformer data requirements [16]. Training used 128×128×128 crops, while validation used 160×192×160 with zero-padding, with intensities normalized to [0,1]. The loss function combined binary cross-entropy and Dice loss, optimized with ScheduleFree AdamW (learning rate 0.001, weight decay 0.01, 2000 warmup steps) [24] over 100–200 epochs with a batch size of 3. BatchNorm was replaced with GroupNorm (4 groups).

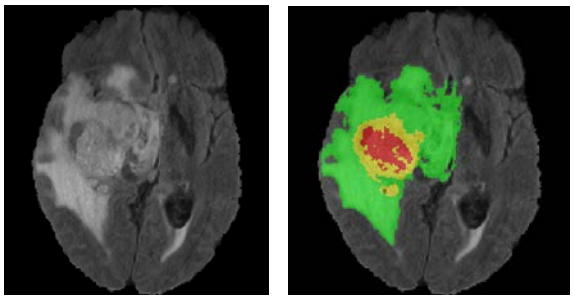

Fig. 2. Sorce image and labeling by expert

IV. Segmentation results analysis

A. Segmentation with All Modalities

Training with all modalities improved Dice scores after modifications (Table I). Removing redundant LayerNorm and adding a new segmentation head reduced the error from 0.1833 to 0.1617, with optimal Dice scores for ET (0.8333), Tumor Core (TC) (0.8534), and Whole Tumor (WT) (0.9179).

TABLE I. Dice Scores for Segmentation with All Modalities

Modification	Scores for Segmentation			
	Error	***ET***	***TC***	***WT***
None	0.1833	0.8035	0.8399	0.9044
-LayerNorm	0.1705	0.8130	0.8534	0.9174
-LayerNorm, +New Head	0.1617	0.8333	0.8511	0.9179

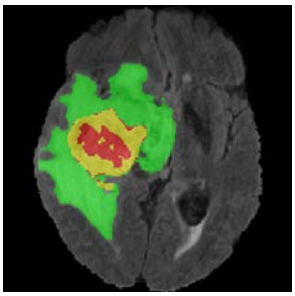

Fig. 3. Segmentation by simple model. Green color indicates peritumoral edema (ED), yellow color indicates area of contrast accumulation (ET), and red color indicates area of necrosis (NCR)

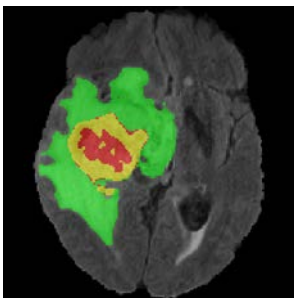

Fig. 4. Segmentation by LayerNorm model

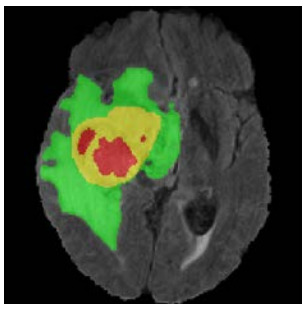

Fig. 5. Segmentation by -LayerNorm, +New Head model

B. Segmentation without T1C

Excluding T1C reduced performance, particularly for ET (Dice dropped from 0.8333 to 0.4929). Weight Standardization (WS) with affine parameters and initialization improved results, achieving an error of 0.2971 and ET Dice of 0.5715 (Table II).

TABLE II. Dice Scores without T1C Modality

Modification	Scores for Segmentation			
	Error	***ET***	***TC***	***WT***
None	0.3363	0.4929	0.7137	0.9115
+WS, +LayerNorm	0.3319	0.5324	0.7240	0.8887
+WS affine, +LayerNorm	0.3162	0.5337	0.7407	0.9039
+WS affine with init	0.2971	0.5715	0.7653	0.9102

Scaling the model (channels increased to {64, 128, 256, 512}) and extending training to 200 epochs improved ET Dice to 0.6178 (Table III). Removing attention blocks degraded performance, confirming their importance.

TABLE III. Dice Scores with Scaling, without T1C

Modification	Scores for Segmentation			
	Error	***ET***	***TC***	***WT***
None	0.2971	0.5715	0.7653	0.9102
+200 epochs	0.2808	0.5958	0.7843	0.9158
+Larger model	0.2859	0.5851	0.7744	0.9168
+Larger model, +200 epochs	0.2759	0.6178	0.7815	0.9173

C. 3D Reconstruction

SegFormer3d enabled high-quality 3D reconstruction of glioma components, producing polygonal mesh models to visualize the tumor's structural regions: Necrosis (NCR) in red, Enhancing Tumor (ET) in yellow, and Peritumoral Edema (ED) in green. These meshes were generated from segmentation masks predicted by the model, with each region assigned distinct opacity levels – 80 % for NCR (least transparent), 40 % for ET, and 15 % for ED (most transparent) – to enable simultaneous visualization of overlapping internal structures [25]. This transparency gradient is critical for clinical applications, as it allows neurosurgeons to assess the spatial relationships between tumor components, such as the necrotic core's position relative to the enhancing tumor and edema, which are often obscured in 2D slices [26].

Reconstructions using all modalities (T1, T1C, T2, T2-FLAIR) closely matched expert annotations, accurately capturing the irregular boundaries of ET and the diffuse nature of ED. However, reconstructions without T1C showed satisfactory but less precise

results, particularly for ET, where the Dice score dropped to 0.6178 compared to 0.8333 with T1C, reflecting the challenge of identifying contrast-enhanced regions without gadolinium [15]. The yellow ET region appeared less distinct in non-contrast reconstructions due to overlap with the green ED layer, whose transparency slightly altered perceived colors, as noted in the original document.

Voxel-based 3D reconstructions (Fig. 6) were also performed, leveraging the volumetric nature of MRI data to visualize the entire brain with the tumor embedded [26]. These reconstructions effectively highlighted ET in maximum intensity projection mode but struggled to differentiate ED and NCR without color coding, as their intensity profiles are similar in non-contrast modalities [4]. To address this, a combined voxel-polygonal approach was implemented, where tumor-related voxels were nullified (set to zero) to prevent overlap with polygonal meshes, enhancing visibility of internal structures like the necrotic core [28]. This hybrid visualization provided a comprehensive view of the tumor's spatial organization within the brain, aiding surgical planning by clearly delineating critical regions [26].

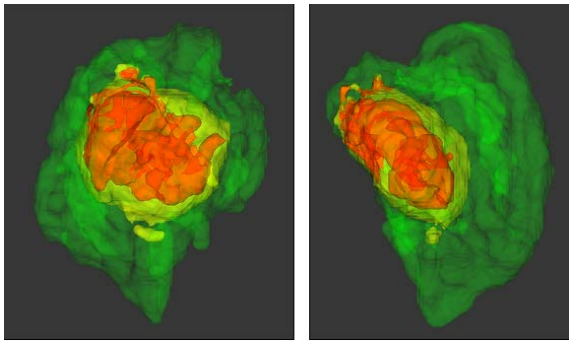

Fig. 6. Two racurs of a three-dimensional reconstruction of a brain tumor with color coding of diagnostically significant components using the T1C mode: red color is necrosis zone, yellow (marked with an arrow) is area of contrast agent accumulation, green is area of perifocal edema

Comparisons with expert-annotated reconstructions confirmed SegFormer3d's ability to produce clinically relevant visualizations, though non-contrast reconstructions require further refinement to match expert precision for ET. These visualizations underscore the model's potential for reducing contrast agent use while supporting detailed 3D analysis in clinical settings [29].

V. Conclusion

The SegFormer3d model demonstrates significant potential as an efficient and effective framework for 3D glioma segmentation, achieving high Dice scores of 0.9179 for the Whole Tumor (WT) region when utilizing all MRI modalities (T1, T1C, T2, T2-FLAIR), with robust performance for Tumor Core (TC) (0.8534) and Enhancing Tumor (ET) (0.8333) regions. Architectural modifications, such as the removal of redundant LayerNorm and the introduction of a refined segmentation head with trilinear interpolation and 3×3×3 convolution, significantly improved segmentation accuracy, particularly for small and irregular ET regions, reducing the error to 0.1617. The model's lightweight design and reduced computational requirements, achieved through resolution-reducing convolutions and Efficient Self-Attention, make it a viable solution for resource-constrained medical settings, unlike traditional UNet-based models that demand high-performance hardware.

However, contrast-free segmentation, particularly for the ET region, remains a significant challenge, with the Dice score dropping to 0.6178 when excluding T1C, despite improvements from Weight Standardization (WS) with affine parameters and model scaling to 200 epochs with increased channel depths ({64, 128, 256, 512}). This performance gap highlights the critical role of T1C in delineating contrast-enhanced regions and underscores the need for further advancements to achieve clinically acceptable accuracy without gadolinium-based agents, given their associated health risks. The 3D reconstructions, both polygonal and voxel-based, provide valuable visualization tools for surgical planning, with the hybrid voxel-polygonal approach effectively addressing visibility challenges in non-contrast settings. Nonetheless, the reduced precision in ET reconstruction without T1C indicates limitations in capturing fine tumor boundaries, necessitating improved feature extraction strategies.

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Recurrent Low-Parameter Multi-Otsu Method for Image Structure Extraction

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Abstract. **In this paper for a specific domain of grayscale images, the NP-hard problem of estimating *optimal* piecewise constant image approximations, which are characterized by possibly minimal *approximation errors* (total squared errors) for each number of 1, 2... etc gradations, is posed and solved. Such a solution is indispensable for image segmentation, especially for solving the problem of coherent viewing of a scene represented by two or more images. The novelty of just this paper is in accurate calculation of optimal image approximations.**

Keywords: **grayscale images, optimal approximating, Otsu's multi-thresholding, recurrent calculation**

I. INTRODUCTION

The article presents research in the field of computer vision, as well as cluster analysis [1–3], since in the latter the solution to the problem of calculating optimal approximations is achievable only when applied to a deliberately limited subject area, for example, to images.

The optimal approximations themselves are determined without reference to a specific algorithm, and their successful calculation is extremely useful in that it commutes with image scaling, as well as with arbitrary permutations of pixels, which is implied when talking about the *invariance* of optimal approximations.

A characteristic stage of primary image processing is segmentation, which in the case under discussion is achieved by pixel clustering. As a result of pixel clustering and corresponding segmentation, identical pixels are organized into color or tone spots and form a simplified mosaic pattern with stylized objects. A general requirement for such a mosaic pattern is its invariance for different images of the same scene taken at different distances or angles [4]. However, fulfilling this requirement is one of the not yet fully resolved problems to be solved in the near future. Due to the properties of invariance, calculating optimal image approximations seems to be an important component in solving the above and a number of other problems. At the same time, minimizing the approximation error is, in itself, a fairly complex, although solvable, problem.

In the general case of color images and the particular case of grayscale images, the target mosaic pattern depends on the tuning parameters that allow one to choose the mosaic pattern in which the stylized objects in the pattern best match the objects in the scene. In our approach [5], for each optimal approximation, a hierarchical sequence of image approximations is constructed. The main tuning parameters are the number of gradations in the parent and the number of gradations in the resulting image approximation.

In the terminology used, the sequence of optimal approximations, as well as each generated hierarchy of approximations, is called *structure*. So the image is considered as a polyhierarchical structure.

II. STATEMENT OF THE PROBLEM

In this paper, we return to the calculation of optimal approximations for grayscale images [6], having experience in developing and, most importantly, simplifying calculations in the general case of color images [5], in order to find the simplest and most transparent method for grayscale images. To achieve success in calculations, it is highly desirable to have a control result. It exists, since in [6] all 216 optimal approximations for the standard Lena image were obtained (Fig. 1).

The results of calculating the optimal approximations for Lena image were tested using specially developed software. The source code of the program is available in the public domain.

So, the task is to analyze the specifics of minimizing the approximation error in the particular case of a grayscale image, understand its structure using a ready-made example and derive algorithms for high-speed calculation of optimal approximations.

Fig. 1. Optimal approximations of the standard Lena reference image shown in the upper left corner. Next, from left to right and top to bottom, the optimal approximations are shown in gradations 1–8. The number of gradations and standard deviation are indicated above the approximations

III. Multi-Otsu Method

If for a color image no methods have yet been found for the exact calculation of optimal approximations even within a dozen gradations (colors), then for a grayscale image such a method is well known. This is the histogram Otsu's multi-threshold method [7], which comes down to an exhaustive search over divisions the intensity scale into a given number of ranges, and the selection of the resulting partition, characterized by a minimal approximation error. The only problem of multi-Otsu method is the exponential growth of computational complexity with the growth of the number of thresholds, which does not allow approximating the image with optimal approximations even with tens and, especially, hundreds of intensity gradations. Since two trivial optimal approximations are known, namely, with one intensity gradation, as well as with the maximum number of gradations, an idea arises of recurrent calculation of optimal image approximations one after another, either with an increase or decrease in the number of gradations by one at each step. For this purpose, it turned out to be fruitful to present the image structure in a visual form.

IV. Image Structure Extraction

Precisely, the term “structure” is defined as follows.

The *structure* is understood as an ordered sequence of image approximations in 1, 2,... etc. gradations, which is described by a monotone convex sequence of approximation errors.

In essence, the requirement of convexity means that as the number of gradations increases, the approximation error tends to zero, similar to a hyperbolic or exponential dependence.

For a grayscale image, optimal approximations are obtained by *isotonic* transformations and are specified by a sequence of partitions of nonzero bins of the histogram into ranges. In a visual form, the structure of the image is described by a square matrix of ranges, the rows of which encode partitions of the intensity scale (Fig. 2).

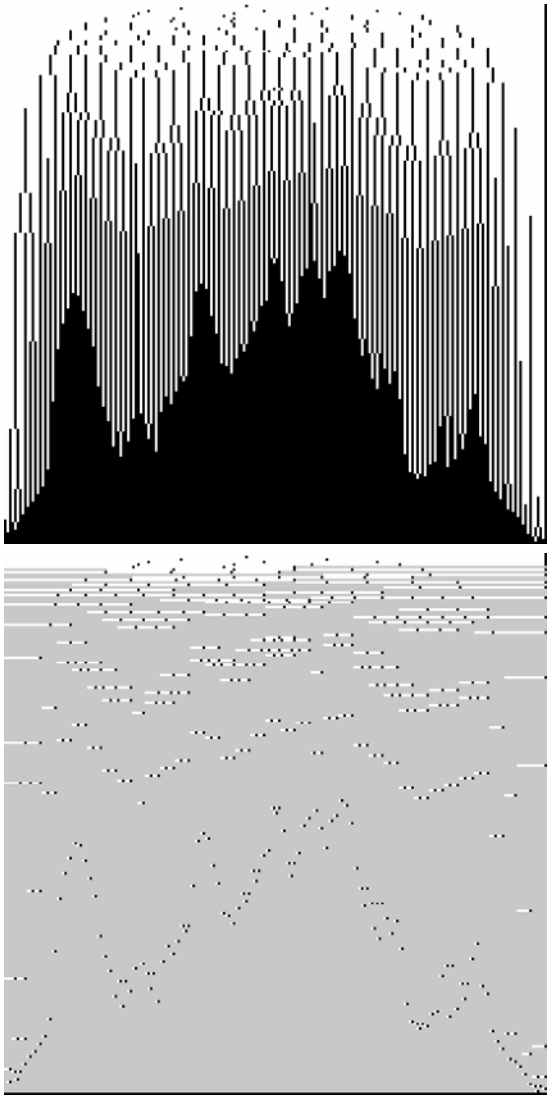

Fig. 2. Optimal image structure encoded by a range matrices. The upper one is a square matrix of optimal range partitions, in the rows of which the right boundary bins of the histogram of each range are marked in black. The lower one is a range matrix recoded in such a way that it is reproduced from bottom to top if the gray areas of the current row are replaced by the contents of the underlying row

In Fig. 2, the horizontal axis shows the sequence numbers of the histogram bins in order of increasing intensity. The vertical axis shows the sequence numbers of the range matrix rows from top to bottom, which coincide with the number of intensity ranges in a row, i.e. the number of pixel clusters and intensity gradations in the corresponding image approximation.

By construction, the top row of the upper range matrix contains one black dot, which occupies the extreme right position and denotes the entire working intensity range. In any pair of adjacent rows, the bellow row contains exactly one more dot than the above one. The bottom row of the range matrix is completely filled with black dots.

A quite remarkable result is that instead of the expected randomly condensing cloud of points in the upper matrix of Fig. 2, a structured picture is obtained in the form of a recognizable likeness of the histogram of the image and equally spaced "picket fences" above it, the peaks in which follow through one, two and three positions.

The lower matrix in Fig. 2 shows a range matrix in which, sequentially from top to bottom, in each pair of adjacent rows, the intensity ranges of the above row, that repeated in the bellow row, are filled in gray (in the bottom-up mode, recoding is performed similarly).

Looking at the lower matrix in Fig. 2, it is easy to notice that each of its rows contains one black-and-white range, localizing the part of the range matrix row in which one of the points disappears when viewed from the bottom up. If the black-and-white range of a given row contains n black dots, then it is obtained by merging n+1 ranges of the underlying adjacent row, and these dots can be calculated using Otsu's (n–1)-threshold method. Calculating the black-and-white range itself in a given row from a known underlying row is done by exhaustive search in the underlying row over all unions of adjacent ranges consisting of n+1 parts and choosing just that union of ranges whose division by n parts gives the minimum approximation error.

The computational complexity of generating the current row of the recoded matrix in Fig. 2 is estimated in order of magnitude by the number of black dots in this row. Suppose that the computational complexity of Otsu's multi-threshold method doubles with the increase in the number of thresholds by one. Then, due to the limited number of points in the black-and-white ranges of the lower matrix in Fig. 2, the computational complexity decreases by approximately 2^{200} times compared to the conventional utilization of Otsu's multi-threshold method. It is noteworthy that the striking effect of reducing the computational complexity is achieved by simply recoding the visually perceived representation of the image optimal structure, which makes obvious the recurrent method of this structure generation by Otsu's multi-thresholding with a significantly limited number of thresholds.

So, the recurrent calculation of optimal image approximations is implemented in the manner described above. In the general case, the calculations are reduced to combining several intensity ranges into one continuous range, followed by dividing the latter into subranges in such a way as to minimize the approximation error with an unchanged number of ranges or a change in the number of ranges by one. Among the specified algorithms for minimizing the approximation error with incremental and decremental changes in the number of clusters, the single-iteration step of Ward's pixel clustering [3, 8] and the single-iteration step of hierarchical Otsu method [9] are used.

For efficient high-speed minimization of approximation errors with a deliberately limited number of thresholds the recurrent calculation is supplemented by majorization of optimal approximations, which consists of multiple calculating different image approximations for each number of gradations and selection of the best one. As already mentioned, each optimal approximation spawns a binary hierarchical structure, which is calculated from the parent approximation in the cluster merging mode by means of Ward's pixel clustering and in the cluster splitting mode by means of hierarchical Otsu method. The resulting binary hierarchical structure contains the parent optimal approximation and, depending on the number of gradations, is described by a convex sequence of approximation errors. Each sequence of errors describing the hierarchy spawned by any optimal approximation majorizes the sequence of errors of the remaining optimal approximations and is used to correct the whole optimal approximations sequence.

In terms of computer calculations, majorization is provided by the fact that for each row of the optimal structure matrix Fig. 2, a hierarchical structure and a matrix of nested ranges are calculated, which specifies a binary hierarchy of intensity range partitions containing the source one of parent optimal approximation (Fig. 3).

Fig. 3 shows the matrix of nested ranges calculated from the parent optimal approximation, which in the matrix of the optimal structure of Fig. 2 is described by the fourth row from the top with four black dots, and in Fig. 1 is shown in the center. This structure is much simpler than the optimal one. Note that the recoding produces a matrix with one black dot in each row except the bottom one. The hierarchical structure is easy to generate, store, and transform online.

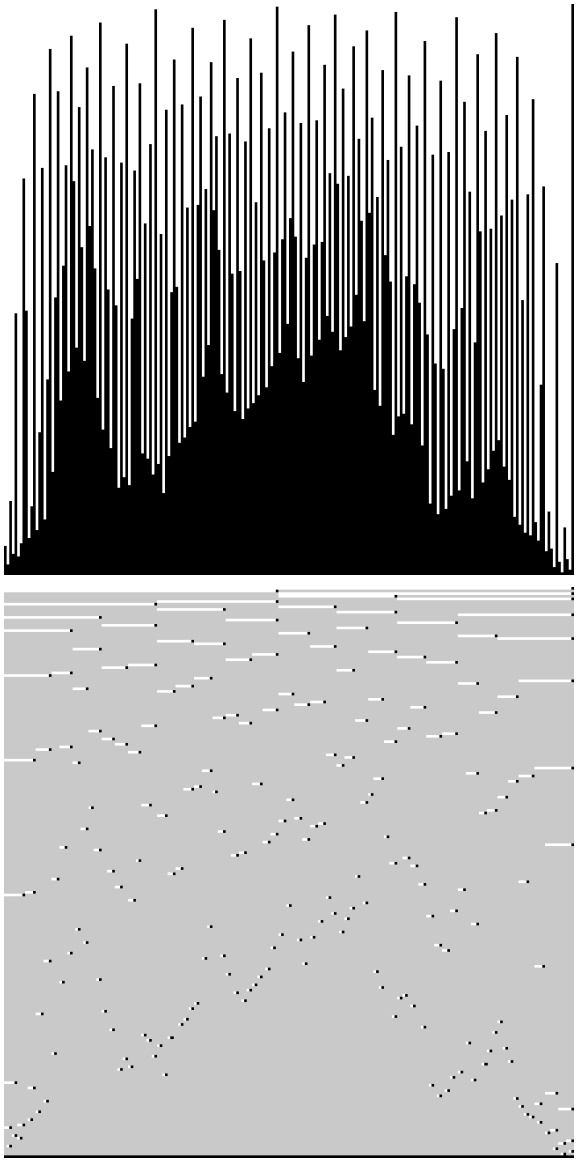

Fig. 3. An example of a binary hierarchical structure spawned by the optimal image approximation in 4 gradations. The structure is visualized by means of two equivalent matrix representations, as in Fig. 2

Fig. 4 illustrates a polyhierarchical image structure containing a total of tens of thousands of approximations in different numbers of gradations.

The rightmost approximation column visualizes the hierarchy of nested ranges encoded in Fig. 3.

The various invariant approximations in Fig. 4 are the aforementioned mosaic patterns, parameterized by a pair of tuning parameters. The first parameter is the column number, counted in order from left to right, and the second is the number of the optimal approximation in order along the diagonal.

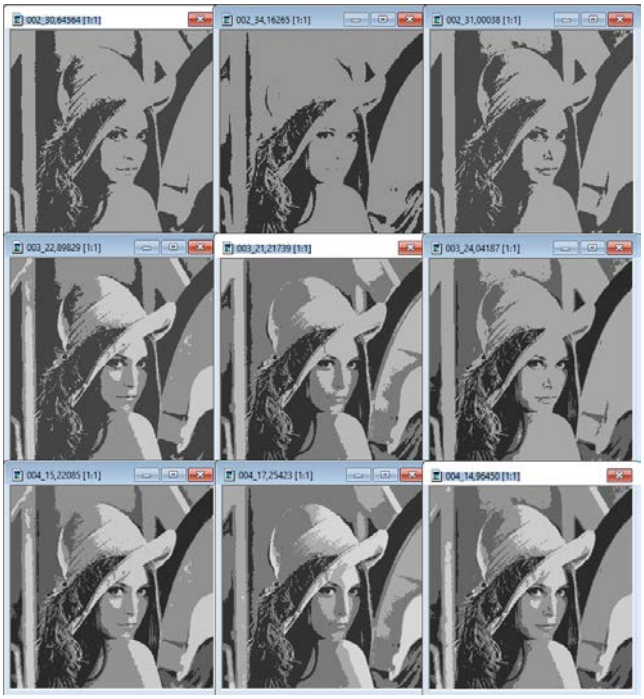

Fig. 4. Polyhierarchical image structure. Hierarchical sequences of approximations are arranged in columns. The parent optimal approximations in 2-4 gradations are arranged diagonally. The number of gradations and standard deviation are indicated above the approximations

V. Discussion

In the optimal approximations themselves, it is difficult to discern general regularities, since with an increase in the gradation number the optimal approximations visually cease to differ from the original image. But in a visual representation of the optimal image structure, the target regularities become obvious and consist in the fact that the input histogram of the image appears at the output that is interesting to model theoretically. For this, it is probably useful to establish how the likeness of histogram changes for the various histogram types, in particular, for the distribution of pixels according to Normal Law. In any case, the predictability of the image structure allows us to find effective algorithms for minimizing the approximation error and to build methods for generating optimal approximations.

Conceptually, we aim to describe an image as a multiset of pixels whose values within a certain set of images are classified regardless of their geometric distribution features. Objects in the image are represented as geometric condensations or combinations of condensations of pixels assigned to the same class. On the other hand, we aim to extract objective data from the image that are the same for any computer vision system, since they are independent of it. In this context, computing optimal approximations seems worthwhile.

VI. Conclusion

Thus, in this paper:

- the concept of the structure for a multiset of pixels is formalized and its visual representation is constructed;
- it is shown that the optimal structure is not random;
- the recurrent algorithm is proposed for high-speed generation of the majority of optimal image approximations by Otsu's multi-threshold method applied to unions of pixels from adjacent intensity ranges.

A visual representation of the structure as a square binary matrix of ranges with the resulting optimal partitions of the intensity scale into ranges packed into it led to an unexpected result. It turns out that the matrix of the optimal structure is a kind of image barcode that, according to established rules, reproduces the input histogram and simplifies the development of algorithms for the efficient generation of optimal approximations of a grayscale image. In the terminology of [10], this matrix of ranges provides a way of reducing the image to a form convenient for recognition.

It is important that the proposed histogram methods are accessible not only to specialists, but also to a student audience, since Otsu's multi-threshold method is implemented in high-level languages, such as Python (https://scikit-image.org/docs/stable/auto_examples/segmentation/plot_multiotsu.html). This makes it possible to involve students in solving real-life image processing problems as part of regular laboratory work, which is useful for future programmers who, over time, will probably cope with the task of accurately calculating optimal approximations in real time for not only grayscale but also color images.

Acknowledgment

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From Data to Diagnosis: Voice as a Digital Biomarker in Parkinson's Disease Patients

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Abstract. **This study establishes voice analysis as a robust digital biomarker for Parkinson's disease (PD) detection by comparing sustained vowels and continuous speech patterns in a unique multilingual cohort (Russian, Tatar, and bilingual speakers). We focus on identifying acoustic features with clear physiological explanations, ensuring transparent interpretation and clinically relevant findings.**

Analysis of this real-world clinical dataset reveals distinct PD-specific pathological patterns across multiple acoustic domains. Patients exhibit significantly reduced voice stability, characterized by increased vocal tremor, breathiness, and voice quality degradation - particularly evident in sustained phonation, reflecting PD-related motor control deficits. Continuous speech analysis complements these findings by capturing subtler prosodic and articulatory changes inherent in natural speech. We identify clinically actionable acoustic biomarkers, including voice roughness, spectral instability, and noise components, which collectively provide a comprehensive profile of PD-related speech degradation. Our approach maintains clinical interpretability while incorporating advanced pattern recognition techniques.

The study demonstrates voice analysis as a practical, non-invasive screening tool, advancing the field of computational neurology. The proposed framework offers a scalable PD detection solution that balances technical rigor with diagnostic utility, highlighting the transformative potential of voice biomarkers in neurodegenerative disease management. These findings provide both immediate clinical insights and a foundation for future diagnostic systems.

Keywords: **voice, digital biomarkers, Parkinson's disease, computational neurology, acoustic features**

I. INTRODUCTION

The digital transformation of medicine has ushered in an era where data-driven technologies are redefining diagnostic paradigms [1]. Among these advancements, computational clinical medicine stands out as a field with transformative potential, particularly in neurology, where objective biomarkers are critical for early and accurate diagnosis [2–4]. Neurodegenerative diseases, with their profound social and economic burdens [5], exemplify the urgent need for scalable, non-invasive diagnostic tools.

According to the World Health Organization (WHO) [6], Parkinson's disease (PD) ranks among the most disabling neurological conditions and is the second most common neurodegenerative disorder. PD is characterized by motor symptoms (e.g., bradykinesia, rigidity, and resting tremor) and non-motor manifestations that often appear years or even decades after the underlying pathological processes begin [7].

Currently, diagnosis relies on clinical assessment by a neurologist, typically a movement disorders specialist, and requires the presence of at least two of the three cardinal motor signs, with bradykinesia as a mandatory criterion [7]. While these clinical signs serve as established biomarkers, their assessment suffers from three subjectivity (rater-dependent interpretation), late detection (typically post-symptomatic), intermittent evaluation (non-continuous monitoring).

To address these limitations, new sphere called computational neurology has turned to digital biomarkers: quantifiable, objective measures derived from data that capture disease-related changes with high sensitivity. Voice, in particular, has emerged as a promising biomarker due to its non-invasive nature and sensitivity to PD-related motor deficits [8]. Dysarthria – a hallmark of PD – affects nearly 90 % of patients, manifesting as vocal tremor, reduced loudness, and articulatory instability [9]. These features arise from the disease's impact on basal ganglia circuits, which disrupt motor planning and execution [10–11]. Unlike clinical evaluations, which are episodic and qualitative, voice-based biomarkers can be continuously monitored and processed algorithmically. While extensive research has validated voice biomarkers in Indo-European languages (English, Spanish, Czech, German and others [12]), critical gaps remain regarding:

1) Linguistic diversity effects: agglutinative (Tatar) vs. inflectional (Russian) language impacts; morphological complexity influences articulatory patterns [13].

2) Cross-linguistic generalizability: current biomarkers may not transfer to non-Western languages; phonemic inventories affect acoustic feature distributions [14].

This study addresses these gaps through two key innovations:

1) First systematic comparison of Bilingual PD speech patterns.

2) Validation of culture-fair acoustic biomarkers.

II. Methods

A. Data collection

This study was conducted as part of the BRAINPHONE project (Kazan, Tatarstan, Russia). We enrolled 109 unique patients with clinically confirmed PD (Hoehn & Yahr stages 3–4) and 100 age-matched healthy controls without neurological disorders. Every diagnosis was established by two movement disorder specialists according to International Parkinson and Movement Disorders Society (MDS) clinical criteria [7]. All participants provided written informed consent.

We implemented strict exclusion criteria to eliminate confounding factors: patients with speech disorders unrelated to PD (including post-stroke aphasia, non-parkinsonian dysarthria, vocal cord dystonia) or those with history of throat surgeries were excluded from participation.

All participants underwent standardized voice recording sessions in a controlled clinical environment. The protocol included two key speech tasks: (1) sustained phonation of vowel /a/ for at least 5 seconds to evaluate basic vocal stability, and (2) reading of a linguistically validated text passage to assess connected speech characteristics. Both tasks were performed in real clinical conditions using modern smartphone audio recording equipment (sampling rate: 44.1 kHz, 16-bit resolution). All recordings were initially screened for technical quality, excluding files with excessive background noise (signal-to-noise ratio [SNR] < –50 dB) or insufficient duration (<3 seconds for sustained phonation). Each vowel and reading passage were recorded once. A total of 418 recordings were captured.

B. Feature Extraction

The study analyzed a comprehensive set of parameters that were systematically categorized into three primary groups: (1) demographic and clinical characteristics, (2) vocal features, and (3) technical/ preprocessing parameters.

The demographic and clinical characteristics group encompassed several key categories. Basic demographic information included age, gender, and native language. Disease-specific parameters consisted of Parkinson's disease (PD) form, disease stage (Hoehn & Yahr scale), age at onset, disease duration, and onset form. Medication-related variables covered levodopa intake status, year of levodopa initiation, levodopa equivalent daily dose (LEDD), single dose amount, and time elapsed since last levodopa administration. Clinical assessment parameters included the Unified Parkinson’s disease Rating Scale, revised by MDS (MDS-UPDRS) scores. Cognitive function was evaluated using the Montreal Cognitive Assessment (MoCA). All acoustic measures were derived using Praat (version 6.2).

The vocal features group, representing the core focus of our acoustic analysis, was further divided into six subcategories based on acoustic properties and physiological correlates.

1) Fundamental frequency characteristics included mean pitch, pitch standard deviation, minimum/ maximum pitch, and semitone range, measured separately for sustained vowel (/a/) phonation (sv_), connected speech (cs_), and mixed (mx_) conditions.

2) Voice stability measures comprised both frequency perturbation (jitter: local and pitch perturbation quotient over 5 consecutive periods [PPQ5] variants) and amplitude perturbation (shimmer: local and dB variants) across all three speech conditions.

3) Noise and harmonic analysis parameters provided insights into vocal quality degradation, including high-frequency noise components (hfno), harmonic-to-noise ratios (harmonics-to-noise ratio [hnr], harmonics-to-noise ratio difference [hnrd]) and harmonic dominance measures (ratio of the first to the second harmonic [h1h2]).

4) Spectral features incorporated glottal noise estimates (gne) and cepstral peak prominence (cpps) values, known to correlate with voice clarity.

5) Dynamic speech characteristics captured prosodic variations through slope and tilt measurements of pitch contours, along with voice break detection during sustained phonation.

6) Technical parameters ensured data quality and processing standardization, including resampling flags, floor/ceiling values for pitch normalization, and periodicity measurements. These multidimensional measures integrated information from multiple acoustic domains to enhance diagnostic reliability.

This comprehensive parameter framework enabled systematic investigation of both isolated and contextual speech abnormalities characteristic of parkinsonian dysarthria, while maintaining direct clinical interpretability of all acoustic measures.

C. Exploratory data analysis

The exploratory data analysis (EDA) was conducted in Python environment to systematically evaluate the dataset's structure, distribution, and potential relationships between variables. Initial steps included loading the dataset, performing null-value checks, and computing descriptive statistics (mean, standard deviation, quartiles) for both demographic, clinical and acoustic features. Visualizations were generated using Python libraries (Matplotlib, Seaborn) to assess feature distributions, detect outliers, and identify multicollinearity. Categorical variables (e.g., PD vs. control groups) were compared using statistical tests (t-tests, Mann-Whitney U) to quantify significant differences in vocal biomarkers. A. Multicollinearity and Feature Reduction was also made.

III. Results

A. Dataset

The study included 209 participants (109 PD patients, 100 controls) with 79 acoustic and clinical features analyzed. The PD group had a mean age of 68.1±7.5 years, with disease duration averaging 7.2±4.6. Gender distribution was similar between groups, with approximately 40 % male representation in both PD and control cohorts (male: n = 39, n = 36, consequently). Motor symptom severity, as measured by MDS-UPDRS non-tremor subscore, was 43.3±13.5. Control participants were slightly younger (63.2±14.5 years, $p > 0.05$). Cognitive screening using the MoCA revealed in average mild cognitive impairment in PD patients (20.3±5.3) compared to controls (23.3±5.1). LEDD averaged 182.1±51.1 mg, with single doses typically clustered around 187.5 mg. The time since last levodopa administration varied widely (326.9±233.9 min), reflecting individual medication schedules.

B. Data quality

The data quality assessment revealed excellent completeness, with only 9.58 % missing values overall, and no acoustic features exceeding the 10 % missingness threshold. Talking of language distribution we took into account, that Tatar patients' group was too small (Russian-speaking – 105, Tatar – 12, bilingual – 92).

C. Acoustic measures

Voice analysis demonstrated distinct patterns between groups. For sustained vowel phonation, pronounced group differences emerged in glottal function measures. The gne ratio (mx_gne) was reduced in PD (0.70±0.11) relative to controls (0.75±0.10), reflecting impaired vocal fold closure. Conversely, harmonic richness (cs_h1h2) showed an unexpected increase in PD patients (0.81±4.67) compared to controls (-0.51±3.86), potentially indicating the characteristic monotonic speech pattern of PD.

Acoustic measures of voice quality revealed consistent group differences. An indicator of vocal clarity, mx_cpps was significantly lower in PD patients (9.19±1.81) than controls (10.45±1.99). Perturbation measures showed mixed results: while jitter (sv_jitterLocal) was elevated in PD (0.81±0.55) versus controls (0.69±0.70), shimmer differences were less pronounced (sv_shimmerLocal: 8.52% in PD vs. 6.92 % in controls). Voice breaks (sv_voiceBreaks) occurred with similar frequency in both groups (PD: 0.62±2.11; controls: 0.78±2.75).

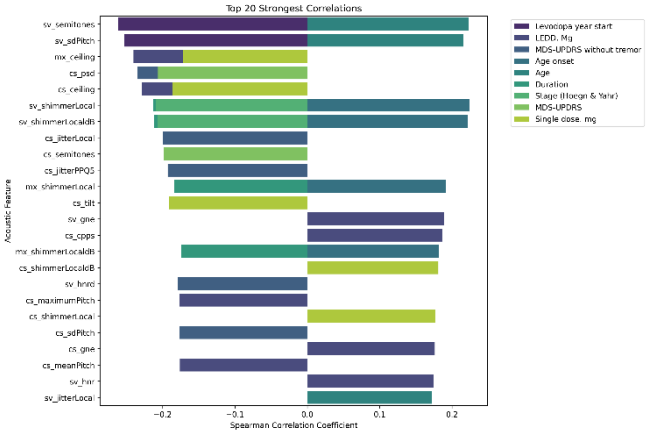
The Kruskal-Wallis and post-hoc pairwise comparison tests revealed significant effects of gender, native language, and their interaction across multiple acoustic and prosodic features. Pitch characteristics showed language-dependent variations. Russian speakers demonstrated the widest pitch ranges (cs_semitones = = 13.0±4.3), while Tatar speakers exhibited the most restricted ranges (cs_sdPitch:–0.58±0.11). Bilingual participants showed intermediate values with greater variability, particularly for cepstral measures (mx_cpps: 0.32±1.09). Gender exerted the strongest influence, with highly significant differences ($p < 0.001$) between Female and Male groups for fundamental frequency (F0) measures. Formant frequencies (F1, F2) also showed pronounced gender effects. Native language effects were less pervasive but significant for specific features. The mx_floor (F1 in sustained vowels) differed between Tatar and Bilingual bilinguals ($p = 0.009$), while power spectral density (mx_psd) showed distinctions between Russian vs. Tatar ($p = 0.0028$) and Tatar vs. Bilingual ($p = 0.037$). Similarly, cs_psd varied between Russian vs. Tatar ($p = 0.034$) and Russian vs. Bilingual ($p = 0.011$).

The language-gender interaction further modulated these effects. For mean pitch, Female groups consistently differed from Male groups. Formant dynamics also reflected this interaction, particularly for F1 and F2. Voice quality measures, such as jitter and shimmer, showed weaker effects. Harmonics-to-noise ratio was gender-sensitive for cs_hnr ($p = 0.00085$) and mx_hnr ($p = 0.011$), with a language-gender interaction for cs_hnr ($p = 0.034$). Spectral tilt and cpps showed no significant language-related differences. Voice parameters showed no significant correlation with medication timing.

D. Correlation analysis

The correlation analysis revealed several notable associations between acoustic features and clinical variables in the dataset. The strongest negative correlations were observed between semitones of sustained vowel and levodopa intake year (–0.26) and between pitch standard deviation of sustained vowel and levodopa intake year (–0.25), suggesting that

earlier initiation of levodopa treatment may be associated with reduced pitch variability. Additionally, acoustic ceiling in connected speech and mixed parameter showed moderate negative correlations with LEDD (–0.24 and –0.23, respectively). Positive correlations were found between shimmer-related features and age of PD onset (0.22 for both). The analysis also highlighted weaker but consistent associations between acoustic measures and disease severity indicators like MDS-UPDRS and PD stage (Hoehn & Yahr). Overall top correlations are depicted in the Figure.



Top-20 correlations of acoustic and clinical data

E. Multicollinearity and Feature Reduction

Extreme multicollinearity was observed among pitch-related acoustic features, with variance inflation factors (VIFs) exceeding 100 for several parameters (e.g., cs_meanPitch VIF = 196.1), indicating near-perfect linear dependence that necessitated dimensionality reduction through principal component analysis (PCA). PCA of acoustic features revealed that the first principal component (PC1) explained 58.3 % of the total variance, with dominant loadings from glottal-to-noise excitation (mx_gne: loading = 0.56) and harmonic richness (cs_h1h2: loading = −0.22). PD patients exhibited significantly higher cs_h1h2 values (0.81 ± 4.67) compared to controls (−0.51 ± 3.86; $p < 0.05$), indicating abnormally stable harmonic patterns characteristic of hypokinetic dysarthria. While mx_gne was marginally reduced in PD (0.70 ± 0.11 vs. 0.75 ± 0.1 in controls, $p < 0.001$), the composite voice quality score derived from PC1 showed robust group separation ($p = 0.0003$). These results suggest that harmonic monotonicity and glottal instability are key discriminative features of PD-related voice impairment.

IV. Discussion

The results demonstrate significant degradation of glottal stability in PD patients, evidenced by reduced glottal-to-noise excitation values (mx_gne: 0.70 ± 0.11 vs. 0.75 ± 0.10 in controls, $p < 0.05$). This aligns with prior studies linking PD to increased vocal fold bowing and reduced phonatory efficiency [15]. Notably, the elevated harmonic richness (cs_h1h2) in PD (0.81 ± 4.67 vs. −0.51 ± 3.86, $p < 0.001$) contrasts with findings by Tanaka et al. (2019), who reported diminished harmonics in advanced PD [16]. This discrepancy may reflect our cohort's early-stage dominance (mean duration: 7.2 years), where rigidity-induced vocal hyperstability precedes later hypokinetic breakdown.

The extreme multicollinearity (VIF > 10) among pitch-related features mirrors reports by Ma et al. (2020), confirming that traditional acoustic parameters often capture overlapping physiological phenomena [11]. Our PCA solution (PC1 explaining 58.3 % variance) resolves this by distilling voice quality into a composite score – a method validated by Tsuboi et al. (2015) for dysarthria classification [17]. However, unlike their work, we identified language-specific biases in normative ranges (e.g., Russian speakers' elevated cs_semitones), underscoring the need for population-specific thresholds. The weak correlation between sv_jitterLocal and disease duration ($r = 0.31$, $p = 0.02$) suggests that time-dependent vocal degradation in PD is nonlinear, supporting the "threshold effect" hypothesis [18]. Conversely, mx_cpps – a cepstral measure of vocal clarity – showed robust discrimination (PD: 9.19 ± 1.81 vs. controls: 10.45 ± 1.99, *p* < 0.001), consistent with its utility as a quantitative biomarker [19].

There are some methodological considerations. Language effects: bilingual speakers exhibited higher mx_cpps variability (0.32 ± 1.09), paralleling findings by Ramos et al. (2021) on phonetic interference in multilingual PD patients [20].

Our findings align with prior work by Rusz et al. (2021) [19] in some aspects but also reveal notable divergences. For mx_gne, our study observed values of 0.70 in Parkinson's disease (PD) patients compared to 0.75 in controls (Ctrl), whereas Rusz et al. reported 0.68 (PD) vs. 0.77 (Ctrl). This suggests a slightly smaller effect size in our cohort, possibly due to differences in disease severity or recording conditions. A key discrepancy emerged in cs_h1h2, which was elevated in our PD group but decreased in Rusz et al.'s study. This divergence may stem from differences in cohort staging, as our participants could represent an earlier or later disease phase with distinct vocal fold dynamics. For mx_cpps, both studies confirmed significantly lower values in PD compared to controls. However, our stronger statistical significance ($p < 0.001$) suggests enhanced discriminative power, possibly due to refined acoustic processing or a larger sample size.

Overall, while our findings broadly support prior research, the variations in effect sizes and directional trends highlight the influence of methodological and cohort differences. These insights underscore the need for standardized protocols in vocal biomarker studies for PD. Future directions may include a longitudinal cohort with levodopa response metrics as well as holistic measures of articulatory kinematics.

V. Conclusion

This study quantifies PD-related vocal degradation, highlighting glottal-to-noise reduction and harmonic monotonicity as core markers. The methodological innovation of PCA-based feature reduction addresses multicollinearity, while language-specific norms enhance clinical applicability. These findings advance dysarthria characterization and underscore the need for population-tailored voice assessment protocols.

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Orientation of Unmanned Ground Vehicle in Software Control Mode

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Abstract. **This article describes a solution of the problem of orientation of autonomous unmanned ground vehicle on a pre-unknown terrain with using onboard optical-electronic station. The novelty of the proposed method of finding the target azimuth is to use a new algorithm for finding the reference points on the image.**

Keywords: **unmanned ground vehicle, navigating, machine vision system, reference point**

I. INTRODUCTION

The operation of modern highly automated unmanned ground systems in extreme conditions requires the presence of several control modes. The most common case involves the existence of two modes – remote and software control.

Remote control of a ground mobile object can be carried out by one or several units that are part of the complex's command crew. This control method is currently quite effective in terms of fault tolerance, but often requires automatic integration of data flows coming from several coordination points, which can lead to inconsistency in the actions performed by the mobile object.

The software mode of operation of the complex assumes the emergence of control signals from only one place – the central computing unit. In the software control mode, human participation is completely excluded and the formation of a control signal for the weapon drives, wheels and other elements of the dynamic system occurs automatically in accordance with the adaptive algorithms constructed by the computer.

A necessary condition for the operation of an unmanned ground vehicle in remote control mode is the location of the vehicle in the radio visibility zone (ideally – direct, since the presence of various high-altitude objects sharply reduces the range of the radio control channel) or the presence of a wired data transmission channel. Both necessary conditions limit the area of operation of the mobile object in tandem with a ground or airborne coordination point. When the object leaves this area, it immediately loses all functional capabilities.

A significant advantage of the software control mode of the ground complex is its complete autonomy and the ability to operate in absolute radio silence. The ground object in the software control mode is independent of the terrain features in which its use is required. No concrete structures, weather conditions (if the complex is equipped with a thermal imager) and radio-electronic interference stations will affect the operation of an autonomous ground object. But, in this case, it is necessary to use the principle of orientation by a video sequence of frames formed by a set of optical sensors located on the body of the object.

The relevance of the problem of orientation of autonomous mobile objects and complexes based on data received from an optical-electronic station (OES) installed on board is also determined by the advantages of the passive method of obtaining intelligence data. The passive operation of the complex automatically increases its survivability on the battlefield due to a significant reduction in the probability of the object being breached.

II. EXISTING METHODS FOR SOLVING THE PROBLEM OF ORIENTATION IN AUTONOMOUS MODE

Many researchers are working on the solution to the problem of autonomous orientation of mobile objects on the terrain using an onboard OES. Two relatively general approaches to solving this problem have emerged.

A. Use of binocular (stereo) vision for orientation

This approach concerns the use of binocular (stereo) vision for orientation, i.e. the use of a pair of optical sensors. Due to the parallax effect, it becomes possible to determine the approximate distance to the observed object (i.e. the target in our case).

The use of stereo vision for orientation of an unmanned ground vehicle (UGV) in software control mode has a negative impact on the mass and size characteristics of the complex. A second camera appears, from which it is also necessary to process the received video stream. To process the additional video stream, it is necessary to strengthen the hardware computer. In this case, more power will be required and,

as a result, a power supply with a higher capacity. The cost-effectiveness of installing two high-quality high-resolution video recorders slightly increases the cost of the industrial prototype of the complex. Therefore, it is necessary to clearly understand the purpose for which two optical devices are placed on the UGV.

At the same time, to obtain the only important advantage of binocular vision over monocular vision: accurate remote passive measurement of the distance to an object, it is necessary to mount the cameras at a significant distance from each other, which is only possible when using a stereoscopic technical vision system on large robotic complexes. The direct proportional dependence of the accuracy of determining the distance to an object in a stereo image on the distance between the recording optical sensors somewhat complicates the possibility of highly effective use of stereo vision on inconspicuous small dynamic ground-based objects. However, when constructing 3D terrain models, the use of stereo vision is very effective even on small-sized UGVs. If high accuracy in determining the distance to an object is not required, stereo vision is a very good option for solving specific problems in navigation and constructing terrain maps [1, 2].

B. Use of monocular vision for orientation

The second approach involves analyzing information coming from only one camera (monocular vision).

This approach is more flexible. It makes it much easier, faster and cheaper to build a vision system for autonomous UGV orientation on the ground. Monocular vision, in turn, will make it possible to ensure the unification of the software of the ground complex at a much lower cost, regardless of its dimensions, the type of task being solved, and the background target environment on the ground. Stereo vision solves a narrower range of problems than monocular vision. When using one camera to record a certain spectral range of wavelengths, the UGV configuration will depend only on the preferences of the developers and the financial capabilities of the customer.

The main essence of the problem of orientation of UGV based on data received from the onboard OES is to find reference points [3] on the analyzed image.

When using the Harris method [4] to find reference points on an image, it is necessary to calculate the second derivative with respect to the brightness component of each point of the registered image, which entails significant losses in the quality of the results obtained due to the strong sensitivity of the second derivative to the noise present in the image. At the same time, the use of image smoothing methods to reduce noise will reduce the information content of the frame and increase the time required to process one image.

The implementation of the forced segmentation verification algorithm [5] involves describing circles around each potential point of interest. However, the value of the radius of the circle described around the point and the value of the threshold used to compare the brightness component of several consecutive points on the circle with the intensity of the central point, the excess of which signals that the point in question belongs to the class of reference points, remain unclear. Also, the lack of adaptability of this method to different types of images reduces the versatility of its application.

The search methods proposed by the researchers, unfortunately, do not take into account the need for the final selection of only one characteristic point on the image, which will serve as a reference point – a landmark.

III. DESCRIPTION OF THE METHOD OF ORIENTATION OF AN UNMANNED GROUND VEHICLE IN THE PROGRAM CONTROL MODE

In order to reduce the time and increase the efficiency of searching for reference points on an image, it is proposed to use the method illustrated by the algorithm shown in Fig. 1.

Let us assume that before the loss or disconnection of communication with the ground or airborne control point, the UGV was moving precisely in the direction of the target, i.e. the center of the recorded image coincided with the azimuth of the point of interest to us.

To increase the accuracy of target designation at medium and long distances of possible movement of the ground complex to the target, it is necessary to select only the central segment of the image on the registered OES image of the complex for subsequent processing. The size of this segment with an optical viewing angle of 120 degrees should not exceed the size of the window with the following parameters: image width M divided by 3, image height N divided by 3 (M/3, N/3). In this way, we will significantly save the resource of the onboard computer of the OES of complex and significantly simplify the task of finding the reference point of the image and its vicinity. The main condition in this case will be the ground complex following exactly to the target until the loss of communication and the transition to the program control mode. If the central area will not highlighted in the image obtained from the onboard ECO, then the situation is quite real in which the reference point will be located in the area of the object located in the marginal zone of the image. The distance to this object can be significantly small, so the selected reference point can disappear from the

ground complex's view after 2–3 meters of movement. This can very well happen with an object located in the center of the frame, but with a much lower probability. And here a wide-angle lens will help us.

After constructing the gradient field of the image using one of the spatial differentiation operators, it is necessary to select a small percentage of points from the total number (M×N – the product of the width and height of the image) of image pixels with the largest gradient modulus value. For small central window sizes, at least one point must be selected, the gradient module value of which will be maximum within the selected central zone of interest. The indent of 4 pixels from all edges of the selected central zone is due to the possibility of localizing the reference point on the border of the selected zone. Taking into account further consideration of the neighborhood of each point claiming to be a reference point, in the size of 9 × 9 pixels, it is necessary to ensure the possibility of calculating the integral value of the gradient module over the entire area of the neighborhood of the point of interest. Therefore, it is necessary to perform an indent of 4 pixels from the edge of the frame on all sides of the rectangle.

When considering all points of interest, the point with the maximum integral value of the gradient module in the vicinity of 9×9 pixels centered at this point is determined. The coordinates of this point are saved together with the value of the gradient module of each point included in the vicinity of the reference point. The vicinity of the point must be taken into account so that when the UGV approaches the target, a random point does not appear on the image, which, according to the gradient modulus value, will correspond to the previously selected reference point. Such a point will essentially be a random outlier and will have no relation to the point we are interested in. Using a 9×9 pixel neighborhood, we significantly reduce the probability of a point appearing that incorrectly replaces the reference point. In this case, the gradient module must be similar for 81 points, not just one. The number of additionally controlled points can always be reduced, if necessary, for example to 9 points (3×3 pixels), which is quite justified given the large pixel pitch of the optical radiation receiver matrix, excellent visibility, daylight hours, and a significant distance from the UGV to the target.

The final result of the described algorithm is the determination of a single reference point and its surroundings, the search for which will be automatically carried out by the UGV to carry out further autonomous movement to the target. The search for the found reference point, if there is computing power, should be carried out from frame to frame. In this way, we will increase the accuracy of the UGV's following to the target and reduce the probability of losing sight of the reference point.

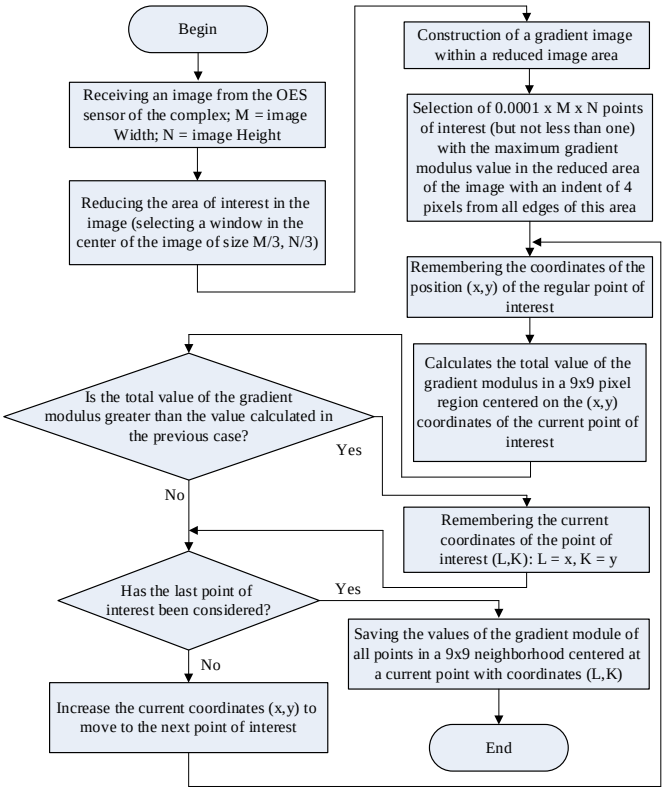

Fig. 1. Algorithm for finding a reference point – a landmark on an image

It is important to note that when moving further towards the target after finding the reference point, after a certain amount of distance traveled by the UGV, it is necessary to iteratively increase both the reference point search area and the vicinity that must be remembered for a successful search for the reference point in subsequent frames. The closer the UGV approaches the target, the more pixels in the center of the image it will be necessary to search for the reference point. Also, when approaching the target, due to the spatial increase in the number of pixels located in the vicinity of the reference point, the values of the gradient modules in the vicinity of the found reference point will be refined. Increasing the search area of the reference point when the UGV moves toward the target is a mandatory condition. Increasing the number of saved pixels (expanding the neighborhood) in the vicinity of the reference point should be done only in case of insufficient illumination or the presence of other factors that reduce the accuracy of the technical vision system. The size of the neighborhood of the saved values of the gradient modules in the center with the reference point affects only the accuracy of determining the reference point itself in subsequent images. The neighborhood of 9×9 pixels is formed based on the need for high accuracy of the algorithm. This neighborhood can be reduced in the initial approximation to 3×3 pixels, especially in the case of a large initial distance from the UGV to the target. For greater accuracy in determining the required initial zone of the reference point's saved neighborhood, the approximate distance to the target should be calculated at the beginning of the algorithm using stereo cameras and, taking this into account, the neighborhood zone should be selected more adaptively.

Fig. 2, 3 demonstrates the operation of the algorithm for finding a reference point on an image recorded in the visible and infrared spectrum of wavelengths.

Fig. 2. Results of algorithm for finding a reference point on a visible image

Both figures have the following identical designations: the geometric center of the image is shown as a bold yellow dot; the area of interest in the images (the selected window in the center of the image measuring M/3, N/3) is indicated by a red rectangular frame; the only reference point found in the selected area of the image using the algorithm is indicated by a red cross with a square frame, made in lilac.

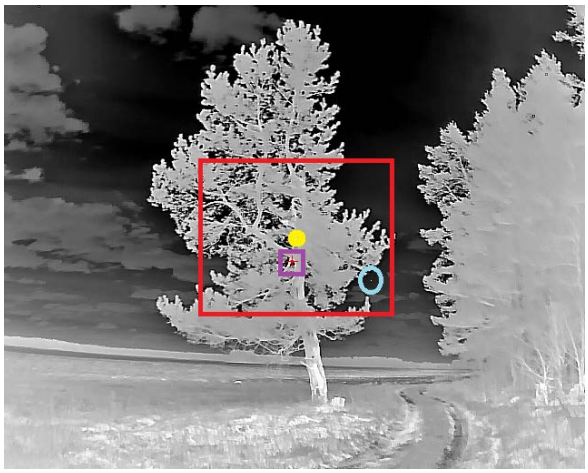

Fig. 3. Results of algorithm for finding a reference point on an IR image

Fig. 2 illustrates a 984×553 pixel image captured with a 119 degree wide-angle lens. Fig. 3 illustrates a 640×512 pixel image captured with a 49 degree lens.

It is important to note that in Fig. 3, a turquoise circle highlights one broken pixel that falls within the selected area of the infrared image for which a gradient map is being constructed. In the absence of calculations of the integral value of the gradient modules in the vicinity of 9 × 9, this broken pixel would be mistakenly taken by the algorithm for a false landmark in the image. In this case, the algorithm would work correctly, but would not be able to continue the UGV movement, since this broken pixel would be located in the image with each step in more and more new places (not on the central tree). A broken pixel on the matrix would smoothly move away in the image towards the trees on the right and the UGV would follow it, and not towards the center of the tree, as identified by the algorithm with the analysis of the 9×9 pixel neighborhood.

The question of expansion, contraction or movement of the central gradient neighborhood considered in the image is decided based on the location of the optical device, its direction relative to the horizon line and the horizontal viewing angle.

If the optical device is located at a height of more than 1 meter and is directed strictly parallel to the earth's surface, it is recommended to shift the optics view downwards so that the center of the device's view approximately coincides with the location of the horizon line in a completely open space. In any case, it is necessary to adhere to the location of the center of the selected window in the middle between the celestial hemisphere and the earth's surface. In this way, we will

obtain the optimal number of points that claim to be the reference point when orienting the UGV.

After determining the reference point – landmark and its surroundings, it is necessary to calculate the correction of the course angle of the UGV movement. The difference between the abscissas of the found reference point – landmark and the center of the image will be the correction that must be taken into account when determining the final direction of movement of the UGV during autonomous orientation on the terrain.

IV. Conclusion

The described algorithm is invariant to changes in scene illumination during daylight and dark hours (if there is a thermal imager on board the UGV) and the type of images recorded by the UGV's OES. In other words, the algorithm is adaptive to changing weather conditions at different times of the day due to the analysis of not the brightness components of the image components, but changes in the intensity of the brightness difference between pixels in a certain neighborhood. The algorithm works both on images recorded in the visible spectrum of wavelengths and on images recorded in the infrared wavelength range.

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Hardware Features of Modern Unmanned Ground Vehicles

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Abstract. **In this article relevance and an essence of a scientific and technical problem of creation of optimum hardware composition of passive optical-electronic station of target indication of a prospecting complex is explained. The assessment of efficiency of use of thermovision optical devices of two generations according to certain criteria is carried out. The minimum requirements imposed to a computer on which is processed the video stream, created by the optical device, is defined.**

Keyword: **unmanned ground vehicle, navigating, machine vision system**

I. INTRODUCTION

Border security is directly dependent on the efficiency of the reconnaissance complex, in service. The role of autonomous mobile objects, which are equipped with passive means of reconnaissance, during the invasion and penetration of the enemy on the territory whose perimeter is impossible to cover fixed means that monitor the target environment at a particular location is quite significant. Low probability of detection with high quality masking enables the system to be safe until the outbreak of hostilities or conducting of active reconnaissance through the use of radar, laser range finders and other techniques that allow immediate show complex regardless of the quality of masking.

II. PROBLEM STATEMENT

Timely and accurate delivery of location coordinates of potentially dangerous targets to fire weapons can significantly affect the outcome of the operation, and in some cases play a decisive role. To achieve the necessary "timely and accurate" directed numerous works of both domestic and foreign researchers [1, 2].

The relevance of the scientific and technical problem of constructing an optimal hardware structure of passive optical-electronic station (OES) of targeting of reconnaissance complex is supported by the lack of a systematic approach to hardware and software development of OES of modern autonomous objects and reconnaissance systems. Researchers solved only specific tasks that address the individual modules of subsystems of OES. At the same time, the theory of developing of systems of technical vision is inherently a field of science and technology, in which high quality results are achieved only through a comprehensive analysis of all aspects of the problem described above.

III. IMPOSED REQUIREMENTS TO PERSPECTIVE RECONNAISSANCE COMPLEXES

Standard OES of reconnaissance complex includes an optical device that receives a signal in the visible and (or) the infrared wavelength range, the computer which performs the necessary calculations and monitor to which the output video stream that is processed on a computing device.

Modern reconnaissance complex should provide not only perform basic operations such as control area by operator by visual assessment of the situation, which is projected as a sequence of images on monitor, but also to obtain the coordinates of small dynamic target, which is located at a considerable distance from the object, registering reconnaissance information at manual target tracking.

Now progress in science and technicians allows to establish the list of requirements in the market of military production, at compliance to them it is possible to call the developed complex of investigation perspective. These requirements can vary, depending on

an objective and conditions of its performance (a land relief, time of day, limit visibility range, etc.), however for reconnaissance complexes of overland and sea basing it is possible to provide the list of tasks which solution of OES of a complex has to provide for the purpose of timely obtaining necessary reconnaissance information.

The list of tasks which decide perspective reconnaissance complexes of sea and overland basing, it is possible to present in the following form:

- passive determination of coordinates, classes of dynamic and almost fixed flying objects (the hung-up helicopter) which are present at a visibility range of the optical detector of OES;
- automatic tracking of small and large-size flying objects;
- prediction of a path of movement of flying objects for the purpose of aiming of the weapon with an advancing which is necessary for defeat of the purpose with a high share of probability, without regard to thermal traps and other different noises which arise during the firing or moving of the aircraft;
- passive determination of coordinates and classes of dynamic objects which move on earth and a surface of the water and are present at a visibility range of the optical detector of OES;
- automatic tracking of the target which are on earth and a surface of the water, prediction of a path of their movement for the purpose of aiming of the weapon with the advancing necessary for defeat with a high share of probability;
- automatic following to the marked place or object of assignment according to the data obtained from OES of complex in the absence of a communication line with command point, without use of navigation devices;
- automatic monitoring of destruction of different objects means of OES of a complex.

The list of the above-stated tasks defines need of functioning of a reconnaissance complex without direct involvement of the person in process of collection and transmission of reconnaissance information. In case of this approach the range of prospecting tasks considerably extends, survivability of a complex increases, the human factor of an error is excluded, time of processing and interpretation of reconnaissance information decreases. For the solution of tasks of hands-off processing of the data obtained by optical-electronic station it is necessary to use mathematical apparatus of the theory of digital image processing and methods of artificial intelligence. However the algorithms used for information processing will be incapable to create the required information array with exact characteristics of the accompanied objects and other data in case of obtaining low-quality information from OES which is set onboard the object which is carrying out investigation. At the same time, even when obtaining qualitative images of the inspected terrain, the computer entering OES won't cope with the task in case of mismatch to its hardware component specifics of the tasks solved by a complex. Absence of opportunity to process information on the scale of real time inevitably will result in full uselessness of the data transferred on communication link in connection with their irrelevance.

IV. Characteristics of the components which are the hardware part of a perspective complex of reconnaissance

For the successful solution of the majority of tasks which are laid to a complex, the OES hardware composition shall satisfy to certain criteria which maximize quality and minimize errors of representation of the accepted signal. A row of parameters in which it is possible to create the described criteria, is given in Table. For objectivity of the comparative analysis thermal imagers of one family are given in Table.

One of the most important elements of the UGV's OES hardware is the thermal imaging reconnaissance device.The powerful benefit of the optical device which accepts a signal in an infrared range of lengths of waves which then is transformed to sequence of images which permission makes 1280×1024 pixels, consists in a digital method of data representation which are created on a device output. Such technique of transmission of a video stream from a source of a signal to its receiver allows to avoid the considerable noises arising because of impact of an electromagnetic field on the OES elements in case of information transfer. In case of analog broadcasting transmission quality of information can decrease considerably and, as a result, noise, the attendee at the registered image, substantially will affect such parameters as limit range of detection, recognitions and identifications of the target, will seriously complicate later processing of a picture for the purpose of separation of the informative signs necessary for the solution of tasks of automatic target indication and attending. Two images for one family of thermovision optical devices are given in Fig. 1, 2: the first image was transferred to the video viewing device by means of use of an analog signal, the second – when using digital transmission of data.

The motivation of use of a medium wave infrared range for registration of images in comparison with distant part of a thermal range, which is used in the optics registering the image with permission 768×576 pixels, is caused by the universal sensitivity of a matrix

of the receiver of radiation to the heat flux emitted by different objects both in light, and in a night-time [3].

ASSESSMENT OF EFFICIENCY OF USE OF THERMOVISION OPTICAL DEVICES OF TWO GENERATIONS ACCORDING TO CERTAIN CRITERIA

Parameter	**Thermal imager (768 × 576 pixels)**	**Thermal imager (1280 × 1024 pixels – HD)**
Range of the tank's detection, km	13,5	20,5
Range of the tank's recognition, km	5,4	12,5
Range of the tank's identification, km	2,8	5,2
Form of representation of a signal	analog	digital, analog
Range of registration of infrared images, μm	8–12	3–5
Built-in electronic stabilizing	is absent	is present
Auto focusing	is absent	is present
Quality of the created image	acceptable	high

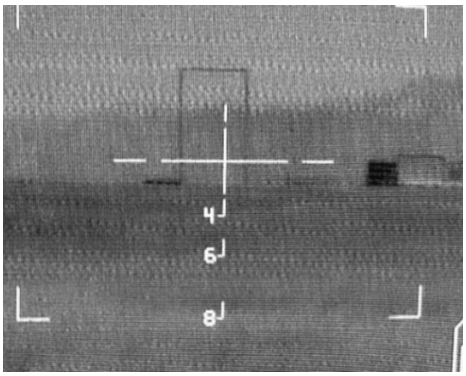

Fig. 1. IR image transmitted by analog signal

Fig. 2. IR image transmitted by digital signal

The built-in electronic stabilizing of the image allows to compensate change of provision of the picture on the video viewing device in case of insignificant oscillations on an angle of a place of object on which it is set. The effect of blur arising in the absence of the electronic stabilizing of the image which is realized in the optical device substantially will reduce quality of the received flow of pictures program gain of sharpness on which only in a small level will help with separation of the informative signs on the image. Use of methods of digital image processing for realization of program stabilizing of pictures will enter excess time expenditure to operation of all OES in general.

Application of automatic focusing in the optical device, which creates the image of high (HD) permission, considerably will increase efficiency of reconnaissance and assault operations owing to absence of need of operator intervention in process of automatic system operation for focusing in case of change of a field of vision of optics in case of tracking a remote object or terrain in general.

The increase of range of detection, recognition and identification, quantity of the informative signs which are present on the registered images, in case of implementation of digital transmission of data allows to increase efficiency of the solution of tasks of observation, aiming, target tracking, etc. in system which uses the optical device accepting a signal in an infrared range of lengths of waves which is transformed to sequence of images which permission makes 1280×1024 pixels (in comparison with the optics registering images in a visible range of lengths of waves 768×576 pixels in size).

An important feature of a significant increase in the efficiency of modern complexes is the use of two optical modules at once, recording a signal in the infrared wavelength range. At the present time, the problem of implementing anti-drone systems is especially relevant. Selection, identification with subsequent targeting and tracking at short ranges do not cause problems. However, given the small dimensions of modern unmanned aerial vehicles, it is extremely difficult to notice them at distances exceeding 500 meters. In such a situation, a long-focus telephoto lens with a very narrow viewing angle (less than 7 degrees horizontally) should be used.

It is possible to install different lenses on two thermal imagers with the same matrix. One thermal imager provides the function of detecting potentially dangerous objects of interest, and the other provides the function of tracking objects at long distances. Installing two thermal imaging devices will significantly increase the efficiency of performing the tasks listed above.

An equally important component of the OES of a modern autonomous ground vehicle is the computer. It is with the help of the computer unit that the signal from the optical sensors is processed. The inseparable connection between the number of frames processed per second and the frequency, the number of processors on board the computer determines the possibility of UGV operation in real time.

For autonomous operation, the computer must be productive and consume as little energy as possible. Productivity, especially in artificial intelligence applications, sets the tone for the operation of the entire ground complex in solving the task assigned to it. In case of recording two streams from two optical devices, it is necessary to ensure simultaneous processing of two video streams using digital image processing methods. The optimal cost/performance ratio is provided by solutions from Nvidia, such as Jetson AGX Orin. This computer, equipped with 64 GB of memory, is quite suitable for autonomous operation of the ground complex when processing two video streams in real time. Jetson Orin NX with 16 GB of memory will be quite enough to process one video stream. AI performance of AGX Orin 278 TOPS, AI performance of Jetson Orin NX 157 TOPS.

The hard drive which is placed in an computer of reconnaissance complex, appears as the buffer of information and the low speed standard according to which on it there is a data record, can reduce significantly overall performance of a computer in general. SSD drives possess the highest speed regulation characteristics, but on reliability and service life they are inferior to mechanical analogs.

V. Conclusion

The solution of a scientific and technical problem of creation of optimum hardware composition of passive OES of target indication of a reconnaissance complex will allow not only to construct effective machines according to specifics of the tasks set for them, but also to avoid thus excess financial expenses. That is very important by development and the subsequent commercial implementation of the final product.

Acknowledgment

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Control of an Anthropomorphic Walking Robot Using Reinforcement Learning

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***Abstract*. This work explores the application of reinforcement learning methods to the control of an anthropomorphic walking robot. The main algorithm selected is the Deep Deterministic Policy Gradient (DDPG), which allows for controlling each joint of the robot's lower limbs within a continuous action space. A reward function has been proposed, taking into account movement speed, stability, energy efficiency, and motion smoothness, thereby promoting the development of stable locomotion without explicit trajectory programming. For simulation purposes, a robotic model was developed in the MATLAB/Simulink environment using Simscape Multibody, providing realistic physical interactions. Parallel computing was employed to accelerate the training process. After 6000 training episodes, the robot demonstrated relatively stable forward movement even in the presence of noise and random disturbances. The obtained results indicate that the DDPG algorithm provides a high degree of autonomy and adaptability, opening prospects for its application in controlling complex mechanical systems. The influence of hyperparameters and the structure of the reward function on training performance is also discussed.**

***Keywords:* reinforcement learning (RL), DDPG, anthropomorphic robot, simulation model, reward function**

I. INTRODUCTION

Anthropomorphic robots are finding applications in various fields such as healthcare, service industries, and manufacturing. In classical control theory, the robot is considered as a single system composed of multiple subsystems, which are in turn controlled centrally. Traditional control methods, such as proportional-integral-derivative (PID) controllers, are effectively used to maintain system stability. However, their implementation becomes more complex as the mechanical design increases in complexity and sensitivity [1]. For example, research shows that PID controllers face challenges under nonlinearities or significant time delays, especially in multidimensional systems such as robots with multiple degrees of freedom [2]. The limitations of traditional control methods become evident in adaptive robotics tasks, where a high degree of autonomy and the ability to learn in real time are required. In contrast, Reinforcement Learning (RL) offers a more flexible approach, enabling robots to learn optimal walking strategies autonomously and adapt to changing environmental conditions [3]. This method has already found successful application in tasks involving the simulation of human walking and motion coordination of anthropomorphic robots, as confirmed by several studies [4].

The goal of this work is to investigate coordinated control methods for the limbs of a humanoid robot in order to simulate human-like walking and perform practical tasks with a high degree of autonomy and adaptability. The proposed system is based on RL methods, which are applied to control the robot's legs and ensure optimal control of each joint during locomotion. This is achieved through the development of a reward function aimed at improving the robot’s stability and adaptability to various environmental conditions. Data normalization plays a key role in enhancing the accuracy and efficiency of the learning process.

II. PRINCIPLE OF REINFORCEMENT LEARNING

The RL method is based on the implementation of a process that maximizes a certain reward signal by exploring various behavior options of the agent. The agent learns to select actions that provide the maximum cumulative reward. Importantly, its actions can influence not only short-term but also long-term outcomes. The formation of long-term reward is a rather complex process; however, a well-designed reward function can significantly reduce training time, improve its stability, and enhance the overall learning performance [5].

The task of RL is for the agent, through interaction with the environment, to use accumulated experience to learn a policy that maximizes the expected cumulative reward over the entire learning process (Fig. 1).

In Fig. 1, s_t represents the agent's state at time t; a_t is the action taken by the agent at time t in the environment; r_t is the reward value received at time step t.

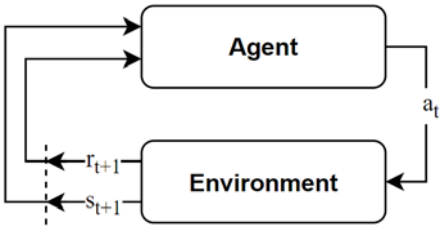

Fig. 1. Principle of Reinforcement Learning

The goal of the agent is to maximize the expected discounted sum of rewards over the entire episode (1) [6]:

$$G_t = \sum_{k=0}^{T} \gamma^k r_{t+k+1}, \quad (1)$$

where G_t – the total reward starting from step t, $\gamma \in [0,1]$ – the discount factor determining the importance of future rewards, T – the episode length.

The agent-environment interaction cycle includes the following stages:

- the agent receives the current state of the environment s_t and the reward value $Q(s_t, a_t, \theta^Q)$;
- based on the current policy, the agent selects an action a_t;
- the environment transitions to a new state s_{t+1} as a result of executing the action a_t;
- the agent receives a reward r_{t+1} for the executed action;
- the agent's policy is updated based on the new data $(s_t, a_t, r_{t+1}, s_{t+1})$.

This process repeats until the episode ends or a specified stopping criterion is met [7].

The DDPG algorithm is a reinforcement learning method that uses two deep networks neural networks: the Actor network and the Critic network. These components work together to develop an optimal control strategy for the system. The Actor, which implements the agent's policy, generates the control action $a_t = \mu(s_t, \theta^\mu)$. The Critic evaluates the quality of these actions using a value function $Q(s_t, a_t, \theta^Q)$, which determines the expected cumulative reward when performing the action a_t in the state s_t. Using (2), the Critic updates its parameters by minimizing the error

$$L(\theta^Q) = \mathrm{E}(s_t, a_t, r_t, s_{t+1})[(y_t - Q(s_t, a_t; \theta^Q))^2], \quad (2)$$

where y_t – represents the target value for the Critic (3). It produces an estimated value that determines the total expected reward the agent will receive if it continues to act according to the Actor's policy

$$y_t = r_t + \gamma Q(s_{t+1}, \mu(s_{t+1}; \theta^\mu); \theta^Q). \quad (3)$$

After that, the Actor adjusts its parameters θ^μ (policy) to maximize the Critic's evaluation using (4):

$$J(\theta^\mu) = \mathrm{E}(s_t, a_t, r_t, s_{t+1}) Q(s_t, a_t; \theta^Q) \quad (4)$$

Thus, the Critic adjusts its parameters θ^Q, using gradient descent to improve the accuracy of its estimates. The resulting error is used for backpropagation and updating the Critic network.

The joint operation of these components enables efficient learning without explicit programming of the agent's behavior.

III. Simulation Model of the Environment and the Interaction Process with the Agent

The developed simulation model of the walking robot acts as a dynamic environment, implemented using the Simscape Multibody library. It provides three-dimensional modeling of the robot's mechanical system. At the center is the RL agent block, which serves as the controller [6]. The model is described by three main terms: *observation, reward,* and *termination criteria* (Fig. 2).

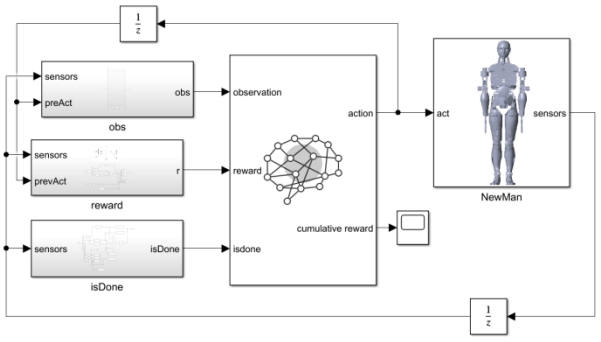

Fig. 2. Scheme of applying the reinforcement learning block together with the robot model

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The *state* represents a complete description of the current situation of the environment, including all parameters necessary for making an optimal control decision. The *observation* provides a partial description of the state. It includes the agent's previous action, a_{t-1}, angular velocities along the axes $\mathbf{w} = [\omega_x \quad \omega_y \quad \omega_z]$, linear displacement along the axes $\mathbf{v} = [v_x \quad v_y \quad v_z]$, linear velocity $\mathbf{P} = [x \quad y \quad z]$, Euler angles (rotation angles) $\mathbf{q} = [q_x \quad q_y \quad q_z]$; indicator of the normal force on the robot's feet for observation $\mathbf{F}_{cont} = [F_r \quad F_l]$, whether the foot is in contact with the ground or not; the position and velocity of each joint $\mathbf{A} = [A_{pose} \quad A_{vel}]$. The proposed control system (Fig. 2) operates on the principle of continuous feedback. At each time step, the environment provides the agent with the current state and the reward value (described in the section on the reward function). Based on this information, the agent generates a control action. The action consists of the torque applied to each joint of the robot's legs. The applied torques can take any continuous value within the range [–1, 1]. Equation (5) describes the transformation of the agent's control signal into a physically valid range of angular values, taking into account the dynamic parameters of the system. The first part of the equation normalizes the input signal u to a specified range $[b_{\max} - b_{\min}]$, based on the current position p. The second part comprises two key components: adaptive stiffness, determined by the coefficient k, and damping, which depends on the current velocity v and the damping coefficient d. Thus, the equation enables parameter-varying control that reflects both the positional and velocity-dependent characteristics of the system.

$$K = \underbrace{\left(\frac{\mathrm{b}_{\max} - \mathrm{b}_{\min}}{2} \cdot (u+1) + \mathrm{b}_{\min} - A_{pose}\right)}_{1} \cdot k - A_{vel} \cdot d \quad (5)$$

where $\mathrm{b}_{\min}$, $b_{\max}$ – lower and upper positions of the joints, u – input signal, the value generated by the agent, k, d – stiffness and damping coefficients.

The torque limitations are defined as follows:

$$sat(K) = \begin{cases} -T, & x < -T \\ x, & -T \le x \le T \\ T, & x > T \end{cases}. \quad (6)$$

The agent generates actions (control signals) within the range [–1, 1], which are then normalized and applied to the corresponding joints according to (5–6), taking into account their physical constraints. Equation (5), using the example of the hip joint, converts the received signal into the appropriate range for the corresponding joint (Tabl. I) and applies it to the environment.

TABLE I. RANGE OF MOTION OF THE HUMANOID ROBOT'S JOINTS

Joint	Range (degrees)
Hip	[–15, 90]
Knee	[0, 90]
Ankle	[–20, 10]

IV. REWARD FUNCTION

To ensure stable simulation of walking, a specialized reward function has been developed. The first necessary step is to introduce a positive reward for the linear velocity $\mathbf{v}_y$ along the Y – axis, aimed at encouraging forward movement of the robot. However, this component alone is not sufficient to form stable behavior. To prevent excessive deviation from the desired trajectory and avoid falls, penalties for deviations along the axes were added X and Z, to ensure that the robot stays on the correct path. The reward function also includes a penalty for the magnitude of the torque applied (p), applied to each joint, which serves as an indicator of energy efficiency and is penalized. This helps avoid abrupt and excessive movements that could lead to instability in the robot's behavior. Thus, the reward function promotes smoother and more natural walking patterns. To prevent the agent from learning a local minimum where the robot falls forward early to quickly maximize the speed reward, a reward for episode duration has been added to the reward function (t_s). It encourages successful task execution over an extended period. To prevent this effect, an additional positive reward for the duration of the episode is introduced, which encourages the agent to maintain balance and avoid falling throughout the entire simulation time.

The final reward function takes the following form:

$$r = w_1 v_y - w_2 x - w_3 z - w_4 p + w_5 t_s, \quad (7)$$

where $w_{1,\dots 5}$ – weight coefficients that determine the relative importance of each component.

Total cumulative reward R for the episode is calculated as the accumulated discounted sum of instantaneous reward values (8), it was formed based on (1):

$$R = \sum_{t=0}^{T} \gamma^t r_t. \quad (8)$$

The reward function is implemented in the MATLAB/Simulink environment as a *Reward* block (Fig. 2). The block receives input data from the sensor block as well as the agent's previous action. The output

is a scalar reward value, which is used to update the agent's policy.

The simulation of an episode ends when one of the following conditions is met: expiration of the maximum episode time, a drop in the robot's center of mass below 0.8 meters (indicating a fall), lateral deviation exceeding 0.5 meters from the target trajectory, or a body tilt angle exceeding 30 degrees, which indicates a loss of stability.

The logic for determining episode termination is implemented in the *isDone* block (Fig. 2), which receives data from sensors and returns a binary signal indicating whether the current iteration should be terminated or continued.

V. RL Settings and Training Process

To ensure effective training of the DDPG agent, it is necessary to configure both the algorithm's hyperparameters and the parameters of the training process. Table.II presents the final set of values used in the experiments.

TABLE II. Hyperparameter Settings for the DDPG Algorithm

Parameter	**Value**
DiscountFactor	0,01
MiniBatchSize	128
ExperienceBufferLength	5e5
TargetSmoothFactor	1e-3
NoiseOptions.MeanAttractionConstant	2e-3
NoiseOptions.Variance	0,5
NoiseOptions.VarianceDecayRate	1e-5

The weights for balancing each term in the reward function were set equal $w_1 = 0.1$, $w_2 = 0.75$, $w_3 = 0.3$ and $w_4 = 0.05$. These values were determined experimentally through multiple trials.

The simulation experiments were conducted on a personal computer equipped with an Intel Core i5-9600KF processor and an NVIDIA Quadro P2000 graphics card.

VI. Results

The training results are presented in Fig. 3, which shows three main metrics: the blue curve represents the reward value for each individual episode, the red curve shows the moving average of the reward, indicating the agent's overall progress, and the green curve ($Q0$) – the initial value Q – the initial value of the function estimated by the Critic based on the initial state

The training stopping criterion was the achievement of a target average reward value, which helped avoid premature termination based on individual successful episodes with high instantaneous rewards.

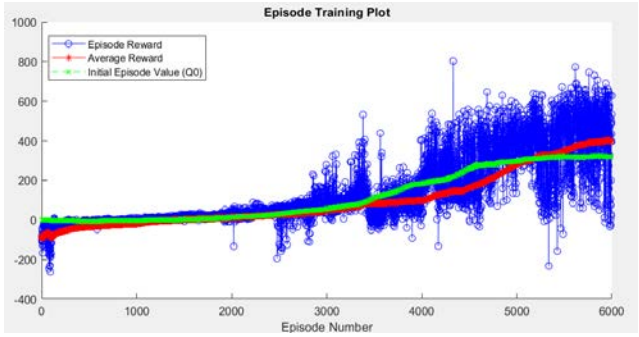

Fig. 3. Training results after 9 hours and 15 minutes

The total number of episodes was 6000. During the initial stages (first 2500 episodes), the episode duration was relatively short, which is associated with the search for feasible solutions. Then, the agent began to find more effective control strategies, and the reward value gradually increased, reaching a level of around 800 units. At the end of training, the blue curves represent rewards for individual episodes, which are still quite noisy. However, there is an overall upward trend, with greater noise evident in the average reward, shown in red. DDPG belongs to the class of high-variance methods, so a monotonic increase in reward is not guaranteed. Nevertheless, a general positive trend is observed, confirming the effectiveness of the learning process.

The analysis of the graph also shows an increase in the average episode duration, indicating that the robot became better at maintaining stability and moving for longer periods compared to the early stages of training.

Fig. 4 shows episode 4331, in which the agent received the maximum reward.

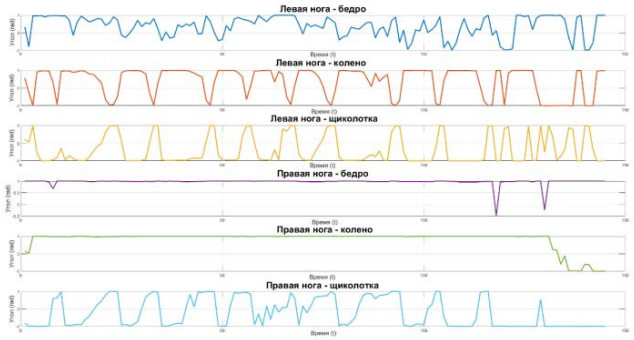

Fig. 4. Torque values for each joint

Upon completion of training, the robot demonstrates relatively stable walking. Although its behavior does not fully match the idealized human locomotion model, it meets the specified criteria of the reward function and allows the robot to move forward without falling. The developed reward function effectively guided the learning process, enabling the agent to achieve the goal – stable forward movement.

To accomplish this task, a computer with six computing cores was used. The training time was 9 hours.

VII. Conclusion

This work implemented an approach to controlling an anthropomorphic walking robot using reinforcement learning, specifically the DDPG algorithm. The proposed control system enabled a high degree of autonomy and adaptability in the robot when operating in a changing environment.

Based on the developed reward function – which accounted for speed, stability, energy efficiency, and smoothness of movement – the agent was able to learn human-like walking behavior without explicit motion programming. The use of a simulation model and environment in MATLAB/Simulink allowed the robot to be trained to perform relatively stable locomotion without predefined trajectories or rigid control laws.

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Optimizing ECG Image Processing: A Multi-Method Approach to Signal Extraction and Recovery

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Abstract. **Digitization of paper electrocardiograms (ECG) is an important task in cardiology, enabling modern analysis techniques, facilitating expert consultations, and ensuring accurate and timely diagnoses. However, the digitization process presents several challenges, including image distortions, scanning artifacts, textual inscriptions, and overlapping signals, all of which greatly affect the signal recovery quality. This paper provides an overview of modern methods for solving the described problems and discuss possible approach to solve signal digitization problems arising from complex cases such as signal overlap and text interference. A common technique for signal binarization involves extracting signals from single-leads black-and-white images by isolating black-colored areas. This approach, however, causes pixel information loss, making grid pixels indistinguishable from signal pixels. Consequently, grid removal often remains incomplete, either leaving behind unwanted artifacts or partial removal of signal elements. This can result in poor signal digitization and even with proper signal mask extraction there is still a chance of missing signal pixels, for example due to poor image quality. To address the described problems, the study evaluates several approaches to removing noisy pixels from the signal and reconstructing missing signal values based on different interpolation methods and training a random forest model. The effectiveness of these methods is assessed in scenarios where signal data is lost due to poor image quality, noise pixels left after removing the grid, and different degrees of signal overlap with text or neighbor signals. Findings indicate that these techniques perform well in restoring partially obscured signals, addressing missing pixels, and slightly signal overlapping with text or neighboring signal. In simple scenarios, where two signals are mistakenly detected instead of one, the proposed methods successfully isolate and digitize signals, enhancing the overall accuracy of ECG digitization.**

Keywords: **ECG digitization, image processing, machine learning**

I. INTRODUCTION

Digitization of paper electrocardiograms (ECG) is an important task in cardiology, as it allows using modern methods of analysis, sharing digital information with experts for consultations and making timely high-quality diagnoses. The process of digitizing paper ECGs is associated with a number of problems, such as image distortions, the presence of scanning artifacts, inscriptions, and overlapping of neighboring signals, which greatly affects the quality of signal recovery.

A. ECD digitization pipeline

A typical pipeline consists of the following steps [1]:

1) Preprocessing: Scanning the paper ECG at high resolution; removing background noise and grid lines using image processing techniques like thresholding and morphological operations.

2) Lead detection and segmentation: Identifying individual ECG leads using deep learning models or traditional image processing methods; cropping and aligning each lead for further processing.

3) Signal extraction: Converting pixel values into voltage readings using grid calibration; applying algorithms like Hough Transform or Viterbi's algorithm to trace signal paths.

4) Noise removal and signal recovery: Using filtering techniques such as wavelet denoising or adaptive filtering to remove artifacts; employing interpolation methods or machine learning models to reconstruct missing signal.

5) Validation and postprocessing: Comparing extracted signals with reference datasets to ensure accuracy; normalizing signals for compatibility with digital ECG formats.

B. The main challenges of digitalizing paper ECGs

1) Image quality and distortions: ECG scans may contain distortions such as tilt, uneven illumination, and noise, making it difficult to accurately extract the signal. To address these issues, tilt correction, binarization, and filtering techniques are used [2]. Noise removal and signal recovery remain challenging, especially for poor-quality source. Overlapping signals and text can lead to inaccuracies in extraction and variability in paper ECG formats requires adaptable preprocessing techniques, Fig. 1.

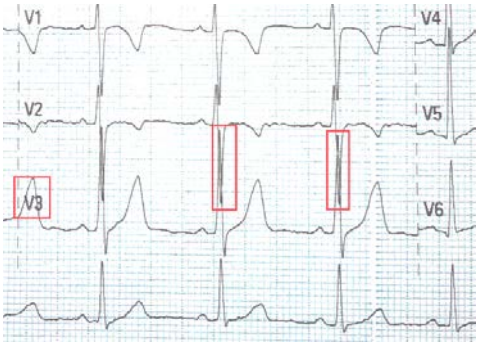

Fig. 1. Example of the scan of paper ECG

2) Lack of standardization: There are many digitization algorithms, but there is no unified database and standardized metrics to evaluate their performance, which makes it difficult to compare different approaches.

3) Accuracy of amplitude and time reconstruction: For clinical use, it is important to accurately reconstruct the amplitude and time characteristics of the ECG signal.

This study provides an overview of modern methods for solving the described problems and discuss possible approaches to solve signal digitization problems arising from complex cases such as signal overlapping and signal-to-text overlapping.

II. Modern Methods of ECG Signal Restoration and Enhancement

A. Noise Removal and ECG Signal Restoration after Digitization

Digitization of paper ECGs is accompanied by various types of noise, including overlaping of neighbor signals, text inscriptions and artifacts caused by printing quality. The following methods are used to effectively remove noise and restore missing data:

1) Wavelet transform: Allows to isolate the useful signal and remove noise while preserving important ECG characteristics. Combines the wavelet transform with the particle swarm optimization (PSO) algorithm to automatically select the optimal filtering parameters, including the choice of basis function, decomposition level and threshold values [3]. The disadvantages of such methods are the dependence of the results on the quality of the initial signal and the need for fine-tuning the PSO parameters to achieve optimal results.

2) Variational and empirical modal decomposition (VMD, EMD): Separates the signal into components, eliminating artifacts and improving the accuracy of reconstruction [4-6]. EMD decomposes the ECG signal into a set of intrinsic mode functions, which allows for effective elimination of various types of noise, including baseline drift and electromyographic interference. Modal decomposition methods have high computational complexity, as well as the possibility of artifacts appearing if the parameters are incorrectly configured.

3) Autoencoders: Autoencoder models with attention and skip connections are used to filter ECG signals. They effectively remove various types of noise, including motion artifacts and underlying fluctuations, improving the quality of the signal for subsequent analysis. Deep autoencoders are trained on incomplete ECG signals to reconstruct the missing segments, ensuring the continuity and integrity of the signal [7, 8].

B. Recovering Missing Data in ECG after Digitization

After noise removal, missing data may occur in the digitized ECG signal, for example due to text overlay, unprinted pixels, or scanning artifacts. Various methods are used to recover such data:

1) Interpolation methods: Interpolation and scaling methods are used to convert pixel coordinates into physical values of time and amplitude. This allows for an accurate recovery of the waveform, taking into account the grid features on the paper ECG [9–12].

2) Deep learning. Deep learning methods, such as convolutional, recurrent, generative adversarial neural networks and segmentation models, are used to automatically extract ECG signals from images [13–16]. Deep neural networks trained on real data can restore both individual signal segments and entire missing leads. Many automated tools use convolutional neural networks to restore lost data and improve the quality of digitized ECG [15]. The disadvantage of models based on deep neural networks is their sensitivity to the quality of the scanned image and the need for a large amount of labeled data for training.

3) Statistical methods and signal analysis. Principal component analysis is used to reconstruct missing data in ECG signals by analyzing correlations between leads. The method allows estimating missing values based on linear dependencies between different components of the signal [17, 18]. Hidden Markov process models are used to model sequences of states in ECG signals, allowing prediction of missing segments based on probabilistic dependencies between observed and hidden states [19, 20]. Disadvantages of statistical methods include their sensitivity to noise and outliers, are not always effective in the presence of nonlinear dependencies, require careful tuning of model parameters and may require a significant amount of training data.

III. Multi-Method Approach to Signal Extraction and Recovery

The process of ECG signal binarization based on extracts signals from single-lead mask (black and white image). However, converting images into black and white results in the loss of pixel information, making certain grid pixels indistinguishable from signal pixels. This approach has several limitations, with one of the main issues being poor removal of the grid in the ECG image, leading to two possible issues: incomplete removal of pixels related to the grid or captions; partial removal of pixels belonging to the signal. This might result in poor signal digitization. Even with correct signal mask extraction, there is still a possibility of missing signal pixels, for example, due to poor image quality.

In this section we discuss some possible approaches to solve signal digitization problems arising from complex cases such as signal overlapping and signal-to-text overlapping. We tested three different interpolation methods combined with Random Forest model (RF) to predict missing signal values. We evaluated these methods for different signal cases: there are missing values in the signal (e.g. due to poor image quality), there is a noise left on the image after grid cleaning, overlapping of signals of different degrees, overlapping of signal and text. The investigated approaches perform well in path selection for signal recovery when the signal is slightly overlapping with text or neighbor signal, as well as for missing pixels (poor ECG print/quality). Also for some simple cases of poor lead detection (two leads were detected instead of one) the investigated approaches can separate and digitize signals.

A. Method description

In the process of signal binarization, we need to obtain a single value *y*-coordinate (signal amplitude) for each *x* - coordinate value (time). On the ECG graph, *x* corresponds to the columns and *y* – to the rows. If, after cleaning the grid and artifacts from the ECG image, the resulting mask still contains pixels from removed artifacts, each value of the *x* – coordinate may correspond to several values of the *y*-coordinate with a fairly high dispertion. The essence of the proposed technique is: 1) approximate the *y* value for each *x*, or if unsuccessful, leave it empty; 2) interpolate the missing values *y*. We tested 3 approaches to approximate the *y* values.

Before cleaning and interpolating the signal, we must make sure that the mask is obtained for only one signal. To do this, we define the dominant line of the signal as the raw of the mask with the maximum number of pixels. We select the top 10 such lines and then compare the distance between them. A large distance (in our experiments more than 30 pixels) indicates the presence of artifacts left over from the neighboring signal, or poor lead detection at the first stages of digitalization (the mask is obtained for two signals at once). If two dominant lines are found, we should separate their masks (the distance to the upper and lower edges of the mask can be used).

The first approach was based on approximating *y* by its mean value for each *x* if the variation of *y* values does not exceed a given threshold, otherwise *y* is equal to *nan*. The threshold value was determined experimentally based on the root mean squared error (RMSE) metric.

The second approach splits all *y* values for every *x* into two clusters depending on the variation value. If the variation is less than θ_1, then *y* is approximated by the mean value, if the variation is greater than θ_1 but less than θ_2, then this indicates the uncertainty of the *y* value (the pixel distribution is excessively wide, making it impossible to determine with certainty whether they correspond to a single signal or multiple signals), so *y* remains unknown. If the variation is greater than $\theta 2$, then the *y* values are clustered into two clusters according to the distance between neighboring pixels in the column. Return the *y* mean from the cluster closest to the dominant line.

Example: Pixels with coordinates *y* = [1, 2, 3, 4, 9, 13, 22, 25, 30, 39] in column *x* will be split into two clusters: y_1 = [1, 2, 3, 4, 9, 13] and y_2 = [22, 25, 30, 39].

In the third approach for every dominant line *L* found, first we find maximum interval [*x*', *x*"] where signal values *y* are located close to the dominant line (for ex., in the range [$L - \eta$, $L + \eta$], where η is a window width we define experimentally). Such interval correspond to the PQ and ST segments of ECG [21] signal which are located close to the dominant line. This segments usually don't overlap with neighboring signals, and with a high confidence it can be stated that pixels from these segments belong to the signal under consideration. Next, starting from *x*' we interpolate the right part of the signal using second approach and after that we interpolate the left part of the signal for *x* from *x*'-1 down to 0.

After signal cleaning, empty values *y* are interpolated using a RF model.

B. Experiment results

To select optimal parameters for the RF model, a dataset was created containing 100 signal masks with minimal noise levels, allowing for high-precision signal binarization. In the experiment, test points were randomly selected and removed from the signal. The remaining data was used to train the RF model, and its accuracy was evaluated on the excluded points.

RF MODEL PERFORMANCE

Maximum depth	R^2 value		
	Test size = 40 %	*Test size = 30 %*	*Test size = 20 %*
10	0.856	0.8766	0.9102
15	0.8811	0.9107	0.9274
25	0.916	0.9065	0.926

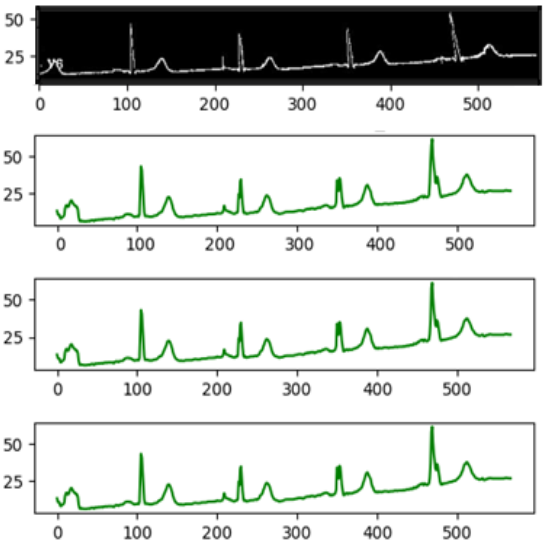

Fig. 2. Signal binarization (scenario with minimal interference and missing entries)

Table presents the test results of the model for different values of the trees maximum depth. We used three different metrics to evaluate the model performance: MSE, RMSE and R^2. Since the proportion of missing points in the cleaned signal is typically small, the optimal parameter value was set to 15.

Fig. 2 and 3 illustrate the reconstructed signals obtained using three different approaches. Figures show from top to bottom the signal mask, the signal restored using the third approach, the signal restored using the first approach, and the signal restored using the second approach. All three methods demonstrate high efficiency in restoring signals in cases without significant overlapping of neighboring signals. However, method 3 slightly reduces the peak amplitudes of the signal, although in complex cases, it may outperform the other methods in terms of accuracy.

IV. DISCUSSION AND CONCLUSION

The process of ECG signal binarization presents several challenges, primarily related to the loss of pixel information and the difficulty of distinguishing signal pixels from grid artifacts. The limitations of the traditional black-and-white extraction method affect signal digitization quality, leading to incomplete removal of grid elements or unintended deletion of signal pixels.

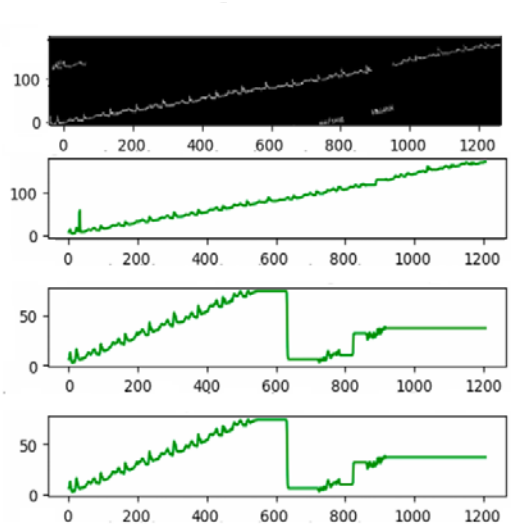

Fig. 3. Signal binarization (scenario with excessive interference and missing entries)

To address these issues, multiple approaches were investigated based on interpolation using a RF model for signal reconstruction.

The experiments revealed that signal recovery is highly dependent on the nature of signal distortions. Missing pixels due to poor image quality, residual noise from grid cleaning, and overlapping signals require different strategies for effective digitization. The tested methods demonstrated strong performance in reconstructing signals when overlapping was minimal, as well as in distinguishing individual signals when artifacts affected detection accuracy. While all three approaches effectively restored signals, the third method exhibited a tendency to slightly reduce peak amplitudes, highlighting potential areas for improvement.

A key challenge in the interpolation process was defining the dominant signal line and handling multiple detected values for a single x-coordinate. Establishing threshold-based clustering and selecting the most representative pixel group proved effective in separating signals. Additionally, the RF-based interpolation method significantly enhanced signal reconstruction accuracy by predicting missing values based on previously learned patterns.

Overall, the proposed methods contribute to refining ECG signal extraction and improving digital signal representation in complex cases. While each approach has its strengths and weaknesses, further refinement through additional experiments and data-driven optimizations could enhance reliability. By improving signal binarization processes, the study paves the way for more precise ECG digitization, facilitating better clinical analysis and automated signal processing applications.

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Decision Support System for Critical IT Service Management Tasks

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***Abstract*. The paper addresses the problem related to the management of computational resources of a critical IT service. An approach to building a decision support system based on a library of neural network models is proposed. A software system implementing this approach has been developed. Experiments were conducted using synthetic and real-world data. The experimental results confirm the system's functionality and demonstrate that the proposed approach enhances the quality of IT service management.**

***Keywords:* decision making, information system, proactive management, uncertain external load, neural networks, multi-model system, model library**

I. INTRODUCTION

Uncertainty in external load and failures of computational equipment lead to disruptions and performance degradation of critical IT systems, resulting in lost operational efficiency in processing information and executing banking and other operations, which in turn can have serious consequences (financial losses, major incidents, etc.).

With the advent of cloud computing, it has become possible to flexibly and dynamically adapt the volume of computational resources for critical IT systems according to current load. Autonomous automated solutions have emerged that can promptly manage scaling of critical IT services without human intervention.

Automation enables systems to respond in real-time to load changes, maintaining stable performance quality in accordance with required service level objectives (SLO).

Moreover, automatic scaling directly impacts the business value of IT services, as it determines both operational costs and customer service quality. Thus, the development of automated resource management methods represents an important direction for ensuring reliability and cost-effectiveness of mission-critical systems.

Generally, scaling represents a task of automated management of computational resources under changing, highly dynamic, complex workloads. An ideal automatic scaling mechanism should minimize both costs and service quality violations. The article [1] presents a framework describing various aspects of auto-scaling, divided into several categories covering specific types, policies, techniques, approaches, metrics, etc. related to scaling. This structure enables classification of different approaches and methods for efficient resource management while maintaining required service levels and optimizing IT system costs.

Despite decades of active research in this field, there remains a significant gap between scaling methods proposed in academic papers and those employed in large-scale industrial deployments [2]. Industrial auto-scaling solutions like Microsoft Azure [3], Amazon Web Services [4], Google Cloud Engine [5], Kubernetes Horizontal Pod Autoscaler (HPA) [6] rely on relatively simple approaches (with predefined thresholds) assuming linear relationships between resources and target scaling metrics.

Research solutions, while typically less adapted for industrial use, tend to be more sophisticated, featuring numerous configuration parameters and system-specific characteristics (alternative metric sets, predefined thresholds for these metrics, workload patterns typical for particular systems, etc.). These solutions employ various approaches [1] including: Application Profiling (AP), Threshold-based Rules (TR), Fuzzy Rules (FR), Control Theory (CTH), Queuing Theory (QTH), Machine Learning (ML), and Time Series Analysis (TSA).

The literature [1] describes numerous research solutions utilizing predictive models (predictors based on neural networks, autoregressive models, etc.) that enable operational decision-making. However, there are certain characteristics that prevent these systems from achieving maximum effectiveness when dealing with complex dynamic loads with uncertainty.

II. METHODS

The key feature of any automated control system lies in its predictive capabilities (forecast accuracy and

responsiveness). Predictions are made based on a sufficiently large set of previously obtained data. A model trained on one dataset (associated with a specific load profile) that demonstrates good predictive performance on a similar profile may show weak results on another profile. Essentially, each load profile may require its own predictive model. Alternatively, the training dataset must contain a sufficiently large number of features that the model can recognize and remember, and then implement some generalization when making predictions.

It is assumed that these models will successfully predict the values of required parameters for other types of loads associated with uncertainty. In these studies, training datasets for models are prepared in advance and contain lengthy time series with a large number of elements. Training on these datasets takes considerable time and requires high-performance computing resources to effectively train models within an acceptable timeframe.

We propose an enhancement to the Dynamic Local Approximation (DLANN) method introduced by the authors in [7], based on a multi-model approach (DLANNLIB). The method enables adaptation to new load patterns involving uncertainty by constructing real-time approximations using neural network models. These models, along with their metadata (training quality metrics, data characteristics), are stored in a model library during operation and subsequently used for forecasting when the system transitions to new states.

The model library serves as an additional predictor to estimate target metrics before sufficient data becomes available to train a new model for an emerging system state - when such a state-specific model is not yet ready.

A hybrid approach is employed, combining reactive and proactive scaling types using DLANN (algorithm code AR90.50.60F) and DLANNLIB (algorithm code AR90.50.60FNNL_LM) predictors.

This approach implements an adaptive control system that learns during operation, builds predictive models matching evolving load patterns, stores and reuses them. As models accumulate, a "forgetting" mechanism is implemented that retains only a specified number of models with the lowest validation errors for each state.

III. Estimation of Management Quality

To evaluate the quality of management, we consider a problem where the target function reflects a trade-off between optimizing computational resource costs and meeting SLO requirements. The problem variables: $\Omega(t)$ – dynamically changing external system load with uncertainty, $R_k(t)$ – the amount of computational resources allocated to the system at the k-th step (system resources change discretely, we assume that the k-th step corresponds to state S_k), $Cost\big(R_k(t)\big)$ – the cost of resource usage at the k-th step, $SLO_k(t)$ – the service level objective metric at the k-th step, $Violation(SLO_k(t))$ – the penalty for SLO violation. $Cost\big(R_k(t)\big)$ and $Violation\big(SLO_k(t)\big)$ are normalized in the interval [0,1] over all states S_k. The target function to be minimized:

$$\arg\min_{A} \begin{pmatrix} \lambda \sum_{k=1}^{N} Cost\big(R_k[A(\Omega(t))]\big) + \\ (1-\lambda) \sum_{k=1}^{N} Violation\big(SLO_k[A(\Omega(t))]\big) \end{pmatrix} \quad (1)$$

with the constraint on the rate of dynamic resource changes

$$|R_k - R_{k-1}| \le \gamma \ , \quad (2)$$

where γ is the maximum allowable resource change.

As a result, the problem reduces to minimizing the target function, achieved by selecting the optimal algorithm A, which generates N system states under external load $\Omega(t)$ with uncertainty. An exact solution to this problem cannot be constructed, so we propose a heuristic algorithm that estimates the target function. From the set of algorithms, we select the one that minimizes the target function.

The load system provides averaged statistics on response time per request over 5 s averaging interval. We introduce a binary penalty indicator for the system in case of exceeding the average response time over 5 s as follows:

$$B_i = \begin{cases} 1, if\ R_i^5 > R_{max} \\ 0 \end{cases}, \quad (3)$$

where R_i^5 is the average response time over 5 s, R_{max} is the specified maximum response time.

Let $N_{\Delta t_j}^5$ be the total number of 5 s intervals during the lifetime Δt_j of state S_j, then the total number of penalties over Δt_j, the total number of penalties across states and the normalized penalty:

$$\mathrm{V}^{norm} = \frac{V}{N_{max}},\ \mathrm{V} = \sum_{j=1}^{N} V_{\Delta t_j},\ V_{\Delta t_j} = \sum_{j=1}^{N_{\Delta t_j}^5} B_j \ , \quad (4)$$

where N_{max} is the total number of 5 s intervals across all states S_j: $N_{max} = \sum_{j=1}^{N} N_{\Delta t_j}^5$.

We estimate the resource cost of state S_j over its lifetime Δt_j as $C_j \Delta t_j$, where C_j is the number of computational modules of state S_j. The total resource cost and the cost normalized across all states:

$$C = \sum_{j=1}^{N} C_j \Delta t_j, \quad C^{norm} = \frac{C}{C_{max} \Delta t} \ , \quad (5)$$

where C_{max} is the maximum number of computational modules and $\Delta t = \sum_{j=1}^{N} \Delta t_j$ is the total lifetime of all states S_j.

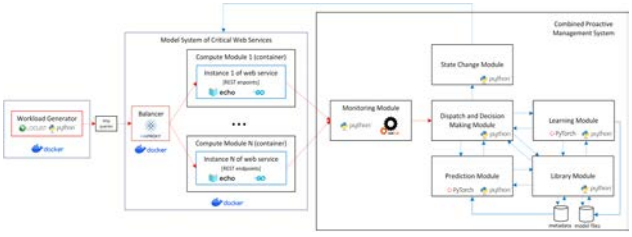
As a result, we obtain the following target function for evaluating management quality:

$$F = \lambda \left[\frac{\sum_{j=1}^{N} c_j \Delta t_j}{C_{max} \sum_{j=1}^{N} \Delta t_j} \right] + (1 - \lambda) \left[\frac{\sum_{j=1}^{N} \sum_{j=1}^{N_{\Delta t_j}^{5}} B_j}{\sum_{j=1}^{N} N_{\Delta t_j}^{5}} \right]. \quad (6)$$

The average response time is not very informative, we use the 95th percentile of response time.

IV. Combined Control System

To manage the resources of the model system, an agent was developed that receives real-time data on the utilization of computational modules and makes decisions about scaling the controlled system. The agent uses a combination of reactive and proactive control. For each state of the controlled system, a data sample is automatically generated, which is used to train a neural network model. This model is saved in the model library and predictions of resource utilization parameters are made by different predictors (based on the trained model and the model library).



Structural diagram of the combined control system

The agent compares the current data on the average load of the computational modules and the forecast results for a specific system state and makes a decision to change the state. Architecturally, the system consists of 6 main modules, which are shown in Figure.

The monitoring module is responsible for collecting performance metrics of the system's computational modules and adding/removing new metrics (when the system state changes). The joblib library [8] is used to collect metrics (every 2 seconds). The state change module is responsible for sending control commands and verifying the correctness of state changes. The dispatch and decision-making module is central. It and other modules are implemented in Python.

The training and prediction modules use the PyTorch library [9]. The training module creates neural network models from datasets for various states of the controlled system and saves the models to the model library. Each model is encoded with a state index. The prediction module loads models from the neural network model library by index and makes utilization forecasts with a certain lead time for various states of the controlled system. SQLite database [10] is used to store model metadata. Process interaction is implemented using the multiprocessing library [11].

V. Experimental Environment and Test Results

The model system, load balancing service, and load testing system operate in Docker containers on a virtual machine running a Linux-based OS – Ubuntu 22.04.1 LTS. The control system is deployed directly in the OS. Tests were conducted on various physical hardware. Final tests were performed on a virtual machine with the following parameters: vCPU – 8 cores, RAM – 16 GB.

We evaluate the performance quality of the combined automatic scaling control system using the previously described methodology. We use the quality metric F with an adjustable weight λ to specify the desired cost-to-penalty ratio. A threshold value of 24 ms is used for the response time penalty function. For calculating maximum cost, we use $C_{max} = 6$. The experiments use 3 load profiles, with brief descriptions provided in Table I.

TABLE I. Description of load profiles for several load types

Profile	Description	Hour
P1	Linear increasing load from 1 to 600 users over 30 minutes and linear decreasing load from 600 to 0 users over 30 minutes	1
P2	Linear increasing load with random noise from 1 to 600 users over 30 min and linear decreasing load with random noise from 600 to 0 users over 30 min	1
P3	Based on real load data describing user requests to NASA Kennedy Space Center web server in Florida on July 6, 1995 [12]. The original profile (RPS) was compressed from 24 hours to 4 hours, scaled to 600 users	4

Each profile was tested with 3 different algorithms. The algorithm name encodes its key operating parameters. The code breakdown is presented in Table II. In each test group corresponding to a specific profile, the test with the reactive algorithm serves as the baseline. The performance of other algorithms is compared against this baseline using quality metrics.

TABLE II. Decoding the algorithm names

Name	Description
AR90.50.60	Reactive
AR90.50.60F	Hybrid (Reactive + DLANN)
AR90.50.60F NNL_LM	Hybrid (Reactive + DLANN + DLANNLIB simplest Last Model implementation)
Add threshold, %CPU_Util = 90 Remove threshold, %CPU_Util = 50 Stabilization period, s = 60	

Table III presents the experimental results of the automated control system operation for 3 different load profiles. The quality metrics were calculated after conducting the experiments, based on the obtained statistics from the load testing system and the control system logs.

TABLE III. EXPERIMENTAL RESULTS FOR 3 TYPES OF WORKLOAD

Algorithms	C^{norm}	V^{norm}	$2F_{1/2}$	$F_{1/3}$	$F_{2/3}$
AR90.50.60 (P1)	0.387	0.727	1.115	0.501	0.351
AR90.50.60F (P1)	0.434	0.515	0.949	0.461	0.367
AR90.50.60FNNL _LM (P1)	0.463	**0.467**	**0.930**	0.465	0.377
AR90.50.60 (P2)	0.382	0.793	1.176	0.519	0.350
AR90.50.60F (P2)	0.431	**0.544**	**0.975**	0.469	0.366
AR90.50.60FNNL _LM (P2)	0.420	0.595	1.015	0.478	0.362
AR90.50.60 (P3)	0.341	0.732	1.073	0.471	0.336
AR90.50.60F (P3)	0.349	0.699	1.048	0.466	0.339
AR90.50.60FNNL _LM (P3)	0.356	**0.668**	**1.024**	0.460	0.341

The obtained results demonstrate that algorithms performing well on synthetic data significantly decrease their effectiveness (from 20 % to 5 % on the $2F_{1/2}$ metric) when applied to complex real-world-based load profiles. However, they still maintain about 10 % better response time efficiency compared to the reactive algorithm.

The baseline reactive algorithm retains its advantage in resource saving. Meanwhile, the DLANNLIB algorithm in its simplest configuration (using the previous state model) demonstrates good performance across most quality metrics when handling real-world-like workloads.

VI. CONCLUSION

The article examines the problem of managing computational resources for a critical IT service under conditions of uncertain external load.

An original multi-model approach (using a model library) is proposed for predicting control decisions, which improves the adaptive properties and stability of the controlled system. Experimental studies were conducted confirming the viability of this approach and the technologies used.

The experimental results show that algorithms that work well on synthetic loads significantly reduce their effectiveness on complex profiles based on real loads. However, they remain about 10 % more effective than the reactive algorithm in terms of response time.

When handling irregular and complex loads, the combined algorithms proved more effective than reactive ones across multiple performance metrics.

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Speech Emotion Recognition Using LSTM-based Neural Network with Local Attention

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***Abstract*. The study experimentally explores the use of recurrent neural networks with long short-term memory and a local attention mechanism for classifying emotions in human speech. Different variants of the classifier based on recurrent networks with one, two, and three hidden layers are presented. Mel-frequency cepstral coefficients (MFCC) are used as acoustic features at the frame level. The proposed solutions are tested on the RAVDESS dataset. A one-layer LSTM-based reccurent neural network showed the best results, with an accuracy of 46.09 % using the UAR metric. Possible improvements to the model are also discussed, which could further enhance the classification quality.**

***Keywords:* emotion recognition, deep recurrent neural networks, LSTM, attention mechanism**

I. Introduction

Speech emotion recognition is a topical problem in the field of natural language processing and computational psychology [1]. In recent years, various approaches based on both statistical methods (classical machine learning) and neural network architectures (deep learning) have been proposed to solve this problem [1–3].

In this paper, we investigate the possibility of constructing an speech emotion classifier using a unidirectional recurrent neural network (RNN) based on long short-term memory (LSTM). Specifically, we compare two different RNN learning strategies: one based on final-frame training, and another using weighted pooling with a local attention mechanism [3]. We use the Ryerson Audio-Visual Database of Emotional Speech and Song (RAVDESS) dataset for the experiments.

II. SER System Based on Recurrent Neural Network

A. General concepts

In this paper, we use mel-frequency cepstral coefficient (MFCC) for speech analysis. MFCC is related to the methods of short-term analysis of the speech signal. It means that speech utterance separated into short frames after that n-dimensional MFCC vector extracted from each frame (Fig. 1).

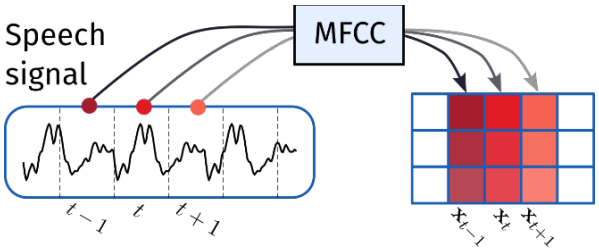

Fig. 1. Transformation of speech signal into sequence of vectors using MFCC

The process of MFCC calculation is presented in Fig. 1. Finally, speech signal transformed into sequence of vectors:

$$\mathrm{X} = [\mathrm{x}_0\ \mathrm{x}_1\ \ldots\ \mathrm{x}_{T-1}], \qquad \mathbf{x}_t \in \mathbb{R}^n, \tag{1}$$

where T is a sequence length (number of frames).

It should be noted that the sequence length T can be of arbitrary size. Thus, in order to solve the classification task using conventional methods like support-vector machine (SVM), linear discriminant analysis (LDA) or multilayer perceptron (MLP) the sequence of vectors (1) should be transformed into fixed-size vector. However, recently, RNN has been recognized as a more natural choice for processing sequential data [4].

B. Final-frame training

According to the classification of tasks [5] that can be solved using RNN, speech emotion recognition can be categorized as a "many-to-one" task (Fig. 2).

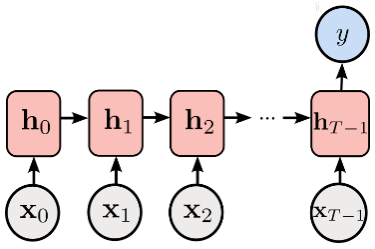

Fig. 2. Emotion classification by RNN using many-to-one scheme

The diagram in Fig. 2 shows that the RNN takes an input vector x_t and produces a hidden state vector h_t. This hidden state passed on to the next time step, where the RNN generates the next hidden state:

$$\mathrm{h}_{t+1} = RNN(\mathrm{x}_{t+1}, \mathrm{h}_t). \quad (2)$$

Last hidden state h_{T-1} is passed through fully connected (FC) layer with softmax(·) activation to obtain emotion label y:

$$y = \mathrm{softmax}(\mathrm{W}_F \mathrm{h}_{T-1} + \mathrm{b}_F), \quad (3)$$

where W_F and $\mathbf{b}_F$ – weight matrix and biases of FC classification layer. The errors obtained at softmax output layer are back-propagated to the beginning of the utterance.

In [3] this approach is referred to as final-frame training. In general, the approach is based on the assumption that the last hidden state contains all the necessary speech information for correct emotion classification. We can also think of RNNs as an adaptive mean to produce a fixed-size vector from a sequence of vectors X.

C. Weighted-pooling with local attention

An alternative to final-frame training approach is to obtain fix-size vector for output softmax layer using pooling over time output vector of RNN. In [3] it was proposed to use weighted-pooling operation for this purpose. Weights for weighted pooling should be computed in adaptive way. In this work we investigate the possibility to use attention map as weights for pooling operation. For generating attention map we used attention mechanism proposed in [6]. The general scheme of the described approach is given in the Fig. 3.

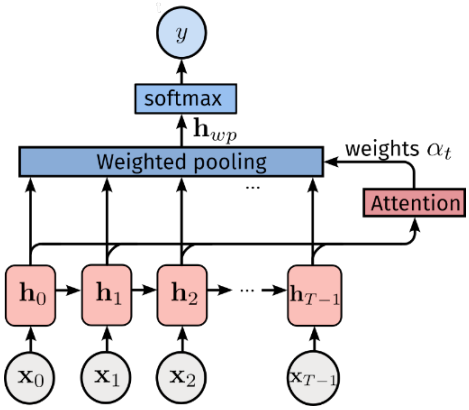

Fig. 3. Emotion classification by RNN with weighted polling

From the Fig. 3 it can be seen that RNN outputs are used in attention block to calculate the wights α_t. These wights are used to perform weighted-pooling operation that generates a vector of fixed length $\mathbf{h}_{wp}$, equal in size to the output vector of the RNN. The vector $\mathbf{h}_{wp}$ is fed into the softmax layer to produce the output (emotion label).

III. LSTM-BASED NN WITH LOCAL ATTENTION

In this work LSTM-based neural networks are used. LSTM is an improved variant of RNN that solves the vanishing/exploding gradient problem, allowing it to efficiently model long-term dependencies in sequential data [7].

Mathematically, an LSTM cell is described by a set of equations for computing the state and output at each time step t:

$$\begin{aligned}
\mathbf{f}_t &= \sigma(\mathbf{W}_f \cdot [\mathbf{h}_{t-1}, \mathbf{x}_t] + \mathbf{b}_f) \quad (\text{forget gate}),\\
\mathbf{i}_t &= \sigma(\mathbf{W}_i \cdot [\mathbf{h}_{t-1}, \mathbf{x}_t] + \mathbf{b}_i) \quad (\text{input gate}),\\
\hat{\mathbf{C}}_t &= \tanh(\mathbf{W}_C \cdot [\mathbf{h}_{t-1}, \mathbf{x}_t] + \mathbf{b}_C)\\
&\quad (\text{Candidate memory cell}),\\
\mathbf{C}_t &= \mathbf{f}_t \odot \mathbf{C}_{t-1} + \mathbf{i}_t \odot \hat{\mathbf{C}}_t \quad (\text{memory cell}),\\
\mathbf{o}_t &= \sigma(\mathbf{W}_o \cdot [\mathbf{h}_{t-1}, \mathbf{x}_t] + \mathbf{b}_o) \quad (\text{output gate}),\\
\mathbf{h}_t &= \mathbf{o}_t \odot \tanh(\mathbf{C}_t) \quad (\text{output}),
\end{aligned} \quad (4)$$

where $\mathbf{f}_t, \mathbf{i}_t, \mathbf{o}_t$ are the forget, input and output gates, respectively, $\mathbf{C}_t$ is the cell memory state at step t, $\mathbf{h}_t$ – network output at step t, σ and tanh are the sigmoid and hyperbolic tangent activation functions, $\odot$ – pointwise multiplication operation, $\mathbf{W}, \mathbf{b}$ are the trainable weights and biases.

LSTM cells can be combined to create a multi-layered RNN. In Fig. 4 an example of two-layer LSTM-based RNN is given.

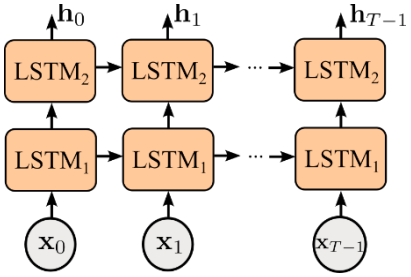

Fig. 4. Example of 2 lyaer LSTM-based RNN

The presence of additional layers in the RNN allows it to produce the representation that contains a greater amount of emotion information.

Fig. 5 shows the sequence of the hidden states produced by the one-layer LSTM-based NN with 64-dimentional hidden representation.

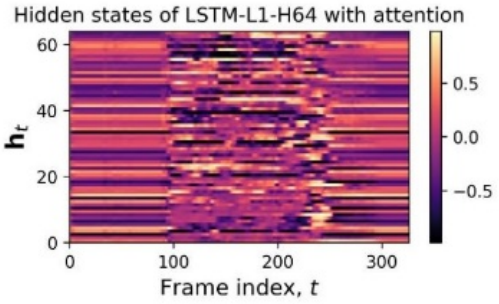

Fig. 5. Sequence of hidden states generated by the LSTM-based RNN

In this work we explore LSTM-based NN with weighed pooling (see Fig. 3) leveraged by local attention. Usually, the term local attention is associated with attention limited to a local window around each position. In the context of this paper, the term local is used in a different, more specific sense. It refers not to a window around a position, but to attention applied to the entire time sequence, but with a focus on locally important sections within utterance.

The proposed approach is based on the idea that speech often contains diverse emotional information: emotions can be expressed unevenly – sometimes during pauses, and sometimes only through specific intonations or individual words. Therefore, instead of using mean pooling to average all frames, it is suggested to use weighted pooling over time, with each frame receiving a weight that reflects its emotional importance.

The implementation of the weighted-pooling over time with local attention algorithm can be described as follows:

1) Calculating an attention score:

$$e_t = \mathbf{u}^T \mathbf{h}_t \tag{5}$$

where $\mathbf{u}$ is a learnable vector of parameters, e_t – is the attention score i.e., the scalar reflecting the "importance" of the $\mathbf{h}_t$.

2) Convert attention scores into pooling weights:

$$a_t = \mathrm{softmax}(e_t) = \frac{\exp(e_t)}{\sum_{\tau=1}^{T} \exp(e_\tau)}, \tag{6}$$

All scores e_t are passed through softmax function over the entire time axis to become normalized weights a_t.

3) Calculate the weighted sum of all frames:

$$\mathbf{h}_{wp} = \sum_{t=1}^{T} a_t \mathbf{h}_t. \tag{7}$$

The resulting vector representation $\mathbf{h}_{wp}$ is the sum of all LSTM outputs, weighted by the importance of each frame. After it $\mathbf{h}_{wp}$ is fed further through a dropout layer to a FC layer with softmax activation for emotion classification.

Fig. 6 illustrates the attention weights obtained for the speech signal. The Fig. 5 also shows the sequence of MFCC vectors fed into the RNN input.

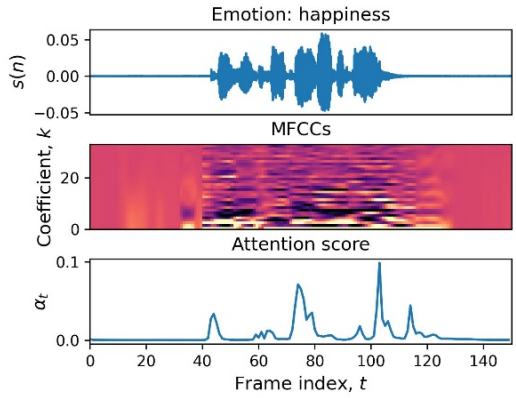

Fig. 6. Example of local attention weights calculation

The results obtained from the attention mechanism demonstrate desirable properties. For example, silence frames are automatically assigned very small weights, while frames with rich emotional information are assigned high weights.

IV. Performance Evaluation

A. NN models

The main goal of this study is to examine the impact of the local attention mechanism on the performance of LSTM-based NNs for speech emotion recognition. Additionally, we investigate the influence of the number of layers and the dimensionality of the hidden representation. Specifically, we explore NNs with 1, 2, and 3 layers, each with a different hidden representation dimensionality: 32, 64, and 128, respectively. In all cases, the neural network receives normalized MFCC vectors with a dimension of 1×34.

A total of 18 NNs were tested: nine networks that follow the final-frame training approach and nine networks based on weighted pooling with local attention. In each group, all combinations of the number of layers and hidden representation sizes were tested.

B. Experimental setup

1) Dataset

In this study we used a part of the RAVDESS dataset, namely, RAVDESS Emotional speech audio. This part of RAVDESS contains 1440 wav-files (16 bits, 48 kHz): 60 entries for each of 24 professional actors (12 males, 12 females). Speech emotions include expressions of neutrality, calmness, happiness, sadness, anger, fear, surprise, and disgust. All emotional states, except for

the neutral one, were voiced at two levels of emotional loudness (normal and increased). The actors repeated each vocalization twice.

2) Training process

Special attention is paid to the initialization of weights and biases. The learnable input-hidden weights of the LSTM-based NNs are initialized using Xavier method, while for learnable hidden-hidden weights orthogonal initialization is used. Orthogonal initialization is a method for setting the initial LSTM weights, in which the weight matrix is formed as orthogonal, which helps to maintain the stability of gradients when training deep recurrent models.

The experiments also showed that models with bias initialization by ones for the forget gates and by zeros for the other layers demonstrated a significant performance improvement compared to models where all biases were initialized uniformly (for example, to zero or random values). This was assumed to be due to an improvement in the network's ability to handle the loss of important temporal dependencies in the data.

All NNs were trained using the Adam optimization algorithm with a learning rate of 3e-3. A step-based learning rate scheduler was used to gradually decrease the learning rate by approximately 0.7943 every 10 epochs, promoting stable convergence. The weight decay was set proportional to the model size, with an initial value of 1e-6 for models with fewer than 10,000 parameters. Each time the number of model parameters increased by 10,000, the weight decay increased by 1e-6 (for example, 2e-6 for models with number of parameters between 20,000 and 29,999). In cases where the baseline learning rate resulted in suboptimal convergence, an alternative configuration with a reduced learning rate of 3e-4 was evaluated, and the more effective configuration was retained for final analysis. All models were trained for 100 epochs using a batch size of one.

To evaluate the accuracy of emotion classification in speech, we used the unweighted average recall (UAR) metric. UAR is a measure that calculates the average performance of a multi-class classification model across all classes. It gives each class equal importance, regardless of the class imbalance:

$$UAR = \frac{1}{N_c}\sum_{i=1}^{N_c}\frac{\mathbf{A}_{ii}}{\sum_{j=1}^{N_c}\mathbf{A}_{ij}}, \quad (8)$$

where $\mathbf{A}$ is the confusion matrix and N_c is the number of the classes.

To test the classifiers, the k-fold cross-validation (CV) method was used. RAVDESS dataset for training and validating the data was split into blocks as shown in Table I.

TABLE I. DATA PARTITIONING FOR 5-FOLD CV

Fold number	***Actors ID***
1	2, 5, 14, 15, 16
2	3, 6, 7, 13, 18
3	10, 11, 12, 19, 20
4	8, 17, 21, 23, 24
5	1, 4, 9, 22

This split order was proposed in [1]. The chosen strategy is that each fold should contain the same number of randomly selected samples for each class. In this case, the condition that each actor is represented either by the training or the validation set, but not by both, should be met.

C. Experimental results

Table II compares classification results of LSTM-based NNs designed using final-frame training approach. From the results we can conclude that increasing number of hidden layers has a negative impact on the model performance. However, increasing number of hidden neurons proved to be useful for 1-, 2- and 3-layer LSTMs since model with the highest number of the hidden neurons (128 in our case) gives the best classification results.

TABLE II. RESULTS FOR LSTM-BASED MODELS WITHOUT LOCAL ATTENTION MECHANISM

Model Name	***Number of Layers***	***Number of Hidden Neurons***	***Number of parameters***	***UAR***
LSTM-l1-h32	1	32	8 968	35,22
LSTM-l1-h64		64	26 120	40,49
LSTM-l1-h128		128	85 000	**43,23**
LSTM-l2-h32	2	32	17 416	34,64
LSTM-l2-h64		64	59 400	39,91
LSTM-l2-h128		128	217 096	**41,47**
LSTM-l3-h32	3	32	25 864	32,62
LSTM-l3-h64		64	92 680	38,02
LSTM-l3-h128		128	349 192	**40,89**

Table III compares classification results of LSTM-based NNs with the local attention mechanism. The results show that increasing number of layers or hidden neurons does not guarantee final UAR improvement. For example, a model with only one hidden layer and only 64 hidden neurons outperformed all other models. As shown in the table, UAR does not improve when using more complex models but the number of parameters increases dramatically: from 26 184 up to 349 192. Therefore, a significant increase in the complexity of the model does not result in its performance increase.

TABLE III. RESULTS FOR LSTM-BASED MODELS WITH LOCAL ATTENTION MECHANISM

Model Name	*Number of Layers*	*Number of Hidden Neurons*	*Number of parameters*	*UAR*
LSTM-l1-h32	1	32	9 000	43,55
LSTM-l1-h64		64	26 184	**46,09**
LSTM-l1-h128		128	85 128	44,60
LSTM-l2-h32	2	32	17 448	41,08
LSTM-l2-h64		64	59 464	42,84
LSTM-l2-h128		128	217 224	**44,86**
LSTM-l3-h32	3	32	25 896	38,35
LSTM-l3-h64		64	92 744	**41,15**
LSTM-l3-h128		128	349 320	38,61

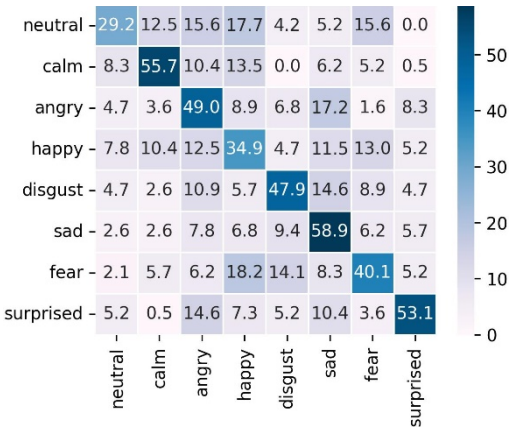

Fig. 7. Confusion matrix for LSTM-L1-H64 model with local attention

In Fig. 7 a multiclass confusion matrix is presented for the best LSTM model with local attention mechanism. Among the emotions, it can be observed that the most frequently misclassified emotion was neutrality (29,2 %). Interestingly, this emotion appeared to be frequently confused with happiness, suggesting some similarities in their acoustic characteristics. Conversely, sadness demonstrated a high recognition accuracy (58,9 %) and was seldom misclassified as another emotion, indicating distinctive features in its acoustic profile.

V. CONCLUSION

The paper shows that LSTM-based NNs in their basic configurations with a simple attention mechanism can be used for speech emotion recognition. The importance of correct initialization of weights and biases, as well as the configuration of hyperparameters (the number of hidden layers and hidden neurons) is also experimentally proven. The hypothesis about the positive influence of local attention mechanism on the final classification accuracy compared to the use of a similar LSTM architecture but without the local attention mechanism is tested and proved. Further improvements can be made by using advanced attention mechanisms. This potentially allows the model to focus on the most informative parts of a time series, enhancing the contribution of key moments in speech to emotion recognition and thereby increasing classification accuracy.

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Development of a Vision System for Determining Geometric Parameters of Objects*

*The article was retracted by the authors

*The article was retracted by the authors

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*The article was retracted by the authors

Practical Aspects of FPGA Implementation of Neural Network for Image Classification Based on Learned Separable Transform

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Abstract. **The paper presents an FPGA implementation of a neural network (NN) for image classification based on a learned two-dimensional separable transform (LST). The LST is based on the idea of using two fully connected layers to generate image embeddings. The first FC layer is applied to each row of an image, and then a second FC layer is applied to the columns of the resulting intermediate representation. Our experience shows that LST can be used as a replacement for the initial FC layers in multilayer perceptrons used for image recognition. We developed a hardware implementation of LST-based NN on an FPGA platform and constructed its reference fixed-point model in Python. Experimental results demonstrate that an NN-based classifier consisting of a single LST layer followed by an FC layer achieved 98.02 % accuracy on the MNIST dataset while having only 9.5k parameters.**

Keywords: **neural network, fully connected layer, MNIST, learned separable transform, FPGA**

I. INTRODUCTION

Deed neural networks (DNN) are a crucial component of many applications related to computer vision and image processing. However, deploying DNNs on resource-constrained platforms, such as Field-Programmable Gate Arrays (FPGAs), requires the development of efficient hardware architectures to achieve optimal performance [1, 2]. The main challenge in implementing a DNN on the FPGA is the high computational cost associated with the large number of network parameters. There are two main approaches to reduce the complexity of DNNs: 1) pruning the parameters of an existing model [3], and 2) designing a model with a reduced number of parameters [4, 5]. Convolutional neural networks (CNNs) can be considered as an example of a model with a reduced number of parameters, as they rely on the concept of weight sharing. However, recently, learned 2D separable transform (LST) was proposed for designing compact and high-performance NNs for image recognition tasks [6].

In this work the practical aspects of designing FPGA-based implementation of NN based on LST are considered. LST is a technique that enables the decomposition of image processing into two sequential stages, significantly decreasing the number of multiplications and the required memory footprint.

II. LEARNED 2D SEPARABLE TRANSFORM (LST)

The LST can be considered as a new type of computational layer that can be used to design a compact NNs for image processing. The key feature of the LST is that it requires significantly fewer parameters for creating a 2D image embedding compared to a fully connected (FC) layer. The LST processes input images in a row-by-column fashion, rather than flattening the image into a vector as is typically done in architectures based on multilayer perceptron (MLP) [7]. This structural change allows for significant parameter reduction while preserving spatial relationships within the image.

Mathematically LST takes image $\mathbf{X}$ of size $d_{in} \times d_{in}$ and produce 2D output image $\mathbf{Y}$ of size $d_{out} \times d_{out}$:

$$\mathbf{Y} = LST(\mathbf{X}) = \sigma(\mathbf{W}_2 \sigma(\mathbf{W}_1 \mathbf{X}^T + \mathbf{b}_1) + \mathbf{b}_2), \qquad (1)$$

where $\sigma(\cdot)$ – activation function, $\mathbf{W}_1, \mathbf{W}_2$ – linear transformation matrices of FC layers for processing rows and columns respectively, $\mathbf{b}_1, \mathbf{b}_2$ – biases.

Graphical representation of LST is given in Fig. 2. It can be seen that LST consists of two stages of processing. In the first stage, the input image is separated into rows and processed by the FC1 layer. We use $\tanh(\cdot)$ as nonlinear activation function. After this, the resulting representation is processed column-wise using the FC2 layer. The size of the obtained embedding is controlled by parameter d_{out}. The number of learnable parameters of LST is equal to

$$N_{params} = 2 \cdot (d_{in} + 1) \cdot d_{out}, \qquad (2)$$

where d_{in} – input image size, d_{out} – output embedding size.

III. NN BASED ON LST FOR IMAGE CLASSIFICATION

A. LST-1 model

The LST layer can be seen as a way to obtain an image embedding of a desired size. This embedding can then be flattened and passed through a FC layer with a softmax activation function for classification tasks. This simplest NN architecture based on LST (Fig. 1) was proposed in [6] and is referred to as LST-1.

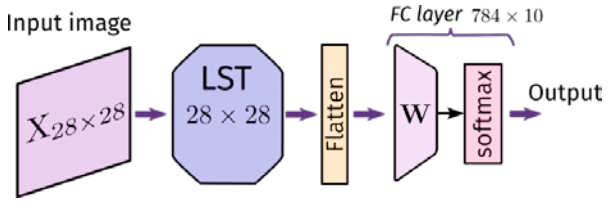


Fig. 1. NN architecture based on LST (LST-1 model)

B. LST-1 training

The LST-1 model is trained on the MNIST dataset. The dataset consists of 60,000 training and 10,000 test grayscale images, each of size 28×28 pixels. From the training set, 1,000 images are reserved for validation, while the remaining 59,000 are used for model training. Prior to training, all images are normalized such that pixel values lie within the range [−1, 1], and the standard deviation is set to 0.5. This normalization improves the stability of gradient descent and accelerates the convergence of the model during training. Cosine scheduler [8] and warm-up strategy are employed to adjust the learning rate. The model is trained for 600 epochs using the negative log-likelihood loss (NLLLoss) function. The Fig. 3 shows the loss function trend over the training period, illustrating convergence toward a value of approximately 0.065, indicating stable model training.

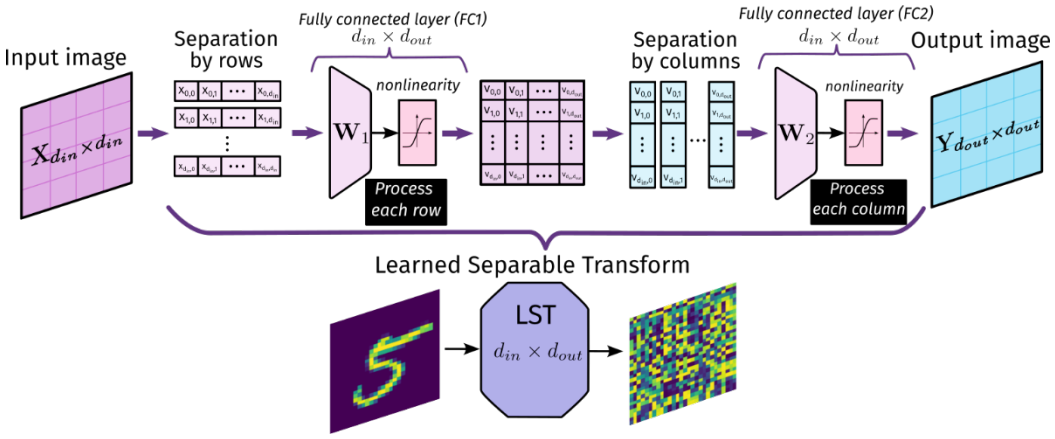


Fig. 2. Learned separable 2D transform

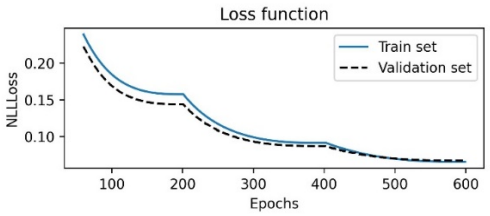


Fig. 3. Loss function on training and testing set

The LST-1 model achieved 98.02 % accuracy on the MNIST test set. An example of image embedding obtained using LST-1 model is given in Fig. 4.

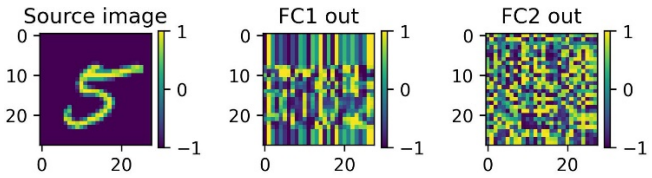


Fig. 4. LST-1 model embedding

C. Fixed-point implementation of LST-1

In order to verify the hardware implementation, a reference model is developed in Python using the Fixpoint package. The reference model employs a fixed-point representation with Q6.7 format. During the conversion from floating-point to fixed-point, a rounding-down approach is used. This method reduces rounding errors and avoids the systematic bias that can occur when rounding to the nearest value. The fixed-point model achieves an accuracy of 97.9 % on the MNIST test set, with only a 0.12 % reduction compared to the original floating-point model. Fig. 5 shows the activations after the FC2 layer for the floating-point and fixed-point LST-1 models. As can be seen, the embeddings generated by the two models have a negligible difference.

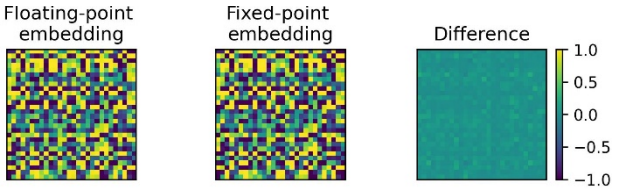


Fig. 5. Comparison of the embeddings for floating- and fixed-point models

IV. FPGA IMPLEMENTATION

In this section, we describe the hardware architecture used for the FPGA implementation of the LST-1 model (see Fig. 1). The interface of the NN IP-block is depicted in Fig. 6.

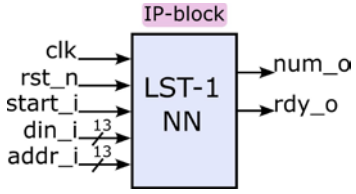


Fig. 6. Interface of NN IP-block

The IP-block receives reset and start control signals, along with the input pixel value and the pixel address, at its input. After the calculation process has finished, the final class label is output to `num_o` and the signal `rdy_o` is set to 1. The proposed design utilizes a single physical computation layer to perform all necessary operations. A detailed block diagram of the LST-1 architecture is presented in Fig. 7.

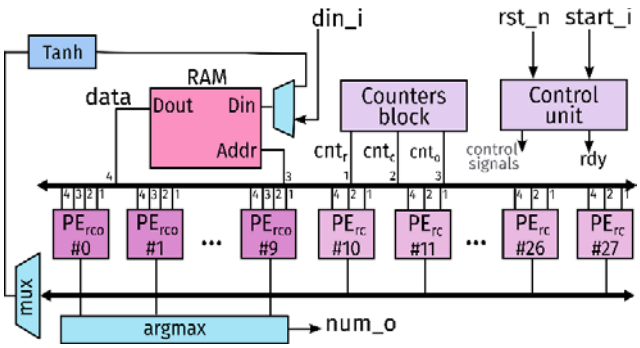


Fig. 7. Structure of the LST-1 NN IP-block

All computations within the LST layer, as well as in the final FC layer, are executed using 28 processing elements (PEs). These PEs are divided into two distinct types, as illustrated in Fig. 8, which aligns well with the 28×28 dimensions of the input images and enables efficient parallel processing.

The LST-1 IP-block utilizes 10 PEs of rco-type, which are reused for computing both the LST layer and the final FC layer. To support this dual functionality, these PEs require additional storage for output layer coefficients and an extra address input for controlling memory access. The PEs of rc-type is dedicated exclusively to performing row and column processing in the LST layer.

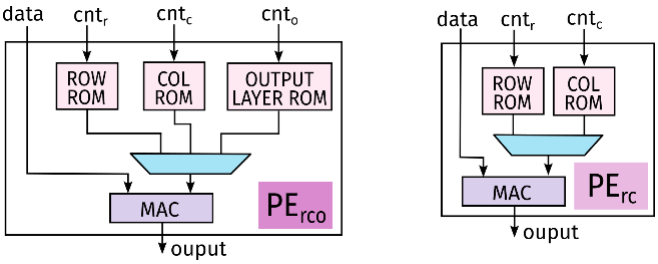


Fig. 8. Structure of PE blocks

A block of counters (see Fig. 7) is used to compute addresses for accessing both the weight memory and the image memory. The RAM stores the intermediate results at all stages of computation: initially the input image, then the output of each FC layer within the LST block.

The non-linear activation function $\tanh(\cdot)$ is approximated using a hardware-friendly piecewise function, as a direct implementation would be computationally expensive. The approximation follows the formula [3]:

$$\tanh(x) \approx F(x) = \begin{cases} \operatorname{sign}(x), & |x| > 2 \\ (1+\frac{x}{4}) \cdot x, & -2 < x < 0, \\ (1-\frac{x}{4}) \cdot x, & 0 < x < 2. \end{cases} \quad (3)$$

The softmax layer (see Fig. 1) is responsible for producing a probability distribution over the 10 output classes (digits from 0 to 9). However, there is no need to use the softmax activation function for inference. Instead, the argmax function can be used to compare all 10 class scores and select the class with the highest score. Additionally, the argmax function uses much less FPGA resources compared to softmax.

The control unit is implemented as a finite state machine with combinational logic for generating the next state and appropriate control signals for the other modules. The control sequence includes the following steps:

1) When the `start_i` signal is set to 1, the input image is loaded into RAM and the `rdy` signal is set to 0.

2) Set current row `cnt_r = 0.`

3) Initialize MAC-cores of PEs with biases of FC1 layer.

4) Perform MAC operations across 28 PEs with current row `cnt_r`.

5) Compute the tanh activations and write the result back to RAM. Set `cnt_r = cnt_r + 1.`

6) If not all rows have been processed (`cnt_r<28`), go to step 3, otherwise, proceed to column-wise processing (step 7).

7) Set current column `cnt_c = 0.`

8) Initialize MAC-cores of PEs with biases of FC2 layer.

9) Perform MAC operations across 28 PEs with current column `cnt_c`.

10) Compute the tanh activation and write the result back to RAM. Set `cnt_c = cnt_c + 1.`

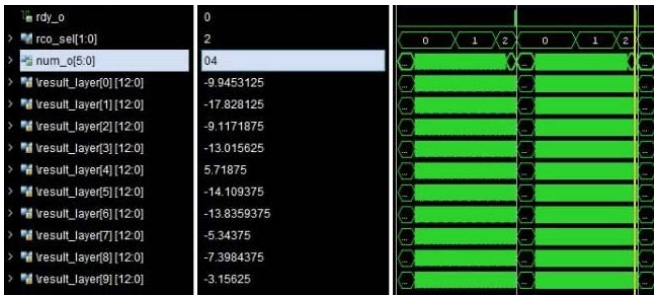
11) If not all columns have been processed (`cnt_c<28`), go to step 8, otherwise, proceed to the output FC layer (step 12).

12) Initialize MAC-cores of PE0…9 with biases of FC output layer.

13) Perform MAC operations across 10 PEs for computing output FC layer.

14) Compute the argmax over the obtained outputs to find the predicted class. Set `rdy` signal to 1.

The result of the post-synthesis timing simulation and the fixpoint implementation are shown in Fig. 9. This result shows the recognition results and the input of the softmax activation function.



a

```
Softmax: [ -9.9453125 -17.828125   -9.1171875 -13.015625    5.71875   -14.109375
 -13.8359375  -5.34375    -7.3984375  -3.15625  ]
Num: 4
```

b

Fig. 9. Simulation result: post-synthesis (a) fixed-point Python-model (b)

V. Experemental results

For the implementation of the LST-1 model, the Zybo development board, based on the Zynq-7000 FPGA, was selected. The Zynq platform integrates an ARM processor with FPGA programmable logic, providing a flexible and efficient hardware/software solution. To facilitate development and testing, the Linux-based PYNQ distribution is employed on this platform. PYNQ allows to interact with FPGA hardware units implemented as IP cores using a Jupyter notebook, which makes the development process more convenient. The uP-AXI4-lite interface converter is used to connect the processor system to the developed IP block. The architecture of the developed system is shown in Fig. 10.

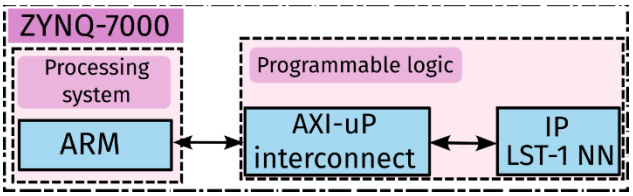


Fig. 10. Prototyping the LST-1 model on the ZYBO Z7

For FPGA testing, 10,000 test images are processed sequentially, and a confusion matrix is generated to evaluate the recognition accuracy for each digit. Fig. 11 and 12 show the confusion matrices obtained from the floating-point model and FPGA implementation, which aligns with the matrix generated by the Python-based fixed-point model. The overall accuracy of the LST-1 model with weights quantized into Q6.7 format is 97.9 %.

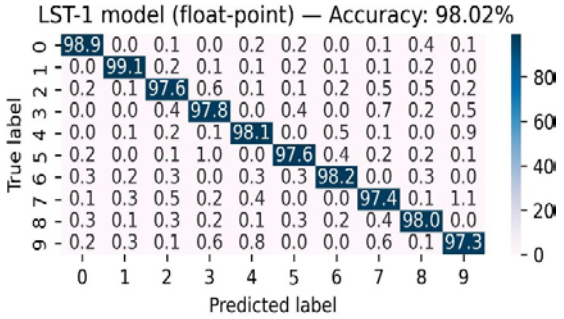


Fig. 11. Confusion matrix on MNIST test set obtained for floating point LST-1 model

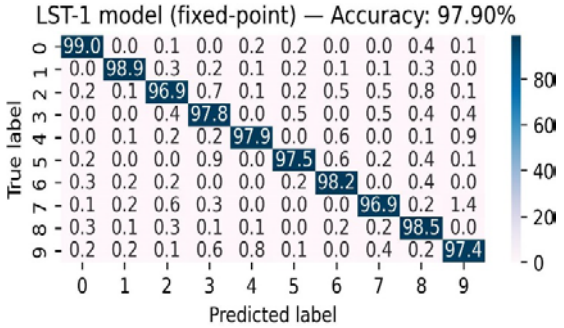


Fig. 12. Confusion matrix on MNIST test set obtained for fixed-point LST-1 model

Based on the obtained results, it can be concluded that the digits 1 and 0 are recognized with the highest accuracy (above 98.9 %), while the digit 7 is recognized with the lowest accuracy (96.9 %). The hardware resource usage, derived from the placement reports of

the FPGA implementation of LST-1 model in the Xilinx Vivado environment, is presented in Table I. The operating frequency of the device is 80 MHz.

TABLE I. HARDWARE COSTS

Block type	Number of blocks		*Usage, %*
	used	*available*	
LUT as logic	1302	17600	7.40
LUT as memory	60	6000	1.00
FF	1461	35200	4.15
BRAM	33.5	60	55.83
DSP	57	80	71.25

Table II shows that the proposed architecture has high efficiency with only 9.5 k parameters. It can be seen that the LST-1 model has from 95 to 12 times fewer parameters than the models based on MLP architectures, with comparable performance.

TABLE II. COMPARISON OF THE LST-BASED NN ARCHITECTURES WITH OTHER DNN

Authors & ref.	**DNN architecture**	**#Params**	*Accuracy, %*
Medus [2]	784-600-600-10	891,610	98.63
Samragh [4]	784-512-512-10	670,208	98.40
Huynh [7]	784-126-126-10	115,920	98.16
Huynh [7]	784-40-40-40-10	34,960	97.20
Westby [9]	784-12-10	9,550	93,25
LST-1 [proposed]	LST-1	9,474	98.02

VI. CONCLUSION

We proposed a hardware implementation of neural network for handwritten digit recognition system based on the learned 2D separable transform. The fixed-point implementation of the LST model on FPGA demonstrates that quantization of the model weights does not result in a significant decrease in accuracy. Therefore, the proposed approach for constructing LST-based neural networks is suitable for designing compact and efficient hardware architectures for image classification tasks. MAC cores based on DSP48 blocks are used as the primary computing units, while weight coefficients and biases are stored in block RAM.

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Comparative Analysis of Deep Learning Models for Lumbar Vertebrae Segmentation in MRI Images

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***Abstract*. Lower back pain is a widespread health concern globally, leading to significant social and medical expenses. Magnetic Resonance Imaging (MRI) is widely used for evaluating lumbar intervertebral disc degeneration due to its non-invasive nature and superior tissue differentiation capabilities. However, traditional 2D image analysis methods are often hindered by noise and various external factors, complicating accurate diagnosis and surgical planning. To address these challenges, this study investigates the application of deep learning models for lumbar vertebrae segmentation in MRI images. We employ U-Net, HRNet, and EfficientNet architectures, to develop an accurate segmentation model. The U-Net model, characterized by its encoding and decoding phases, demonstrated superior performance with a Precision of 0.9809, Recall of 0.9715, F1-score of 0.9742, and mAP of 0.7084. Comparatively, HRNet and EfficientNet also showed promising results, with HRNet achieving a Precision of 0.6684, Recall of 0.9153, F1-score of 0.77208, and mAP of 0.6568, while EfficientNet achieved a Precision of 0.7995, Recall of 0.9247, F1-score of 0.8491, and mAP of 0.7666. Our findings indicate that deep learning models, particularly U-Net, can significantly enhance the accuracy and efficiency of lumbar vertebrae segmentation in MRI images. This advancement holds potential for improving clinical diagnostics and surgical planning. Future work will focus on refining these models with larger datasets and exploring additional architectures to further enhance segmentation performance and robustness.**

***Keywords:* Medical Image Segmentation, U-Net, Convolutional Neural Network, Lumbar MRI, Performance Evaluation**

I. INTRODUCTION

Lower back pain is a prevalent health issue globally, resulting in substantial social and medical costs [1]. Magnetic resonance imaging (MRI), due to its non-invasive nature and ability to differentiate various tissues, is considered an ideal tool for evaluating lumbar intervertebral disc degeneration in clinical and research settings. Traditional detection methods in two-dimensional imaging are susceptible to noise, equipment, human, and environmental factors, significantly hindering physicians in diagnosing and planning surgeries based on the obtained images [2, 3]. Spinal image segmentation, which utilizes pixel features to separate pathological regions from muscle tissue, is crucial for analyzing spinal pathological structures and guiding spinal surgeries.

With the rapid development of artificial intelligence, convolutional neural networks (CNNs), known for their powerful nonlinear feature extraction capabilities, have greatly advanced research in image segmentation [4]. Deep learning based image segmentation methods can achieve excellent results in medical image segmentation. In terms of segmentation efficiency, deep learning have significant advantages over traditional machine learning algorithms [5]. This study aims to construct an accurate lumbar MRI segmentation model using CNN frameworks, specifically U-Net, HRNet, and EfficientNet architectures.

II. RELATED WORK

Accurately segmenting disease areas and key tissues from various medical images provides a visual basis for clinical treatment, addressing visualization issues in many diagnoses. Traditional spinal image segmentation methods are mainly divided into semi-automatic and non-automatic categories [2]. Non-automatic segmentation methods can be completed based on differences in image thresholds and pixel values. Semi-automatic segmentation methods somewhat alleviate the operational pressure on physicians, but the segmentation speed still falls short of real-time segmentation requirements [6]. Although traditional medical image segmentation techniques have significantly advanced modern medical imaging, they struggle to meet the faster, more accurate, and more efficient demands of modern medical technology [7].

Deep learning-based image segmentation techniques have emerged in new forms. Long et al.[8] proposed Fully Convolutional Networks (FCN), which hold significant importance in the history of image semantic segmentation development. FCN addresses many

bottlenecks in semantic segmentation, surpassing traditional advanced levels and providing end-to-end, pixel-to-pixel segmentation solutions. However, FCN, as the first-generation semantic segmentation model, has many areas for improvement. Ronneberger et al. [9] modified FCN's network structure to change network connection patterns, proposing the U-Net model that emphasizes the connection of image features during training. U-Net, with its lightweight structure and good training effect on small sample sets, has become a classic end-to-end method in the segmentation field (Fig. 1). Prior research indicates that U-Net demonstrates superior performance in MRI vertebral segmentation.

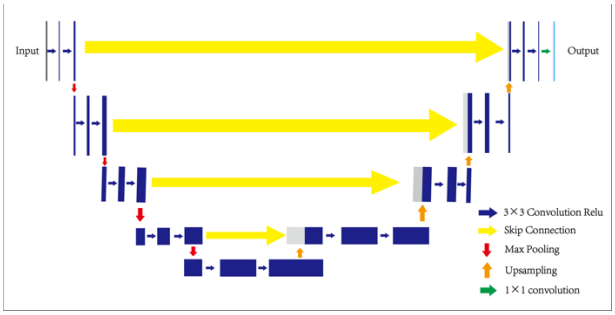

Fig. 1. U-Net Model

HR-Net [10] is a high-resolution network designed to achieve precise feature extraction and classification by maintaining high-resolution feature maps. The core design principle of HR-Net involves processing feature maps at different resolutions through multiple parallel branches, with feature exchange occurring at each stage of the network to preserve high-resolution information. The main structure of HR-Net comprises four stages, each containing multiple parallel convolutional modules that process feature maps of varying resolutions, which are then fused through feature exchange layers. The key feature is the maintenance of high-resolution feature maps to enable accurate feature extraction and classification (Fig. 2). Previous studies have shown that HR-Net achieves excellent results in human keypoint detection tasks, effectively identifying key body parts [10–12].

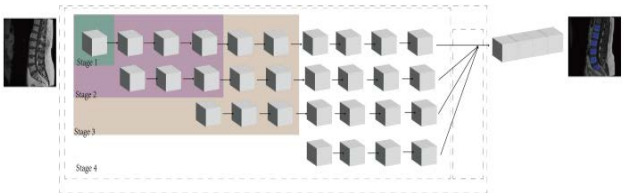

Fig. 2. HR-Net Model

EfficientNet [13] is an efficient CNN model that achieves high performance with reduced parameters and computational cost through comprehensive scaling of network depth, width, and resolution, thereby enabling efficient feature extraction and classification. EfficientNet-B0, the smallest version of EfficientNet, boasts fewer parameters and lower computational requirements. The main structure of EfficientNet-B0 consists of two convolutional modules, sixteen MBConv modules, a global average pooling layer, a dropout layer, and a fully connected layer, with the core being the sixteen MBConv modules, which achieve efficient feature extraction through the continuous stacking of multiple MBConv modules (Fig. 3). Existing research suggests that EfficientNet can effectively identify vertebrae and intervertebral discs in vertebral MRI [14].

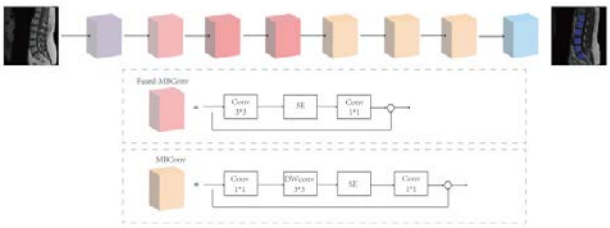

Fig. 3. EfficientNet model

However, the relative performance of the U-Net Model, HR-Net Model, and EfficientNet model in MRI vertebral segmentation, and which algorithm offers the optimal application effect, remains a subject of ongoing debate and lacks a definitive consensus.

III. Proposed Apporach

Our segmentation method is based on the convolutional neural networks, utilizing U-Net, HRNet, and EfficientNet architectures. The dataset comprises a total of 514 lumbar spine MRI images, which were divided into training, testing, and validation sets according to a distribution ratio of 70 %, 15 %, and 15 %, respectively.

A. Image Dataset

The training, testing, and validation datasets contain 514 lumbar MRI images with various lumbar diseases. The lumbar vertebrae mainly include the L1-L5 and S1 regions. All images were manually annotated and verified by experts, outlining the vertebrae contours.The partial images of the dataset are shown in Fig. 4.

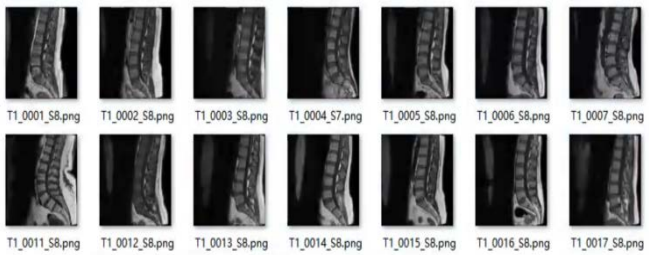

Fig. 4. The partial images of the dataset

B. Experimental environment

The experimental environment for Comparative Analysis of Deep Learning Models for Lumbar Vertebrae Segmentation in MRI Images is shown in Table.

EXPERIMENTAL ENVIRONMENT

Software and hardware names	Specific parameters
CPU	Intel(R) Xeon(R) Gold 6226R
Memory	64GB
GPU	Quadro RTX 5000
Operating system	Window 10 Professional Edition
Software environment	Python3.12.7+torch2.6.0+cu118

C. Results and Discussion

In our experiments, we concentrated on precise vertebrae segmentation in lumbar MRI images. The U-Net model employed in this study features an encoding phase consisting of convolution operations and max-pooling layers, while the decoding phase utilizes convolution operations and deconvolution layers, culminating in a Softmax layer for classification. We also incorporated HRNet and EfficientNet models for comparative analysis. Following the input of lumbar MRI image data into the U-Net, HRNet, and EfficientNet models for segmentation prediction, the resulting segmentation masks are illustrated in Fig. 5-7, respectively.

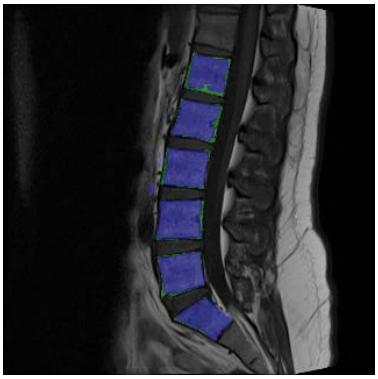

Fig. 5. Vertebrae segmentation by U-Net model

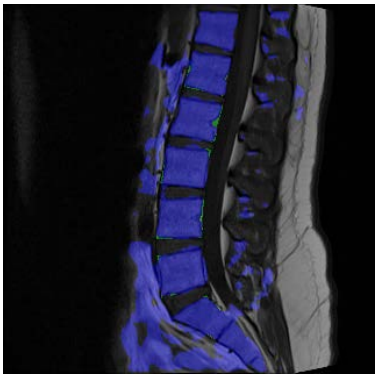

Fig. 6. Vertebrae segmentation by HRNet model

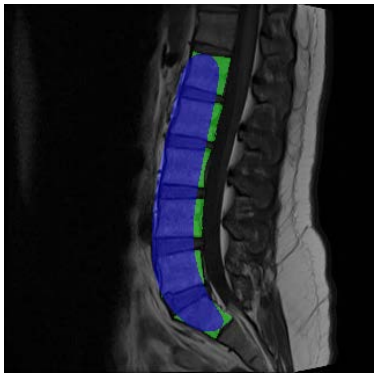

Fig. 7. Vertebrae segmentation by Efficient Net model

Quantitative evaluation metrics for each model are summarized as follows: U-Net achieved a Precision of 0.9809, Recall of 0.9715, F1-score of 0.9742, and mAP of 0.7084. HRNet obtained a Precision of 0.6684, Recall of 0.9153, F1-score of 0.77208, and mAP of 0.6568. EfficientNet yielded a Precision of 0.7995, Recall of 0.9247, F1-score of 0.8491, and mAP of 0.7666.As shown in Table II.

TABLE I. ERFORMANCE OF DIFFERENT MODELS

	U-Net	HRNet	Efficient Net
Precision	0.9809	0.6684	0.7995
Recall	0.9715	0.9153	0.9247
F1 Score	0.9742	0.7208	0.8491
mAP	0.7084	0.6568	0.7666

IV. CONCLUSION

This study explored the application of deep learning models, specifically U-Net, HRNet, and EfficientNet, for precise vertebrae segmentation in lumbar MRI images. Our results demonstrate the feasibility of these architectures for this task. While all models showed promise, U-Net achieved the highest overall performance in terms of Precision, Recall, F1-score, and mAP. This suggests its suitability for automated lumbar vertebrae segmentation.

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An Approach to Resource-Efficient Optimization for Real-time Computer Vision-based OHS Monitoring on Resource-constrained Industrial Objects

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Abstract. **This paper proposes and investigates a methodology for the resource-efficient optimization of real-time AI-based computer vision technologies for occupational health and safety (OHS) monitoring tasks on industrial objects, specifically targeting deployment in resource-constrained systems. The core of the methodology enables the efficient use of CPU-based server devices by introducing two key improvements: a two-stage detection mechanism with dynamic Region of Interest (ROI) selection to significantly reduce the computational load on the primary object detection model, and a static background subtraction algorithm for pre-filtering the video stream and removing non-informative scene areas. A detailed analysis of the performance (in terms of processing speed for real-time capability) and accuracy of various configurations implementing this approach, based on models from the YOLO family, is conducted. A conceptual scheme for integrating the proposed optimization techniques into a typical video analytics pipeline is described, along with a methodology for creating and annotating a specialized dataset. The paper demonstrates that the developed methodology achieves an acceptable balance between violation detection accuracy and video stream processing speed necessary for real-time operation on CPUs, opening prospects for the wider adoption of intelligent safety systems in environments with limited computational resources.**

Keywords: **occupational safety, health and safety, personal protective equipment (PPE), computer vision, YOLO, object detection, neural network optimization, edge computing, industrial safety, background subtraction, focus of attention, optimization methodology, video analytics.**

I. INTRODUCTION

Ensuring a high level of occupational health and safety (OHS) is a critical task for all industries, especially for sectors with high production risks, such as oil and gas enterprises. Statistics on occupational injuries in these sectors, despite the measures taken, remain high, which requires the search for new, more effective approaches to control and prevent incidents [1, 2]. Non-compliance with established norms and rules for the use of personal protective equipment (PPE), as well as violation of safety procedures, are among the main causes of occupational injuries and emergency situations. Traditional control approaches, based on inspections and human observation, have significant drawbacks, including subjectivity, high cost, limited coverage, and the inability to ensure continuous real-time monitoring, which is crucial for timely intervention.

The development of computer vision and deep learning technologies provides opportunities for creating automated OHS monitoring tools. Modern neural network architectures, such as YOLO (You Only Look Once) [5], SSD (Single Shot MultiBox Detector), and Faster R-CNN [8], show high results in object detection tasks in images and videos. The effectiveness of using computer vision for industrial safety monitoring is confirmed by a number of studies. However, their widespread practical application for real-time monitoring at remote or mobile industrial objects often faces the problem of high demands on computational resources. Providing broadband internet for video stream transmission to a centralized cloud service is not always technically feasible, and the use of high-performance servers with GPUs at each facility is frequently not economically viable, necessitating resource-efficient solutions that can operate on existing or limited hardware.

The authors of this paper propose a methodology for the resource-efficient optimization of real-time computer vision-based OHS monitoring, adapted for effective operation on devices with limited computational capabilities, primarily CPUs, commonly found in resource-constrained systems at industrial sites. A key improvement proposed in the article is the integration of algorithmic components into a common processing pipeline designed to significantly reduce

computational load and enhance processing speed: a two-stage "focus of attention" mechanism and static background subtraction. This approach offers an effective, resource-efficient, and affordable way to enhance industrial safety, reduce injury risks, and improve the overall safety culture at enterprises through wider adoption of intelligent real-time monitoring technologies.

II. Existing approaches to object detection and methods for their optimization for CPU

A. Object Detector Architectures

The task of automatic object detection in images and video is one of the fundamental tasks in computer vision. Over the past decades, a number of successful approaches have been proposed, among which methods based on deep convolutional neural networks (CNNs) have taken a dominant position.

Modern CNN-based object detectors can be broadly divided into two main families: one-stage and two-stage detectors.

Two-stage detectors: A prominent representative of this family is the R-CNN (Regions with CNN features) architecture and its more advanced versions, such as Fast R-CNN and Faster R-CNN. Their operation is based on two main stages. In the first stage, a set of potential regions (region proposals) where objects might be located is generated. For this, Faster R-CNN uses a special Region Proposal Network (RPN) module. In the second stage, each of these regions is analyzed by a classifier to determine the object class and refine its boundaries (bounding box regression). Two-stage detectors generally demonstrate high detection accuracy, especially for small objects and in scenes with a large number of overlapping objects. However, their sequential architecture leads to higher computational costs and, consequently, lower processing speed compared to one-stage counterparts.

One-stage detectors: This family includes popular architectures such as YOLO (You Only Look Once) [10] and SSD (Single Shot MultiBox Detector) [5]. Unlike two-stage detectors, they predict object classes and coordinates in a single pass of the neural network through the image. The image is divided into a grid of cells, and for each cell, bounding boxes, objectness score, and class probabilities are predicted.

YOLO: The YOLO family has undergone significant evolution: from YOLOv1 to more modern versions such as YOLOv3, YOLOv4 [9], YOLOv5, and the newest YOLOv7, YOLOv8 [3]. Each new version brought improvements in architecture (e.g., using more efficient backbone networks like DarkNet, CSPDarkNet, or without them in recent versions), feature aggregation mechanisms (Feature Pyramid Network FPN [4], Path Aggregation Network PANet [4]), loss functions, and data augmentation techniques. YOLO models are known for their high processing speed, making them ideal for real-time tasks. However, earlier versions could be inferior to two-stage detectors in the accuracy of detecting small objects.

SSD: The SSD architecture uses a set of anchor boxes of various scales and aspect ratios on multiple feature maps of different resolutions. This allows for effective detection of objects of different sizes. SSD is also a fast detector, but its accuracy can depend on the correct selection of anchor box configurations for a specific task.

In the context of PPE monitoring on CPUs, one-stage detectors, especially modern YOLO versions, are of greatest interest due to their optimal balance of speed and accuracy, making them suitable candidates for resource-efficient real-time applications.

B. Methods for Optimizing Neural Network Models for CPU

For efficient operation of object detectors on CPUs with minimal compromise to accuracy, various optimization strategies are applied, such as quantization, knowledge distillation, and algorithmic optimizations.

Quantization: This method involves reducing the bit precision of the model's weights and/or activations [6]. Instead of 32-bit floating-point numbers (FP32), 16-bit or 8-bit integers are used. This leads to a reduction in model size, decreased memory bandwidth requirements, and accelerated computations.

Knowledge Distillation: This approach involves training a more compact "student" model using knowledge obtained from a larger and more accurate "teacher" model [7]. The "student" is trained not only on true labels but also on the "soft" predictions (class probabilities) of the "teacher". This allows the transfer of the generalization ability of the large model to the small one, often achieving better quality than when training the small model from scratch only on true labels.

Algorithmic Optimizations:

- Optimization of the data processing pipeline itself: minimizing data copying, efficient cache utilization, parallelization of independent operations.
- Use of specialized libraries and frameworks for CPU inference, such as ONNX Runtime. These tools provide optimized implementations of operations for various processor architectures,

support quantized models, and can automatically apply various graph optimizations.

The choice of a specific method or combination of optimization methods depends on the specifics of the task, requirements for accuracy and performance, as well as available tools and hardware platform. For the task of PPE monitoring at drilling sites, where real-time operation on a CPU is required, a combination of lightweight architectures, quantization, and algorithmic optimizations, such as Region of Interest Cropping and background subtraction, appears to be the most promising for achieving resource efficiency.

III. Proposed Optimization Methodology for OHS Monitoring

The proposed methodology aims to create an efficient video data processing pipeline for detecting OHS violations, which can be implemented on devices with limited computational resources. It is based on two main components: a "focus of attention" algorithm and a static background subtraction method, integrated into a common sequence of operations.

A. Static Background Subtraction

At many industrial monitoring sites, including drilling rigs, video cameras are often installed stationary. Under such conditions, a significant part of the observed scene remains unchanged over time (static background), while the changes of interest are primarily related to the movement of personnel and, to a lesser extent, the operation of some equipment. Effective separation of moving objects from the static background can significantly reduce the amount of data for subsequent analysis by neural network models.

We propose to use an adaptive background subtraction method based on Gaussian Mixture Models (GMM) [8]. The choice of GMM is due to its ability to effectively model a background that is not absolutely static, and its relative robustness to phenomena characteristic of an industrial environment, such as:

- Shadows: GMM can model changes in pixel intensity caused by moving shadows and not classify them as foreground objects.
- Lighting Changes: The adaptive nature of GMM allows it to gradually adjust to slow and moderate changes in the overall scene illumination level.
- Periodic movements of background elements: At drilling rigs, elements performing repetitive movements may be present (e.g., slight swaying of wires, rotor rotation at low speed if it is not the main object of interest). GMM can incorporate such regular changes into the background model, highlighting only more significant, atypical movements, such as people moving, as foreground.

Thus, the use of GMM allows filtering out a large part of irrelevant information (Figure), leaving for subsequent analysis by the neural network model only those areas of the frame where significant moving objects are present with high probability, primarily personnel.

Example of adaptive background subtraction

Integrating GMM as a preprocessing component can significantly reduce the amount of data fed to the input of subsequent detector stages, leading to an overall reduction in computational load.

B. Region of Interest Cropping

The main idea of this component is to intelligently reduce the volume of data fed to the input of the main, resource-intensive neural network detector model. Instead of processing each video frame entirely with a "large" high-accuracy recognition model, a two-stage process is proposed:

- Stage 1: Preliminary localization of regions of interest (ROI). At this stage, a fast and computationally "light" model (e.g., YOLOv8n) is used for coarse detection of key objects (people) that are highly likely to contain or be associated with the target monitoring objects. Due to its low complexity and small number of target classes, this stage requires insignificant resources. The result is a set of bounding boxes outlining potential ROIs.
- Stage 2: Detailed analysis of ROI. ROIs identified in the first stage (with some configurable padding to capture context and PPE) are cropped from the original frame. These fragments are passed to the input of the main, more accurate model (YOLOv8s) for detecting all target PPE classes. Due to the small ROI sizes, the main detector processes significantly fewer pixels, which reduces inference time while maintaining high accuracy.

IV. Experimental Study and Discussion of Results

To assess the effectiveness and practical applicability of the proposed optimization methodology, a comprehensive experimental study was conducted.

The key goals were a quantitative assessment of the performance gain (FPS) and an analysis of the impact of optimization components on the accuracy (mAP) of neural network detection of OHS violations.

A. Dataset Formation and Selection of Evaluation Metrics

For this study, a specialized dataset was created that maximally reflects the operating conditions at drilling rigs.

The basis of the dataset consisted of 12 video recordings obtained from surveillance cameras installed at various sections of active drilling platforms. The total duration of the source video material was about 8 hours. The recordings covered various work operations and times of day.

Individual frames were extracted from the video recordings. To ensure diversity and reduce data redundancy, a mixed approach was used: every 25th frame was extracted (at an original video FPS of 25 frames/sec, this gave approximately 1 frame per second), and additional frames containing significant changes in the scene or rare views of personnel and equipment were also selected. The total number of images extracted for annotation was about 11,500. The original video resolution varied, but for the dataset, images were resized to a standard Full HD (1920×1080 pixels) and HD (1280×720 pixels) resolution to assess the impact of resolution on performance and accuracy. Data annotation was performed manually using the CVAT (Computer Vision Annotation Tool). The following 8 object classes were defined: *helmet, no_helmet, vest, no_vest, person_front, person_back, gloves, no_gloves*.

During annotation, attention was paid to cases of partial object occlusion, different views, and scales. The class distribution was somewhat imbalanced: the *person_front* and *person_back* classes occurred more frequently than cases of explicit PPE absence, however, they were used in a separate model for fast ROI search, which let us avoided additional data balancing

The resulting dataset was randomly split into training (70 %), validation (15 %), and testing (15 %) sets, while maintaining class proportions in each set.

For quantitative evaluation of the effectiveness of the proposed solutions, commonly accepted metrics in object detection tasks were used: mAP (mean Average Precision), Precision, and Recall for each class, as well as FPS to assess the system's operating speed.

B. Analysis of Experimental Results

Experiments were conducted to evaluate the impact of the proposed optimization methods on performance and accuracy. The following main configurations were tested using the YOLOv8s model as the primary detector (input video resolution – HD, 1280x720):

1) Configuration A (Baseline): YOLOv8s processes the full video frame.

2) Configuration B (ROI Cropping): YOLOv8n for detecting people (ROI) + YOLOv8s for PPE analysis in the identified ROIs.

3) Configuration C (ROI Cropping + Background Subtraction): Sequential application: first background subtraction (GMM), then ROI detector (YOLOv8n), and then YOLOv8s on the final ROIs.

All measurements were performed on a test machine with an Intel Core i7-10700 CPU without using a discrete graphics card.

SUMMARY RESULTS OF PERFORMANCE AND ACCURACY

Type	***FPS***	***mAP@0.5***				
		Overall	***Helmet***	***Vest***	***No helmet***	***No vest***
A	8.5	0.812	0.953	0.930	0.821	0.791
B	16.2	0.863	0.972	0.955	0.881	0.845
C	***24.1***	0.835	0.965	0.942	0.843.	0.810

The data from Table clearly show that the proposed optimization methodology allows achieving a significant increase in performance (FPS) when working on a CPU. The baseline configuration (A) with full HD frame processing by YOLOv8s demonstrates 8.5 FPS. Background removal and applying the model to ROI allows accelerating frame processing to 24.1 FPS while increasing the overall mAP@0.5 accuracy metric from 0.812 to 0.835.

V. CONCLUSION

This paper proposed and experimentally validated a methodology for optimizing the application of neural network technologies for automated OHS monitoring, focused on effective functioning under limited computational resources on a CPU. The methodology, based on a combination of a dynamic ROI algorithm and static background subtraction, demonstrated the ability to significantly increase the video stream processing speed of YOLO models (up to 2.8 times) while maintaining an acceptable level of violation detection accuracy. This opens up opportunities for wider and more economically effective implementation of intelligent video monitoring systems for safety in industrial facilities.

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A Demodulation Method for DDMA-MIMO in Strong Clutter Background

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Abstract. **Frequency modulated continuous wave multiple-input multiple-output (FMCW-MIMO) millimeter-wave radar is widely used in the field of automatic driving. Doppler division multiple access (DDMA) achieves waveform orthogonality through phase coding in the Doppler domain. However, when the antenna array has a large number of elements, under the strong clutter background, there would occur many clutter peaks in the range-Doppler (RD) spectrum during DDMA demodulation process. These issues result in a sharp decline in target detection performance. Therefore, a demodulation method for DDMA-MIMO radar in strong clutter background is proposed in this paper to improve the target detection accuracy. Specifically, the demodulation method includes two steps, i.e. the background clutter suppression method based on multi-frame signals and the peak correction method of RD spectrum based on variable threshold. Several experimental results of the real-data confirmed that the demodulation method achieved DDMA demodulation in both vehicular scenario and UAV scenarios. The relative radial velocities between radar and target were accurately estimated, which verified the effectiveness and wide applicability of the proposed method.**

Keywords: **FMCW, DDMA demodulation, background clutter suppression, peak correction**

I. INTRODUCTION

Frequency modulated continuous wave multiple-input multiple-output(FMCW-MIMO) radar has become a key technology in the field of autonomous driving [1–3]. MIMO radar significantly improves the angular resolution through combining transmitting and receiving antennas under the premise of orthogonal transmission. Doppler division multiple access (DDMA) is a widely used orthogonal waveform design method using phase coding schemes. DDMA realizes orthogonal demodulation through peak detection in the range-Doppler (RD) spectrum of the received signal [4].

DDMA modulation introduces Doppler ghost peaks in the RD spectrum of the intermediate frequency (IF) signals. In order to achieve DDMA demodulation, the uncoded spectral peaks must be extracted from multiple peaks [5]. At present, there are many studies on DDMA demodulation [6–8]. Usually, DDMA demodulation is realized through inserting empty-bands into the IF signal RD spectrum and combining the noncoherent integration (NCI) method [5]. M. Jeannin et al. [9] proposed a multiplexing spurs cancellation method , and validated the DDMA demodulation performance with an antenna array of 3 transmitters and 4 receivers (3TX4RX). Moreover, stable DDMA demodulation is achieved through multiple subbands coherent accumulation [10]. In both [9] and [10], experiments were carried out through 3TX4RX and 4TX4RX antenna arrays respectively. However, in these experiments, the target peaks in the IF signal RD spectrum are prominent, and the background clutter is negligible. These conditions result in DDMA demodulation easily. In general, current DDMA demodulation studies focus on antenna

arrays with few elements and lack experiments in the strong clutter background [6–8].

In this paper, a DDMA demodulation method is proposed to suit scenarios with a large number of array elements and strong clutter background. Firstly, the background clutter suppression method based on multi-frame signals is applied to overcome the lack of background priors. Secondly, the peak correction method is proposed to correct the subband peak power distortion in the Doppler domain. Finally, several DDMA demodulation experiments of real-data in vehicular scenario and UAV scenario are carried out in the strong clutter environment.

II. Signal Model

The single-input single-output FMCW signal model is established, and the transmitted signal is expressed as

$$s(t)=A_{\mathrm{t}}\exp\left[-j2\pi\left(f_0 t+\frac{1}{2}\mu t^2\right)\right],(0<t<T), \quad (1)$$

where A_{t} is the amplitude of the transmitted signal, f_0 is the carrier frequency, $\mu=B/T$ is the slope of frequency modulation, B is the bandwidth, T is the pulse repetition interval (PRI), t is the fast-time in a single chirp. Suppose the radial distance of the target from radar is R, and the relative radial velocity is V. The received signal and the transmitted signal are mixed to obtain the IF signal, as

$$s(n_{\mathrm{r}},n_{\mathrm{v}})=A_{\mathrm{IF}}\exp\left[j2\pi\mu\frac{2R}{c}n_{\mathrm{r}}T_{\mathrm{s}}\right]\cdot\exp\left[j2\pi\frac{2V}{\lambda}n_{\mathrm{v}}T\right]+ \quad (2)$$
$$+w(n_{\mathrm{r}},n_{\mathrm{v}}),$$

where A_{IF} is the amplitude of the IF signal, $n_{\mathrm{r}}\left(n_{\mathrm{r}}=1,\ldots,N_{\mathrm{r}}\right)$ is the index of fast-time, $n_{\mathrm{v}}\left(n_{\mathrm{v}}=1,\ldots,N_{\mathrm{v}}\right)$ is the index of slow-time, T_s is the sampling period, $\lambda=c/f_0$ is the signal wavelength, $w(n_{\mathrm{r}},n_{\mathrm{v}})$ is the noise component. The radial distance and relative radial velocity can be determined by the fast Fourier transform (FFT) of the IF signal $s(n_{\mathrm{r}},n_{\mathrm{v}})$. Assuming that the DDMA-MIMO radar adopts the PRI phase coding scheme on M_{t} transmitting antennas and l empty-bands, $m_{\mathrm{t}}\left(m_{\mathrm{t}}=1,\ldots,N_{\mathrm{sub}}\right)$ is the index of subbands, $N_{\mathrm{sub}}=M_{\mathrm{t}}+l$ is the number of subbands. The DDMA IF signal can be represented as: [3]

$$s_{\mathrm{DDMA}}(n_{\mathrm{r}},n_{\mathrm{v}},m_{\mathrm{t}})=s(n_{\mathrm{r}},n_{\mathrm{v}})\cdot\exp\left(j2\pi\frac{m_{\mathrm{t}}-1}{N_{\mathrm{sub}}}n_{\mathrm{v}}\right). \quad (3)$$

Fig. 1 shows the spectral distribution of m_t-th subband after performing FFT on (3). $S(p,q)$ is the spectrum of $s(n_{\mathrm{r}},n_{\mathrm{v}})$, where $p\left(p=1,\ldots,N_{\mathrm{P}}\right)$ is the distance index, and $q\left(q=1,\ldots,N_{\mathrm{Q}}\right)$ is the Doppler index. As shown in the second term of (3), the RD spectrum of IF signal can be evenly divided into N_{sub} subbands along the Doppler domain. When $m_{\mathrm{t}}\in[1,...,M_{\mathrm{t}}]$, subbands of $\mathrm{TX}_1,\ldots,\mathrm{TX}_{M_{\mathrm{t}}}$ are distributed in the positive Doppler direction by cyclic shift. The maximum unambiguous velocity for a single transmitting antenna and the velocity interval length of subband can be expressed as:

$$V_{\max}=\frac{c}{4f_0T},\ \ and\ V_{\mathrm{sub}}=\frac{2V_{\max}}{N_{\mathrm{sub}}}. \quad (4)$$

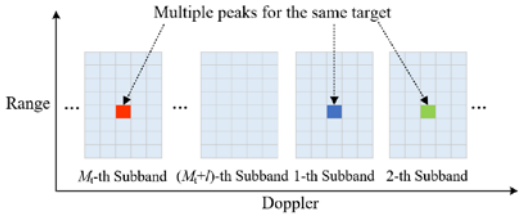


Fig. 1. The RD spectrum for DDMA-MIMO radar

When $m_{\mathrm{t}}\in[1,...,M_{\mathrm{t}}]$, phase coding of $\mathrm{TX}_1,\ldots,\mathrm{TX}_{M_{\mathrm{t}}}$ forms M_{t} target peaks with $\Delta\varphi=2\pi/N_{\mathrm{sub}}$ as the interval in the Doppler domain. In the RD spectrum of IF signal, subbands do not contain the target peaks when $m_{\mathrm{t}}\in[M_{\mathrm{t}}+1,..,N_{\mathrm{sub}}]$. The ideal RD spectrum shows obvious high-power peak subbands containing target peak and low-power empty-bands. NCI locates the uncoded target peak of TX_1 to achieve DDMA demodulation [5].

III. Background Clutter Suppression Method and Peak Correction Method

Under the condition of strong background clutter, there would exist many clutter peaks in the RD spectrum of the IF signal, in which the NCI process became invalidated [5]. Meanwhile, the increase of the numbers of antennas would further complicate the peak and subband distribution, which brought challenges to peak detection. Therefore, DDMA demodulation processing should achieve the suppression of RD spectrum clutter before the extraction of target peaks.

In this paper, a demodulation method combining background clutter suppression and peak correction method is proposed. The processing flow is shown in Fig. 2. Firstly, the 2D-FFT and window filtering on the received IF signals are performed respectively. Subsequently, the background clutter suppression is carried out, and then, the peak correction method is developed to extract the target peaks from the denoised

RD spectrum of IF signals. Finally, the DDMA demodulation is implemented and CFAR detection can be conducted for accurate parameter estimation.

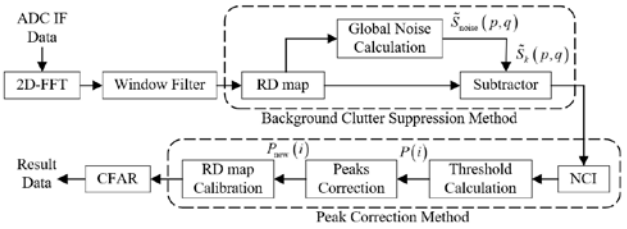


Fig. 2. Flowchart of DDMA demodulation process

A. Background Clutter Suppression Method

The field tests in strong clutter environments show that target peaks occupy few resolution units and are obscured by clutter. These issues make target detection difficult without prior knowledge. In this paper, a multi-frame background clutter suppression method is proposed. The average RD spectrum of continuous K frames of IF signals from the same scenario is calculated and regarded as the estimation of clutter level. $S_k(p,q)$ is the RD spectrum of the k-th IF signal frame. $\tilde{S}_{\text{noise}}(p,q)$ is the estimated noise result, expressed as:

$$\tilde{S}_{\text{noise}}(p,q)=\frac{1}{K}\sum_{k=1}^{K}|S_k(p,q)|, \tag{5}$$

where K is the total number of signal frames, and k is the frame index. The RD spectrum $\tilde{S}_k(p,q)$ after clutter suppression can be obtained through subtracting $\tilde{S}_{\text{noise}}(p,q)$ from $S_k(p,q)$, which can be expressed as:

$$\tilde{S}_k(p,q)=dB\left(|S_k(p,q)|\right)-dB\left(\tilde{S}_{\text{noise}}(p,q)\right). \tag{6}$$

B. Peak Correction Method

In the strong background clutter, power distortion may occur in both the empty-bands and the peak subbands. Two common cases of the subband outlier distribution are shown as Fig. 3. Fig. 3a shows the ideal subbands distribution, in which peak subbands and empty-bands are clearly divided. The red arrow indicates the target peak without phase encoding, which denotes obvious rising edge characteristics. A high-power outlier in the peak subbands is presented in Fig. 3b. The outliers in Fig. 3b and (c) may lead to misjudgment of the peaks indicated by the red arrow. Under strong clutter interference, the RD spectrum of IF signal may contribute more subband outliers, which significantly reduces the DDMA demodulation performance. Therefore, to improve the DDMA demodulation performance, a peak correction method based on variable threshold is proposed. In detail, the power values of Doppler domain across subbands are sorted firstly. And then, the mean value of the l_t smaller power values are set as the threshold $P_{\text{Threshold}}$.

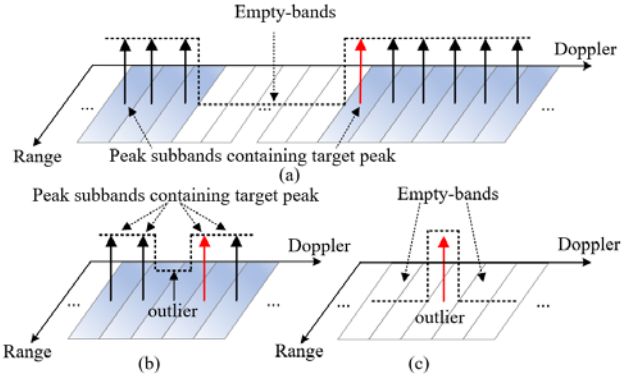


Fig. 3. Ideal subbands and subbands with outlier: Distribution of ideal subbands (a); Outlier appears in the peak subbands (b); Outlier appears in the empty-bands (c)

Subsequently, the subbands are labeled as '0' for low power and '1' for high power, which can be expressed as:

$$P(i)=\left[p_1,\ldots,p_{N_{\text{sub}}}\right]_{1\times N_{\text{sub}}},\ \textit{and}\ p_i\in\{0,1\}, \tag{7}$$

where p_i is the power label marked by index i. (7) transforms DDMA demodulation into a rising edge detection in $P(i)$. The outliers in $P(i)$ are corrected by comparing the left neighbor $L(i)$ and the right neighbor $R(i)$ of p_i:

$$\begin{cases} L(i)=\left[(i-2)\bmod\left(M_t+l\right)\right]+1, \\ R(i)=\left[i\bmod\left(M_t+l\right)\right]+1. \end{cases} \tag{8}$$

When $p_i = 0$ and $L(i)=R(i)=1$, p_i is identified as a low-power outlier and the value is corrected as 1. Conversely, if $p_i = 1$ and $L(i)=R(i)=0$, p_i is corrected as 0:

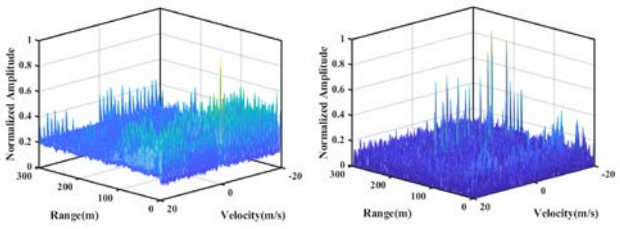
$$P_{\text{new}}(i)=\begin{cases} 1, \left(p_i=0\right)\cap\left(L(i)\odot R(i)\right), \\ 0, \left(p_i=1\right)\cap\left(L(i)\odot R(i)\right), \\ p_i\ , \textit{others}. \end{cases} \tag{9}$$

After the correction processing, the distorted subbands are calibrated. The rising edge detection is performed through analyzing two adjacent detection units of the calibrated data $P_{\text{new}}(i)$. The detected rising edge is served as the Doppler unambiguous position of TX_1, which is used to achieve DDMA demodulation. After the suppression of the target Doppler domain and two adjacent Doppler domains, only the NCI peak in the subband of TX_1 is remained.

IV. Experimental Analysis

A. Experience Environments And Equipment

The radar system adopts a planar array with 24TX32RX. The carrier frequency of the transmitted signal is set to 80 GHz, with the bandwidth of 180 MHz. The system adopts 20MHz ADC sampling rate with the PRI of 48μs and 512 fast-time samples per pulse. Each frame of signal consists of 1024 pulses. The RD spectrum of IF signal contains 8 empty-bands. The real-data is acquired in both vehicular and UAV scenarios.

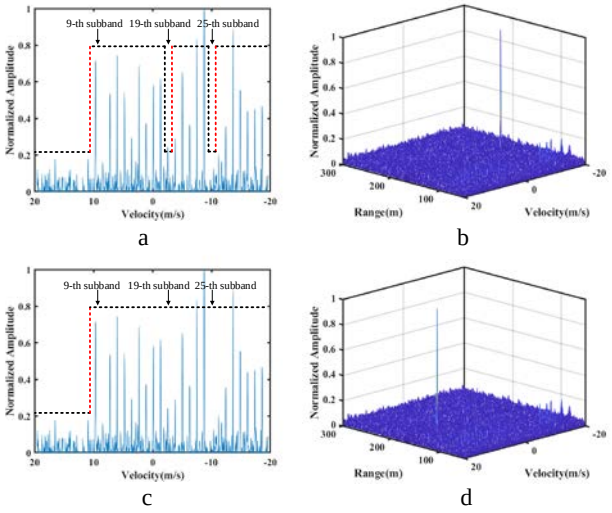


a b

Fig. 4. Denoising comparison of RD spectrum of the 64-th frame: Raw RD spectrum (a); Denoised RD spectrum (b)

B. Experimental Results in Vehicular Scenario

In the vehicular scenario, the radar is mounted on a stationary vehicle roof with a 0º depression angle. An armored vehicle target does a variable velocity straight reciprocating motion on the test road, and returns after moving 250 m away from the radar platform. The relative radial velocity ranging [–11 m/s, 11 m/s]. During operational testing, 90 signal frames are collected at intervals of 1s, and 10 or more average frames are used for background noise estimation.



a b

c d

Fig. 5. Comparison of calibrated RD spectrum results of different methods of the 64-th frame: Doppler-domain data result and calibrated power envelope (a); NCI result: the velocity estimation result is –11.21m/s (b); Doppler-domain data result and the calibrated power envelope (c); Proposed method result: the velocity estimation result is 9.67m/s (d)

The comparison of the RD spectrum of the 64-th frame signal before and after denoising is presented in Fig. 4. The RD spectrum of the IF signal is donated in Fig. 4a. The target signals are obscured by strong clutter. The denoised RD spectrum is donated in Fig. 4b, which clearly shows 24 target peaks. The results of NCI and peak correction methods are presented for comparison in Fig. 5. Subbands are renumbered along the Doppler positive direction. The peak distribution in Doppler domain is shown in Fig. 5a. The target peak of TX_1 is in the 9-th subband and low-power outliers are in the 19-th subband and 25-th subband, which leads to a misjudgment that the 26-th subband is the position of the target peak of TX_1. The calibrated RD spectrum is shown in Fig. 5b, and the estimated velocity is –11.21 m/s, which is inconsistent with the actual motion. The peak distribution after peak correction method is shown in Fig. 5c. The calibrated RD spectrum is shown in Fig. 5d, and the estimated velocity is 9.67 m/s , which is consistent with the experimental conditions. Relative radial velocities of 90 frames are donated in Fig. 6. The velocity is negative in 12-th to 42-th frames, positive in 56-th to 87-th frames. In 43-th to 55-th frames, the vehicle is out of the experimental range. Except for the 34-th frame, accurate velocity is achieved in 60 frames of signal, which verifies the effectiveness of the proposed algorithm.

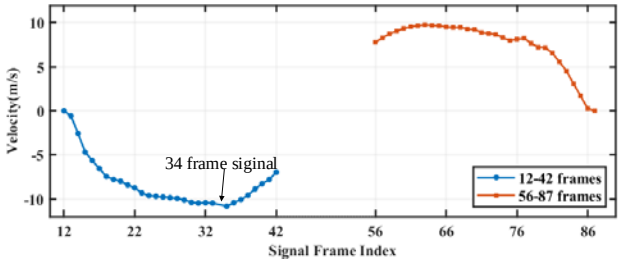
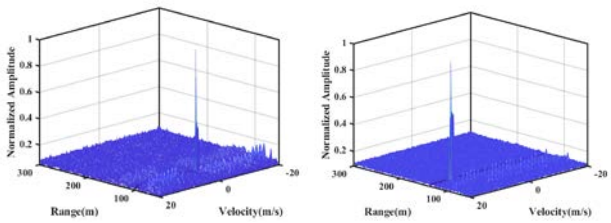


Fig. 6. Estimated velocity results in vehicular scenario

C. Experimental Results in UAV Scenarios

In this scenario, two UAV-mounted radar experiments are tested. The radar system is mounted underneath the UAV fuselage to observe the target at a downward angle of 30º. During the first experiment, the drone hovers at a height of 50m above the roadside to detect a moving armored vehicle. Since the moving direction of the target is almost perpendicular to the radial direction, the relative radial velocity is approximately [–0.2 m/s, 0]. During the second experiment, the borne flies forward along the road centerline at a height of 100 m to detect a stationary armored vehicle, and the relative radial velocity is approximately [8.66 m/s, 17.32 m/s]. The calibrated RD spectrums for two scenarios are presented in Fig. 7. The relative radial velocity under the first experimental condition is shown in Fig. 7a, which is –0.19 m/s. The relative radial velocity under the second

experimental condition is shown in Fig. 7b, which is 13.28 m/s. To sum up, the estimated velocity values after DDMA demodulation are within the given velocity range.



a b

Fig. 7. Comparison of calibrated RD spectrum results of different environments. (a) Drone hovers at 50 meters altitude to detect moving target of 50-th farme, the velocity estimation result is –0.19 m/s; (b). Drone flies at 100 meters altitude to detect stationary target of 53-th farme, the velocity estimation result is 13.28 m/s

V. Conclusion

The paper presents a background clutter suppression method based on multi-frame signal for DDMA-MIMO radar with large antenna numbers, which can overcome the interference from strong clutter background and highlight the target signal. Moreover, the peak correction method based on variable threshold effectively solves the problem of power distortion in subbands under strong clutter background. Furthermore, several experiments are carried out in vehicular and UAV scenarios. In the vehicular scenario, the effectiveness of the background clutter suppression method and the peak correction method is verified by comparation. And the accurate DDMA demodulation results of 60 frames are achieved. In the UVA scenario, DDMA demodulation is achieved in two experiments: stationary radar observing moving targets and moving radar observing stationary targets. Accurate relative radial velocity estimation is realized in both scenarios. These results demonstrate the wide application of the DDMA demodulation method under different scenarios.

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Multi-Camera Pairwise Calibration Through Joint Optimization Method

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***Abstract*. The calibration of multi-camera systems is crucial for the deployment of vision-based mobile robots and autonomous vehicles. Conventional checkerboard-based calibration methods typically require complete overlapping field of view of calibration patterns across all cameras, a condition often difficult to satisfy in complex configurations of multi-camera systems. To address this limitation, this study proposes a multi-camera calibration method based on joint optimization of adjacent nodes. The proposed approach establishes local overlapping constraints between neighboring cameras, estimates the intrinsic parameters of individual cameras and extrinsic parameters between adjacent cameras in a phased manner, then achieves global parameter unification in a unified coordinate system through recursive transformation of extrinsic parameters via intermediate nodes. This methodology effectively resolves the calibration challenges in multi-camera systems with non-overlapping fields of view. Experimental results demonstrate the high accuracy of the proposed algorithm.**

***Keywords:* multi-camera calibration, checkerboard, pairwise calibration, joint optimization**

I. INTRODUCTION

Perception and comprehension of the surrounding environment by mobile robots and autonomous vehicles constitute a critical capability for autonomous intelligent systems [1]. Cameras demonstrate significant applicability in intelligent systems due to their advantages of low manufacturing/maintenance costs, lightweight construction, and minimal power consumption. Compared to monocular cameras, multi-camera systems enhance environmental understanding through expanded field of view, enabling comprehensive spatial perception around vehicles. This capability facilitates robust implementations of visual localization, three-dimensional reconstruction, and Simultaneous Localization and Mapping (SLAM) [2]. To achieve accurate environmental perception and improve system reliability and precision in intelligent systems, rigorous calibration of multi-camera configurations prior to deployment represents an essential procedural requirement.

The core objective of multi-camera system calibration resides in determining the intrinsic parameter matrices of individual cameras (encompassing focal length, principal point coordinates, and distortion coefficients) and establishing the inter-camera pose transformation matrices (rotation matrices and translation vectors). Based on dependency on artificial reference objects, existing calibration methodologies can be classified into target-based calibration [3, 4] and target-free calibration [5, 6]. Target-free calibration eliminates reliance on dedicated calibration targets, enabling online implementation; however, its accuracy is contingent upon the performance of Structure from Motion (SfM) algorithms and feature point extraction efficacy in three-dimensional environments. In contrast, target-based calibration achieves comparatively higher precision through controlled reference objects, thereby reducing computational time and complexity while enhancing system stability.

The checkerboard pattern represents a classical and simplified calibration target selection [7], characterized by its regular geometric configuration and high contrast ratio, which facilitates direct detection of reliable and high-precision corner points for correspondence

computation. However, checkerboard applications exhibit inherent limitations in multi-camera calibration scenarios, primarily because each sub-camera in the system must fully capture the complete checkerboard pattern. Failure to satisfy this requirement may induce correspondence ambiguity during calibration due to the pattern's inherent symmetry. To circumvent these limitations while preserving high-precision estimation capabilities, this paper proposes a calibration methodology for non-overlapping multi-camera systems. The approach establishes local overlap constraints between adjacent cameras, implements phased estimation of monocular intrinsic parameters and inter-camera extrinsic parameters, then achieves global parameter unification within a unified coordinate system through recursive transformation of extrinsic parameters via intermediate nodes.

II. Related work

In multi-camera vision systems, the spatial poses of individual cameras exhibit diverse connection relationships contingent upon practical application environments. Traditional checkerboard-based calibration mandates complete pattern capture by all cameras in the system. Failure to meet this requirement introduces correspondence ambiguity during calibration due to the inherent symmetry of checkerboard patterns. To mitigate these limitations while preserving high-precision estimation characteristics, recent methodologies incorporate meticulously designed encoded markers within each checkerboard square. These markers eliminate the necessity for full-pattern capture, as exemplified by Fiala et al.'s ARTag calibration board [8–9], which systematically integrates square-coded markers on checkerboard planes. Building upon this foundation, Atcheson et al. [10] developed the CALTag calibration board. However, such marker-enhanced approaches demonstrate heightened vulnerability in low-resolution or high-noise environments compared to conventional checkerboard calibration, primarily due to the inherent unreliability of region detection compared to corner detection.

Herout et al. [11] proposed identity encoding through grayscale variation between adjacent squares, enabling real-time camera pose estimation. Nevertheless, this method's dependency on line fitting and vanishing point estimation renders it susceptible to calibration failure under lens distortion conditions. Xing et al. [12] introduced the TCAD calibration board, substituting CALTag's binary-coded markers with diverse identity labels or textures in checkerboard squares. While circumventing calibration failures caused by region detection, this approach introduces complexity in corner detection algorithms and intricate label design requirements.

Another category of calibration targets encompasses three-dimensional structures, where specialized spatial configurations enable extrinsic parameter calibration under non-overlapping field-of-view conditions. Zhang's one-dimensional calibration target [13] employs multiple collinear feature points with known intervals for multi-camera pose estimation, though its limited feature quantity constrains calibration accuracy. Edward et al. implemented rapid multi-camera calibration using rigidly interconnected spherical markers [14], yet their algorithm exhibits significant sensitivity to image noise and illumination variations. Zhao et al. developed a spherical calibration method [15] leveraging the omnidirectional visibility of spheres, which enhances reliability in limited-field image center extraction compared to planar circle detection approaches. However, this method suffers from compromised calibration precision due to challenges in maintaining precise inter-spherical distances. Liu et al. achieved improved extrinsic calibration accuracy through pre-calibration of multiple spatial targets using high-precision FARO 3D scanning apparatus [16], albeit with substantial experimental equipment and cost requirements.

Critical analysis of existing literature reveals inherent limitations in multi-camera calibration techniques employing physical targets: fabrication complexity directly impacts parametric accuracy, while current research demonstrates insufficient academic exploration in high-precision checkerboard-based multi-camera calibration methodologies.

III. Methodolgy

Consider a multi-camera system composed of N cameras, denoted as $\{C_1, C_2, \dots, C_N\}$. In this system, adjacent camera pairs $C_i, C_j)$ can simultaneously observe the same checkerboard plane (termed co-visible edges), while non-adjacent camera pairs cannot directly observe the same checkerboard plane (termed non-co-visible edges). The objective is to estimate the intrinsic parameter matrices $\{K_i\}$ and extrinsic parameter matrices $\{T_i\} \in SE(3)$ (relative to the global coordinate system O_w) for all cameras based on the calibration results from co-visible edges, such that the reprojection error across all cameras is minimized. Here, $SE(3)$ denotes the Special Euclidean group in three-dimensional space, representing rigid-body transformations. This optimization process aims to establish globally consistent calibration parameters that satisfy both geometric constraints from co-visible observations and the intrinsic constraints of individual cameras.

A. Monocular Camera Calibration

Let the coordinate of checkerboard corner point p in the world coordinate system be denoted as $X_p =$

$= (x_p, y_p, 0)^T$ (since the checkerboard plane lies on $Z_w = 0$). The projection equation for camera C_i is given by:

$$s\begin{bmatrix} u_p^i \\ v_p^i \\ 1 \end{bmatrix} = K_i[R_i \quad t_i]\begin{bmatrix} X_p \\ 1 \end{bmatrix} = K_i\left(R_i\begin{bmatrix} x_p \\ y_p \\ 0 \end{bmatrix} + t_i\right), \quad (1)$$

where K_i represents the intrinsic parameter matrix of the camera. The rotation matrix $R_i \in SO(3)$ and the translation vector $t_i \in \mathbb{R}^3$ constitute the extrinsic parameters in the monocular system, describing the pose of the checkerboard plane relative to the camera. Here, SO(3) denotes the Special Orthogonal group of 3D rotation matrices, ensuring orthonormality (i.e., $R_i^T R_i = I$) and a determinant of +1, while t_i represents the 3D displacement vector from the camera's optical center to the origin of the checkerboard coordinate system. Together, R_i and t_i define the rigid transformation that maps points on the checkerboard plane (in the world coordinate system) to the camera's coordinate frame. s is an arbitrary scaling factor, (u_p^i, v_p^i) are the normalized image coordinates of the projected corner point.

Under the constraint that the checkerboard plane coincides with the $Z_w = 0$ plane in the world coordinate system, the projection equation reduces to:

$$H_i = K_i[r_{i1} \quad r_{i2} \quad t_i]\,. \quad (2)$$

Here, r_{i1}, r_{i2} denote the first two column vectors of the rotation matrix, the homography matrix H_i is estimated by minimizing the reprojection error between the observed image points and their projected counterparts, formulated as:

$$\min_{H_i} \sum_p \left\|\pi(H_i, X_p) - u_p^i\right\|^2 . \quad (3)$$

B. Calibration of Co-visible Cameras

For co-viewing camera pairs capable of synchronously capturing multiple sets of images of the same checkerboard pattern, the essential matrix E_{ij} corresponding to matched corner pairs $u_p^i \leftrightarrow u_p^j$ satisfies the following constraint:

$$u_p^{jT} K_j^{-T} E_{ij} K_i^{-1} u_p^i = 0, E_{ij} = [t_{ij}]_\times R_{ij}\,. \quad (4)$$

For each image set, checkerboard corners are extracted and matched to construct a candidate correspondence set $\mathcal{M} = \{(u_p^i, u_p^j)\}$. The RANSAC algorithm is iteratively applied to: 1. Randomly select 8 matched point pairs. 2. Compute the essential matrix. 3. Evaluate inlier count under the epipolar constrain $[u_p^j]^T E_{ij} u_p^i = 0$. The hypothesis achieving the maximum inlier consensus is retained. Finally, the optimal essential matrix E_{ij} is refined over the final inlier set through least-squares minimization:

$$\min_E \sum_{(u_p^i, u_p^j) \in \mathcal{M}_{\text{inlier}}} \left(u_p^{jT} K_j^{-T} E K_i^{-1} u_p^i\right)^2 . \quad (5)$$

Upon performing singular value decomposition (SVD) on the essential matrix E_{ij} to extract the relative rotation matrix R_{ij} and translation vector t_{ij}, a nonlinear optimization is subsequently conducted to refine the extrinsic parameters through geometric error minimization:

$$\min_{R_{ij}, t_{ij}} \sum_p \left\|\pi(K_j, R_{ij}, t_{ij}, \pi^{-1}(K_i, u_p^i)) - u_p^j\right\|^2 . \quad (6)$$

The nonlinear least-squares problem is solved using the Levenberg-Marquardt algorithm to obtain the optimal extrinsic parameter estimation R_{ij}, t_{ij} from camera i to camera j, thereby determining the relative pose transformation between co-viewing camera pairs (camera coordinate system →other camera coordinate systems).

C. Calibration of Non-Overlapping Cameras

When cameras C_i and C_j lack direct overlapping fields of view, extrinsic parameters are propagated through an intermediate camera chain $C_i \to C_k \to \cdots \to C_j$:

$$T_{ij} = T_{k_1 k_2} \cdot T_{k_2 k_3} \cdot \cdots \cdot T_{k_{m-1} k_m} \,. \quad (7)$$

The extrinsic parameters along the camera chain $C_i \to C_k \to C_j$ are defined as:

$$T_{ij} = T_{kj} \cdot T_{ik} = \begin{bmatrix} R_{kj}R_{ik} & R_{kj}t_{ik} + t_{kj} \\ 0 & 1 \end{bmatrix}. \quad (8)$$

Let the covariance matrix of the extrinsic parameter estimation between cameras C_a and C_b be denoted as $\sum_{ab}$, which is computed via reprojection error minimization:

$$\Sigma_{ab} = J_{ab}^{+} \cdot \text{diag}(\sigma_1^2, \sigma_2^2, \ldots) \cdot (J_{ab}^{+})^T . \quad (9)$$

where J_{ab} denotes the Jacobian matrix computed during the calibration process.

For the camera chain $C_i \to C_k \to C_j$, the composite covariance matrix is formulated as:

$$\Sigma_{ij}^{\text{path}} = J_{ik}\Sigma_{ik}J_{ik}^T + J_{kj}\Sigma_{kj}J_{kj}^T , \quad (10)$$

where the Jacobian matrix $J_{ik} = \frac{\partial \log(T_{ij})}{\partial \log(T_{ik})}$ quantifies the sensitivity of error propagation in the Lie algebra parameterization.

Define the graph model with Vertices representing camera poses $\{T_i\}$ (relative to the world coordinate system O_w), edges encoding directly observed co-visibility constraints and their associated covariance

matrices Σ_{ij}. The joint optimization of all parameters is formulated as minimizing the following cost function:

$$\mathcal{L} = \sum_{(i,j)\in\mathcal{E}} \rho\left(\left\|\log(T_{ij}^{-1}T_jT_i^{-1})\right\|^2_{\Sigma_{ij}^{-1}}\right) + \lambda\sum_{\text{loops}}\left\|\log(T_{\text{loop}})\right\|^2 , \quad (11)$$

where ρ denotes the Huber robust kernel for outlier suppression. The loop transformation $T_{\text{loop}} = T_{i_1i_2} \cdot T_{i_2i_3} \cdot \cdots \cdot T_{i_ki_1}$ represents the composite transformation along the cyclic closure path, which theoretically should equal the identity matrix I in a drift-free scenario.

If no physical loop closure exists, we construct a virtual loop constraint through transitive pose chains(e.g., $C_1 \rightarrow C_2 \rightarrow C_5 \rightarrow C_1$) and enforce the condition:

$$\log(T_{15} \cdot T_{52} \cdot T_{21}) \approx 0 . \quad (12)$$

By introducing virtual constraints to enforce structural rigidity, we mitigate drift artifacts induced by redundant degrees of freedom within the system.

IV. Experiments

In this section, the multi-camera system requiring calibration in this study is introduced. Furthermore, the high accuracy of the proposed joint calibration algorithm is validated through comprehensive experimental verification conducted on the physical multi-camera setup.

A. System

The multi-view top-view configuration is illustrated in Fig. 1, where cameras are arranged in two tiers with a symmetrical configuration. Specifically, the inner tier contains a single central camera, while the outer tier incorporates eight peripherally distributed cameras. The numbering convention follows a systematic pattern: the central camera in the inner tier is designated as No. 01, with the peripheral cameras in the outer tier being sequentially numbered from No. 02 in a counterclockwise direction along the circumference.

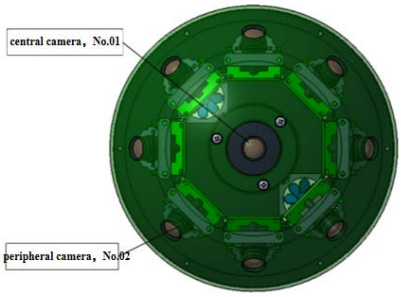

Fig. 1. Top-view Schematic of the Multi-view Camera System

Fig. 2 presents a multi-view camera system prototype developed based on the architectural configuration shown in Fig. 1. The system housing exhibits a maximum outer diameter of 170 mm, with its imaging units arranged in a dual-tier topology: a central camera positioned at the inner tier and eight peripherally distributed cameras forming the outer tier, collectively establishing an axisymmetric configuration. Each imaging module demonstrates a horizontal field of view (FoV) of 80°(H) × 51°(V) with resolution specifications of 320×240 pixels.

Fig. 2. Multi-Cameras System

Fig. 3 illustrates the checkerboard grid employed in this experiment, where each cell exhibits dimensions of 24 mm with a 6:7 aspect ratio.

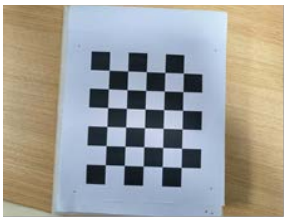

Fig. 3. Checkerboard calibration plate

B. Experimental Results and Analysis

To quantitatively evaluate the performance of the proposed algorithm, this study employs the standard reprojection error as the accuracy validation metric. Comparative experiments were systematically conducted across multiple camera configurations. The experimental results, as documented in Tables I and II, demonstrate the algorithm's precision characteristics under varying system conditions.

TABLE I. Comparison of Intrinsic Parameters of Partial Camera

Camera	f_x, f_y	o_u, o_v	Reprojection error
01	175.31,240.09	157.121,121.21	0.21 pixel
02	169.6384,221.936	178.414,125.014	0.19 pixel
05	190.268,280.10	165.427,133.094	0.19 pixel
06	177.093,236.093	185.376,121.183	0.27 pixel
07	207.617,269.53	158.208,134.181	0.19 pixel
09	190.50,274.70	159.22,122.46	0.27 pixel

As evidenced by Tabl. I, the intrinsic projection errors for all cameras remain below 0.3 pixel, satisfying the sub-pixel level accuracy requirement and collectively demonstrating high calibration accuracy for intrinsic parameters. Extrinsic analysis in Tabl. II reveals that the baseline angle distribution among different camera pairs spans a wide range, establishing complementary

observation topologies. Specifically, the near-opposite configuration of camera pair 01-09 (178.92°) enhances scene coverage capacity, while medium-low angle combinations such as 01-05 (53.42°) and 02-09 (47.38°) demonstrate superior suitability for binocular stereo matching applications. The extrinsic calibration reprojection errors are constrained below 0.32 pixel, significantly outperforming traditional multi-view geometry systems (typical values >0.5 pixel).

TABLE II. COMPARISON OF INTRINSIC PARAMETERS OF PARTIAL CAMERA

Camera	External	Reprojection error
01-05	53.42°	0.27 pixel
01-09	178.92°	0.26pixel
02-09	47.38°	0.22 pixel
06-07	128.03°	0.31pixel

Notably, a strong correlation emerges between intrinsic calibration quality and extrinsic errors, consistent with error propagation theory. The 06-07 pair incorporating camera 06 (highest intrinsic error: 0.27 pixel) exhibits the maximum extrinsic error of 0.31 pixel, whereas the 02-09 pair utilizing camera 02 (optimal intrinsic precision: 0.19 pixel) achieves the minimum extrinsic error of 0.22 pixel. These quantitative relationships align precisely with theoretical predictions of error propagation mechanisms.

V. CONCLUSION

This study proposes a recursive multi-camera system calibration method based on co-visibility relationship constraints, achieving high-precision parameter estimation through the establishment of geometric constraint models between adjacent cameras. The methodology constructs local constraint relationships based on common-view features between neighboring cameras, realizing system parameter calibration in the global coordinate system through progressive parameter transmission and recursive optimization of intermediate camera parameters. By developing parameter propagation chains, this approach effectively overcomes the dependence of traditional Zhang's checkerboard method on global common-view features, significantly enhancing algorithm applicability while maintaining calibration accuracy.

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Inter-channel Attention Transformer for POLinSAR Image Classification

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***Abstract*. Polarimetric interferometry synthetic aperture radar (POLinSAR) increases the information of remote sensing in cloudy, atrocious and nonluminous all-weather. Automatic target recognition (ATR) and terrain classification play an important role in agriculture, industry, transportation and urban development. Deep neural networks (DNNs) are widely applied to SAR object detection since convolutional neural networks demonstrate high performance in optical image processing. The paper proposes a novel object classification method for POLinSAR images with inter-channel attention transformer framework that combines the relationship of channels to extract polarimetric interferometry features with attention mechanism. The experiments demonstrate that the developed method attained more accurate classification than SOTA algorithms on Flevoland, San Francisco and ESAR Oberpfaffenhofen datasets.**

***Keywords:* POLinSAR, classification, attention, transformer**

I. INTRODUCTION

Synthetic aperture radar (SAR) can provide high-resolution images in all-weather conditions at any time. It is suitable for automatic target detection, marine resource utilization, environmental surveillance and planetary exploration [1]. Due to radar microwave scattering imaging and phase coherent processing characteristics, SAR images are different from optical images and difficult to process directly. However, SAR images contain rich target information, such as position, velocity, geometry, even surface structure. PolSAR obtains the polarization scattering data of the target by changing the polarization mode of transmitting and receiving electromagnetic waves. Different polarization modes of electromagnetic waves contain more information. POLinSAR combines polarization measurement with interferometry technology, which is not only sensitive to the shape and direction of the scatterer, but also to their spatial distribution and height [2]. It can distinguish the mixed scattering mechanisms occurring in the same resolution unit, thereby determining the heights corresponding to different dielectric layers in the overburden. The principle of SAR radar imaging is seen in Fig. 1. The airborne radar emits electromagnetic pulses to the target and receives echo signals.

SAR image classification refers to the process of using image data acquired by remote sensing data to identify and classify targets, such as ship, vehicle, road, bridge, forest, river, building, grassland and etc. SAR image classification methods mainly relies on machine learning and deep learning techniques. Methods based on machine vision include obtaining sample images, dividing them into different image regions, using a encoder to extract features of targets and classifier. Classic classification methods include linear classification, SVM, Gaussian Process, Conditional

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Random Field, Decision Tree and Adaboost. Traditional algorithms require artificial design features to distinguish between background and foreground targets in SAR images. Iervolino and Guida considered both the ocean clutter and the signal noise from remote targets in SAR images, and developed a generalized-likelihood ratio test (GLRT) model [3]. The type of methods require manual specification of features with a lot of computation, so they are not generalized well.

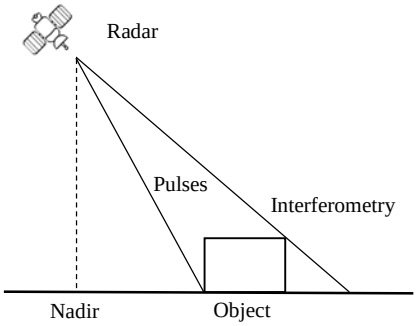

Fig. 1. Radar imaging principle

With the development of deep learning, the accuracy and efficiency of SAR image classification have been continuously improved in recent years. Such as convolutional neural network (CNN) models based on deep neural network can achieve high-precision target detection and classification efficiency in complex environments. With the continuous optimization of algorithms and the improvement of computing power, SAR image classification become more intelligent and automated. The framework diagram of RCNN consists of region proposal extractor and CNN feature extractor, and then uses SVM classifier for classification [4]. Compared with RCNN, Fast-RCNN improved both speed and precision. Its training is single-stage with multi-task loss. All network layers can be updated during training, also no additional storage on the hard disk is required [5]. Transformer architecture is a model proposed by Vaswani and Shazeer [6]. It uses the decoder and encoder architecture, but there is attention layers between them, which is used to help the decoder focus on the relevant parts of the input data. ViT is the application of transformer in the image field [7]. It divides the optical image into fixed-size patches, which are flattened and mapped into fixed-length vectors through linear transformation. The vector sequences are concatenated to a learnable classification tag, followed by learnable position encoding of the corresponding position. The corresponding features are extracted and input into the classifier for training. Jamali proposed local window attention transformer for PolSAR image classification [8]. The model is a vision transformer-based framework, which utilizes 3D and 2D convolution as feature extractors with local window attention for PolSAR image classification. The effective accuracy depends on multi channels of SAR image. However, the interrelated relation of each channel is available for decrease computation for POLinSAR data with more channels.

Aiming at the above problems, an improved visual transformer method is proposed for POLinSAR image classification called inter-channel attention transformer (ICAT). The main contributions of our work can be summarized as follows:

- A deep learning framework for POLinSAR data is proposed based on CNNs and local window vision transformer for accurate classification of imagery.
- The developed model conducts inter-channel attention, which improvs the feature generalization capability in a local region with multi-channel information sharing.
- The results of experiments show more effective than the state-of-the-art models with the polarimetric interferometry dataset.

The paper introduces the ICAT model in Section II as following. The experiments are presented with quantitative and qualitative analysis in Section III. The conclusion is drawn in Section IV.

II. Proposed Classification Model Experiments

Statistical modeling of polarimetric interferometric SAR data has always been a research hotspot, and the statistical characteristics derived from targets of SAR data play an important role in image classification. The classic statistical model is complex multivariate Gaussian distribution of the scattering vector and the covariance coherence Wishart distribution.

For a uniform region, *k* follows a complex Gaussian distribution with a mean of 0, and its probability density function is Eq. (1):

$$p(k) = \frac{1}{\pi^q|\Sigma|}\exp(-k^H\Sigma^{-1}k)\ . \tag{1}$$

In Eq. (1) q is the number of channels, Σ is covariance matrix. Polarimetric SAR multi-look processing is performed by averaging several independent single-look covariance matrices as

$$C^* = \frac{1}{L_{Att}}\sum_1^L kk^H\ . \tag{2}$$

L_{Att} is attention coefficient, is not means as traditional covariance matrix processing. So multi-look SAR probability distribution is improved as Eq. (3).

$$p(C^*) = \frac{L_{Att}|\mathrm{C}|^{L_{Att}-q}\exp[-L_{Att}tr(\Sigma^{-1}C^*)}{R(L_{Att},q)|\Sigma|^q}. \tag{3}$$

In Eq. (3), tr(.) is trace of matrix. In inter channels, a multi-head attention mechanism based on local window attention is used to realize the association operation of L_{Att}.

Transformer consists of two parts including an encoder and a decoder. Both encoder and decoder contain n blocks. The attention relationship between inter channels of SAR data is calculated with L_{Att} weight. The diagram of the proposed ICAT model for polarimetric SAR Image Classification is shown in Fig. 2. The SAR data is split into several patches (8×8×20). 8×8 is the local window size. 20 is the number of channels of polarimetric interferometric SAR data. Firstly, the data features are extracted by 3D convolution and 2D convolution as shown in Fig. 3. The each layer is also normalized by layer_norm module.

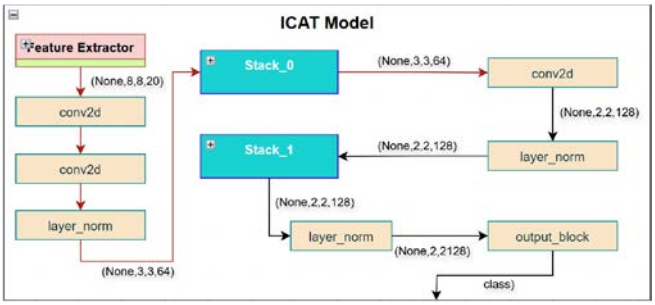

Fig. 2. Diagram of ICAT model

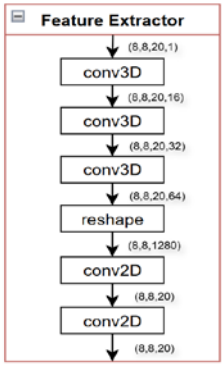

Fig. 3. Module of feature extractor

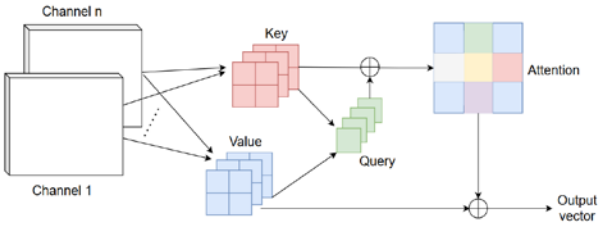

Fig. 4. Inter-channel attention mechanism

The local window attention (LWA) create the local neighborhood window and limits the receptive field of each query token to fixed-sized neighboring pixels [8]. It utilizes the relationship of multi channels with 3D convention, however computation cost is high. ICAT combines LWA to utilize the attention of same region from each channel to decrease duplicate computation as shown in Fig. 4.

The neighborhood of a pixel at a spatial position (i, j) in a lth feature map within a local window, is expressed by τ (i, j, l). ICAT adds a finite set of indices belonging to pixels position close to the location (i, j) of each channel feature map. Query, Key and Value are processed by linear transformation from data X:

$$q = W_q X, k = W_k X, v = W_v X. \quad (4)$$

Attention matrix in Fig. 4 is calculated as seen Eq. (5). ch is channel number, b is the relative positional bias. Channel weights are computed by $q(i, j, l, ch)$. $1/\sqrt{D}$ aims to decrease the scale of attention map without gradient disappear.

$$A = softmax(q(i,j,l,ch)k_\tau^T + b_{(i,j,l,ch)}/\sqrt{D}). \quad (5)$$

The ICAT conducts overlapping convolutions rather than non-overlapping ones. The developed model consists of multi levels. Each level has three ICAT blocks. Unlike local window attention, ICAT is not constrained to operate on inputs by D depth channel. The size of the pixel's neighborhood of inter channels is greater than the size of the feature map.

III. Experiments

In the section, experiments are conducted on ESAR_Oberpfaffenhofen, NASA/JPL AIRSAR Flevoland and San Francisco in [9] to evaluate the effectiveness of the developed model. Experimental implementations such as datasets, settings, and evaluation metrics are introduced. Data of Flevoland are situated in the Netherlands, on August 16, 1989. The Flevoland image is 750×1024 pixels in size, which have 12 channels. 15 classes of land cover are labeled in pixels, including bean, forest, potato, alfalfa, wheat, bare land, beet, rape, pea, grass and water as shown in Fig. 5. The data of San Francisco is a NASA/JPL AIRSAR L-band image, which resolution is 900×1024 pixels with 12 channels, where four terrain classes are shown in Fig. 6, including sea, mountains, grass, and buildings. The data of Oberpfaffenhofen is ESAR German city, which resolution is 1200×1300 pixels with 20 channel. They are famous benchmarks for both polarization and interference SAR as shown in Fig. 7 including wood, buildings and open area.

Fig. 5. Flevoland Pauli RGB composite image

Fig. 6. San Francisco Pauli RGB composite image

Fig. 7. Oberpfaffenhofen Pauli RGB composite image

We extract 12×12×12 image patches for Flevoland, 8×8×12 image patches for San Francisco, 8×8×20 image patches for Oberpfaffenhofen. For the dataset, we split the data into training sets and validation sets. The features and principles of the developed model are analyzed as following.

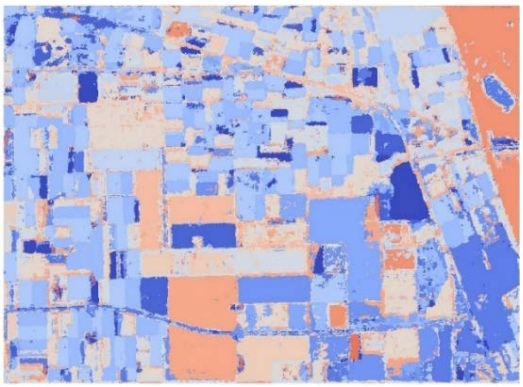

Fig. 8. Flevoland classification result composite image

Flevoland classification result is shown in Fig. 8. ICAT model achieves effective classification. San Francisco and German Oberpfaffenhofen classification result are shown in Fig. 9, 10, which are qualitatively better than SOTA models.

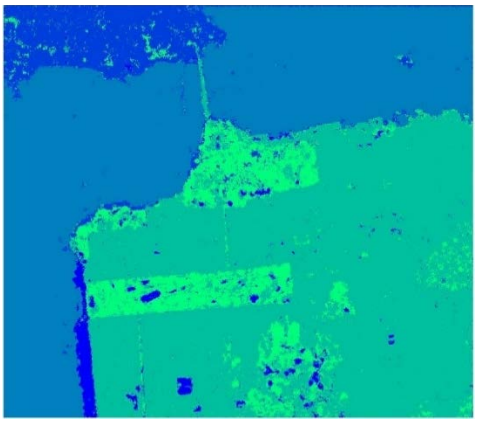

Fig. 9. San Francisco classification result composite image

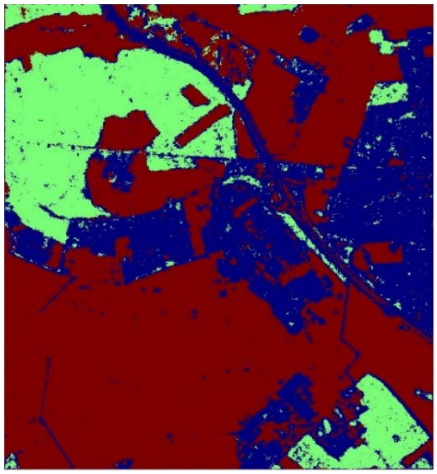

Fig. 10. Oberpfaffenhofen classification result composite image

The precision of the method on datasets are quantitatively analyzed correspondingly. In terms of accuracy and loss, the value are shown in Table I under 100 training epochs. The overall accuracies of training on the datasets are 99.1 %, 97.8 %, 95.9 %, which are up to SOAT methods. Meanwhile the losses are 0.026, 0.059 and 0.109 on SAR data from Flevoland, San Francisco and German Oberpfaffenhofen. The accuracy curves of training on the datasets are shown in Fig. 11. The experiments show the developed model is accurate and effective with low computation cost.

ACCURACY AND LOSS OF ICAT MODEL ON DATASETS

100 epochs	**Datasets**		
	Flevoland	***San Francisco***	***Oberpfaffenhofen***
Accuracy	0.991	0.978	0.959
Loss	0.026	0.059	0.109

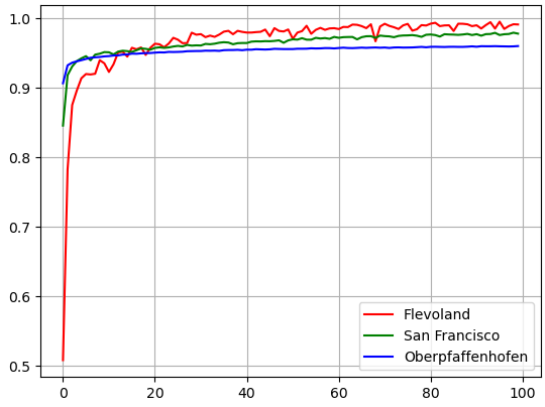

Fig. 11. Accuracy curves of training on datasets

IV. Conclusion

In the paper, a novel model ICAT is designed for POLinSAR image classification. ICAT take advantage of attention relationship of inter channels of polarimetric interferometry SAR data. The method improves the feature extraction capabilities globally between channels and reduces training cost and time consumption. The results on three polarimetric and interferometry SAR benchmark datasets show that the proposed ICAT model has comparable performance to state-of-the-art models. In the future, we will analyze the function and impact of the correlation between key channels with attention framework on SAR image classification.

Acknowledgment

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A Fast Bayesian Compressive Sensing Super-Resolution Method for Forward-Looking Imaging Radar

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Abstract. **Super-resolution imaging techniques are widely employed in azimuth-elevation two-dimensional (2D) forward-looking imaging with real aperture radar (RAR). However, most existing methods suffer from high computational complexity, particularly in 2D super-resolution imaging scenarios where the dimensionality of the echo matrix increases substantially. This significantly degrades algorithmic efficiency and limits practical implementation in real-world systems. To address this issue, a fast Bayesian compressive sensing (FBCS) method for 2D super-resolution imaging is proposed. First, the sparse characteristics of the scene are utilized to constrain the target prior. Then, the relevance vector machine (RVM) is employed to estimate the posterior probability. Finally, the algorithm is accelerated by maximizing the marginal likelihood function. Simulation results demonstrate the superior efficiency of the proposed method, showing a 90 % reduction in runtime compared to conventional super-resolution methods.**

Keywords: **fast Bayesian compressive sensing (FBCS), real aperture radar, super-resolution imaging**

I. INTRODUCTION

Real aperture radar (RAR) serves as a critical sensor for forward-looking imaging applications, including airport monitoring, topographic mapping, maritime navigation, and precision delivery systems [1], 2]. Although RAR achieves stable measurements, its azimuth and elevation resolutions remain fundamentally constrained by the physical antenna size.

Super-resolution techniques offer a promising pathway to enhance angular resolution without hardware modifications. In scenarios such as airport reconnaissance and maritime surveillance, where targets are sparsely distributed relative to potential grid points. Therefore, some sparse signal processing methods, including Bayesian methods, spectral estimation, and regularization-based approaches have demonstrated potential for resolution enhancement. In [3], a two-dimensional (2D) super-resolution imaging method based 2D fast Fourier transform is developed to improve the azimuth-elevation resolution. In fact, 2D deconvolution is the problem of imaging processing, and there are various classical methods which can be used to solve the 2D super-resolution problem, such as Wiener fltering [4] and Richardson–Lucy methods [5]. These methods can be implemented in the frequency domain using the FFT and inverse FFT. There are also some effective timedomain methods to solve 2D deconvolution problem, mainly including regularization methods [6, 7], spectral estimation methods [8], 9]. In [10], a 2D sparse super-resolution imaging method based on the l1 norm is reported and the problem is solved by the alternating direction method of multipliers (ADMM) algorithm. In [11], the Tikhonov regularization super-resolution method, which introduces the l_2 norm is brought up to smooth noise and improve angular resolution. Iterative adaptive approach (IAA) is a parameter free spectral estimation method. In [12], a fast conjugate gradient 2D-IAA is proposed to reconstruct the azimuth-elevation 2D target scatterings more effciently.

However, most of the aforementioned methods require extensive iterative computations and involve matrix inversion operations, resulting in prohibitively high algorithmic complexity. Furthermore, this study focuses on azimuth-elevation 2D forward-looking super-resolution imaging, where the dimensionality of the echo matrix is significantly larger compared to one-dimensional azimuth-only super-resolution. This leads to a dramatic increase in the dimensions of the observation matrix, further exacerbating computational demands and limiting practical applicability. To address these challenges, we propose a Fast Bayesian compressive sensing (FBCS) algorithm that not only maintains high imaging fidelity but also substantially reduces computational complexity, thereby enhancing the operational efficiency of super-resolution imaging.

The rest of this paper is organized as follows. In section II, the 2D signal model of the real aperture radar is introduced. In section III, the proposed FBCS method are discussed in detail. In section IV, simulation results are presented to illustrate the performance of the proposed method. Finally, section V covers the conclusion.

II. SIGNAL MODEL

The azimuth-elevation imaging geometry of a real aperture radar is illustrated in Fig. 1.

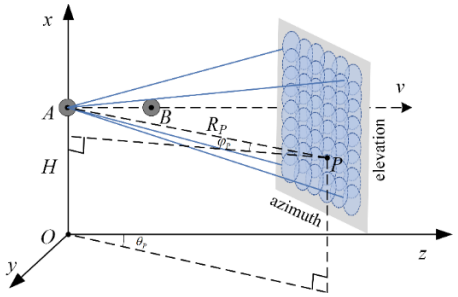


Fig. 1. Imaging geometry of a real aperture radar

Considering additive noise for the same range slice, the azimuth-elevation echo model after pulse compression can be written as follows

$$y(\theta,\varphi) = a(\theta,\varphi) * \sigma(\theta,\varphi) + n(\theta,\varphi), \tag{1}$$

where $*$ denotes the 2D convolution operation. $a(\theta,\varphi)$ is equal to a 2D convolution kernel. For mathematical simplicity, the 2-D imaging model (1) can be rewritten as a matrix form

$$\mathbf{Y} = \mathbf{AXB} + \mathbf{N}, \tag{2}$$

where $\mathbf{Y} \in \mathbb{C}^{M\times N}$ represents a matrix containing the sampling of measurement data at the corresponding azimuth and pitch angles, $\mathbf{X} \in \mathbb{C}^{K_1\times K_2}$ represents the unknown target scattering coeffcient, $\mathbf{A} \in \mathbb{C}^{M\times K_1}$ and $\mathbf{B} \in \mathbb{C}^{N\times K_2}$ denote the azimuth and elevation antenna pattern convolution matrix, and $\mathbf{N} \in \mathbb{C}^{M\times N}$ denotes the additive noise. Using the Kronecker product, model (2) can be transformed into a matrix-vector form, expressed as

$$\mathbf{y} = \mathbf{Fx} + \mathbf{n}, \tag{3}$$

where $\mathbf{y}$, $\mathbf{F}$, $\mathbf{x}$, $\mathbf{n}$ respectively satisfy the following relations,

$$\begin{aligned} \mathbf{y} &= \mathrm{vec}(\mathbf{Y}) \in \mathbb{C}^{MN\times 1}, \\ \mathbf{F} &= \mathbf{A} \otimes \mathbf{B} \in \mathbb{C}^{MN\times K_1K_2}, \\ \mathbf{x} &= \mathrm{vec}(\mathbf{X}) \in \mathbb{C}^{K_1K_2\times 1}, \\ \mathbf{n} &= \mathrm{vec}(\mathbf{N}) \in \mathbb{C}^{MN\times 1}, \end{aligned} \tag{4}$$

where vec(·) denotes vectorization, and $\otimes$ the Kronecker product.

III. PROPOSED METHOD

Model (3) can be solved using traditional super-resolution methods [13]. However, the dimensionality of the vectorized model is extremely high, which is unfriendly to the hardware platform. In this paper, we are committed to deriving a fast 2D sparse reconstruction algorithm based on BCS.

A. Hierarchical Sparseness Prior

First, assume $\mathbf{x}$ follows a Gaussian distribution with zero mean. Its probability density function can then be expressed as

$$p(\mathbf{x}\,|\,\boldsymbol{\alpha}) = \prod_{i=1}^{N} \mathcal{N}(x_i\,|\,0,\alpha_i^{-1}), \tag{5}$$

with α_i the precision (inverse-variance) of a Gaussian density function. Assuming the hyperparameter of noise is denoted as α_0, and to maintain consistency with the signal hyperparameters, it is also defined as the reciprocal of the noise variance, i.e., $\alpha_0 = 1/\sigma_0^2$. Further, a Gamma prior is considered over $\boldsymbol{\alpha}$

$$p(\boldsymbol{\alpha}\,|\,a,b) = \prod_{i=1}^{N} \Gamma(\alpha_i\,|\,a,b). \tag{6}$$

By marginalizing over the hyperparameters, the overall prior on is then evaluated as

$$p(\mathbf{x}\,|\,a,b) = \prod_{i=1}^{N} \int_0^{\infty} \mathcal{N}(x_i\,|\,0,\alpha_i^{-1})\Gamma(\alpha_i\,|\,a,b)d\alpha_i. \tag{7}$$

The density function $\Gamma(\alpha_i\,|\,a,b)$ is the conjugate prior for α_i, when x_i plays the role of observed data and $\mathcal{N}(w_i\,|\,0,\alpha_i^{-1})$ is a likelihood function.

B. *Fast Bayesian CS Inversion via relevance vector machine*

According to the BCS theory, the sparse reconstruction of the original signal is achieved by maximizing its posterior probability. The posterior probability distribution of the unknown variables can be expressed as:

$$p\left(\mathbf{x},\boldsymbol{\alpha},\alpha_0|\ \mathbf{y}\right)=\frac{p\left(\mathbf{y}|\ \mathbf{x},\boldsymbol{\alpha},\alpha_0\right)p\left(\mathbf{x},\boldsymbol{\alpha},\alpha_0\right)}{p(\mathbf{y})}. \quad (8)$$

We cannot directly compute the posterior probability $p\left(\mathbf{x},\boldsymbol{\alpha},\alpha_0|\ \mathbf{y}\right)$ from (8) due to the intractability of calculating $p(\boldsymbol{y})=\int p(\boldsymbol{y}\,|\,\mathbf{x},\boldsymbol{\alpha},\alpha_0)p(\mathbf{x},\boldsymbol{\alpha},\alpha_0)d\mathbf{x}d\boldsymbol{\alpha}d\alpha_0$.

Therefore, we decompose the posterior probability into the following expression for solution:

$$p(\mathbf{x},\boldsymbol{\alpha},\alpha_0|\ \mathbf{y})=p(\mathbf{x}|\ \mathbf{y},\boldsymbol{\alpha},\alpha_0)p(\boldsymbol{\alpha},\alpha_0|\ \mathbf{y}), \quad (9)$$

where

$$\begin{aligned}p(\mathbf{x}|\ \mathbf{y},\boldsymbol{\alpha},\alpha_0)&=\frac{p(\mathbf{y}\,|\,\mathbf{x},\alpha_0)p(\mathbf{x}\,|\,\boldsymbol{\alpha})}{p(\mathbf{y}\,|\,\boldsymbol{\alpha},\alpha_0)}\\&=(2\pi)^{-\frac{(N+1)}{2}}\left|\boldsymbol{\Sigma}\right|^{-\frac{1}{2}}\exp\left\{-\frac{1}{2}\left(\mathbf{x}-\boldsymbol{\mu}\right)^T\boldsymbol{\Sigma}^{-1}\left(\mathbf{x}-\boldsymbol{\mu}\right)\right\}\end{aligned} \quad (10)$$

The mean and variance of the posterior probability are respectively,

$$\begin{aligned}\boldsymbol{\mu}&=\alpha_0\boldsymbol{\Sigma}\mathbf{F}^T\boldsymbol{y}\\\boldsymbol{\Sigma}&=\left(\alpha_0\mathbf{F}^T\mathbf{F}+\boldsymbol{\Lambda}\right)^{-1}\end{aligned} \quad (11)$$

where $\boldsymbol{\Lambda}=diag\left(\alpha_1,\cdots,\alpha_N\right)$.

From the above two equations, it can be observed that solving for the mean $\boldsymbol{\mu}$ and covariance $\boldsymbol{\Sigma}$ requires first estimating the parameters α_0 and $\boldsymbol{\alpha}$. For the second part of (9), we have $p\left(\boldsymbol{\alpha},\alpha_0\,|\,\mathbf{y}\right)\propto p\left(\mathbf{y}\,|\,\boldsymbol{\alpha},\alpha_0\right)p\left(\boldsymbol{\alpha}\right)p\left(\alpha_0\right)$. When the Gamma distribution is assumed to be uniform (i.e., uninformative priors for $\boldsymbol{\alpha}$ and α_0), this simplifies to, $p\left(\boldsymbol{\alpha},\alpha_0\,|\,\mathbf{y}\right)\propto p\left(\mathbf{y}\,|\,\boldsymbol{\alpha},\alpha_0\right)$. Thus, the problem reduces to estimating $p\left(\mathbf{y}\,|\,\boldsymbol{\alpha},\alpha_0\right)$. By marginalizing over the sparse weight coefficients $\mathbf{x}$, we obtain

$$\begin{aligned}p(\mathbf{y}\,|\,\boldsymbol{\alpha},\alpha_0)&=\int p\left(\mathbf{y}\,|\,\mathbf{x},\alpha_0\right)p\left(\mathbf{x}\,|\,\boldsymbol{\alpha}\right)d\mathbf{x}\\&=\left(2\pi\right)^{-N/2}\left|\alpha_0^{-1}\boldsymbol{I}+\mathbf{F}\boldsymbol{\Lambda}^{-1}\mathbf{F}^T\right|^{-1/2}\\&\exp\left\{-\frac{1}{2}\boldsymbol{y}^T\left(\alpha_0^{-1}\boldsymbol{I}+\mathbf{F}\boldsymbol{\Lambda}^{-1}\mathbf{F}^T\right)^{-1}\mathbf{y}\right\}\end{aligned} \quad (12)$$

Taking the logarithm of both sides of the equation yields

$$\begin{aligned}L\left(\boldsymbol{\alpha}\right)&=\log\left(p\left(\mathbf{y}\,|\,\boldsymbol{\alpha},\alpha_0\right)\right)\\&=\log\left(\int p\left(\mathbf{y}\,|\,\mathbf{x},\alpha_0\right)p\left(\mathbf{x}\,|\,\boldsymbol{\alpha}\right)d\mathbf{x}\right)\\&=-\frac{1}{2}\left[N\log\left(2\pi\right)+\log\left(\mathbf{C}\right)+\mathbf{y}^T\mathbf{C}^{-1}\mathbf{y}\right]\end{aligned} \quad (13)$$

where

$$\mathbf{C}=\alpha_0^{-1}\mathbf{I}+\mathbf{F}\boldsymbol{\Lambda}^{-1}\mathbf{F}^T. \quad (14)$$

Considering the dependence of $L(\boldsymbol{\alpha})$ on a single parameter α_i (where $i\in\{1,2,\ldots,K\}$), (14) can be decomposed as

$$\mathbf{C}=\sigma_0^2\mathbf{I}_K+\sum_{j\neq i}\alpha_j^{-1}\mathbf{F}_j\mathbf{F}_j^T+\alpha_i^{-1}\mathbf{F}_i\mathbf{F}_i^T=\mathbf{C}_{-i}+\alpha_i^{-1}\mathbf{F}_i\mathbf{F}_i^T \quad (15)$$

where $\mathbf{C}_{-i}$ denotes the matrix $\mathbf{C}$ with the contribution of the *i*-th basis vector removed.

Using theorems related to matrix determinants and inversion, the terms of $L(\boldsymbol{\alpha})$ can be further expressed as:

$$|\,\mathbf{C}\,|=|\,\mathbf{C}_{-i}\,|\cdot\left|1+\alpha_i^{-1}\mathbf{F}_i^T\mathbf{C}_{-i}^{-1}\mathbf{F}_i\right|, \quad (16)$$

$$\mathbf{C}^{-1}=\mathbf{C}_{-i}^{-1}-\frac{\mathbf{C}_{-i}^{-1}\mathbf{F}_i\mathbf{F}_i^T\mathbf{C}_{-i}^{-1}}{\alpha_i+\mathbf{F}_i^T\mathbf{C}_{-i}^{-1}\mathbf{F}_i}. \quad (17)$$

Substituting (15)–(17) into (13) yields:

$$\begin{aligned}L(\boldsymbol{\alpha})&=-\frac{1}{2}\left[\begin{array}{l}K\log(2\pi)+\log|\,\mathbf{C}_{-i}\,|+\mathbf{y}^T\mathbf{C}_{-i}^{-1}\mathbf{y}-\\\log\alpha_i+\log\left(\alpha_i+\mathbf{F}_i^T\mathbf{C}_{-i}^{-1}\mathbf{F}_i\right)-\frac{(\mathbf{F}_i^T\mathbf{C}_{-i}^{-1}\mathbf{y})^2}{\alpha_i+\mathbf{F}_i^T\mathbf{C}_{-i}^{-1}\mathbf{F}_i}\end{array}\right]\\&=L(\boldsymbol{\alpha}_{-i})+\frac{1}{2}\left[\log\alpha_i-\log(\alpha_i+s_i)+\frac{q_i^2}{\alpha_i+s_i}\right]\\&=L(\boldsymbol{\alpha}_{-i})+l(\alpha_i)\end{aligned} \quad (18)$$

where

$$s_i=\mathbf{F}_i^T\mathbf{C}_{-i}^{-1}\mathbf{F}_i, \quad (19)$$

$$q_i=\mathbf{F}_i^T\mathbf{C}_{-i}^{-1}\mathbf{y}. \quad (20)$$

Here, s_i is referred to as the sparsity term, representing the portion of the model already explained by the basis vector $\mathbf{F}_i$, while q_i is called the quality term, equivalent to $q_i=\sigma_0^{-2}\mathbf{F}_i^T\left(\mathbf{y}-(\mathbf{F}\mathbf{x})_{-i}\right)$, which can be interpreted as the correlation between $\mathbf{D}_i$ and the noise in the model.

By decomposing the marginal probability density in (18) into $L(\boldsymbol{\alpha}_{-i})$ (the marginal density excluding $\mathbf{F}_i$ and $l(\alpha_i)$, the parameter α_i is effectively isolated. The conditions for $L(\boldsymbol{\alpha})$ to reach its maximum with respect to α_i are as follows

$$\alpha_i=\frac{s_i^2}{q_i^2-s_i},\quad q_i^2>s_i, \quad (21)$$

$$\alpha_i = \infty, \quad q_i^2 \le s_i . \tag{22}$$

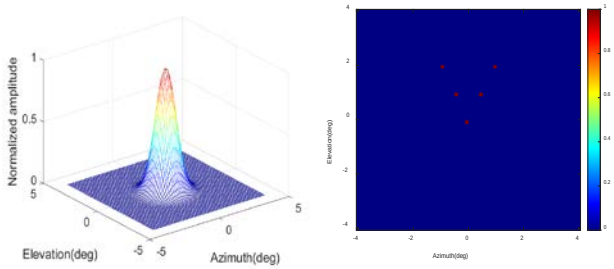
Based on the above derivation, the function $L(\boldsymbol{\alpha})$ attains a unique maximum with respect to α_i .

IV. Numerical Results

To verify the performance of the proposed method, this section gives the 2D imaging performance comparison about l_1-ADMM and 2D-IAA methods. The specific parameters are shown in 0Fig. 2a shows the 2D antenna pattern function, the mainlobe width is 1°×1°. The five spaced point targets, which are located at (0°,0°), (-0.4°,1°), (0.4°,1°), (-1°,2°) and (1°,2°) are considered to demonstrate the effectiveness of the developed method in this paper. Fig. 2b shows the original scene.

Simulation Parameter

Parameter	Value
Carrier frequency	80 GHz
Bandwidth	15 MHz
Field of view in azimuth/elevation	±4°
Azimuth/elevation beamwidth	1°
Sampling number in azimuth/elevation	32



a b

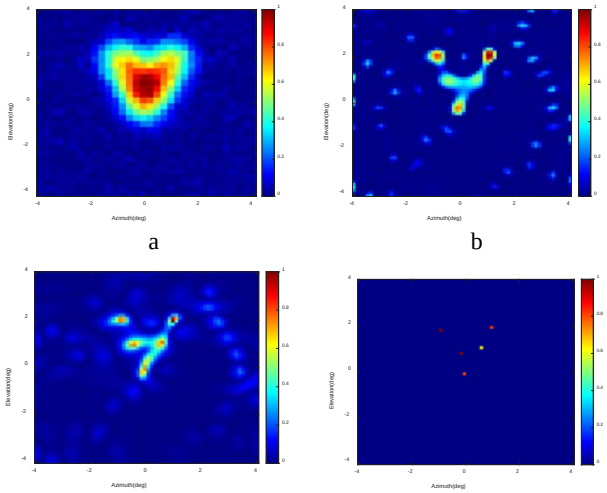
Fig. 2. Antenna pattern and real scene of simulation: Antenna pattern (a), Real scene (b)

A. Imaging performance

The processed results of different methods are illustrated in Fig. 3, where Fig. 3a is the real beam echo with signal-tonoise ratio (SNR) of 20 dB. We can find that the resolution of the echo imagery is coarse, and we cannot distinguish the number of targets from it. Fig. 3b is the processed result of l_1-ADMM. It can be seen that the two central targets is notably poor, with significantly lower amplitudes compared to the other three targets, resulting in subpar image quality. Fig. 3c shows the results of 2D-IAA method. It can be observed that the target positions canbe constructed roughly, but its performance is limited by higher sidelobes. In contrast, the result based on the proposed FBCS method maintains higher resolution and lower side lobes as shown in Fig. 3d.

B. Computational efficiency

Compared with conventional methods, the proposed FBCS super-resolution imaging method in this study eliminates the need for large-scale matrix inversion operations. To compare the computational complexity of different methods, we maintain the dimensions of the high-resolution images (i.e., K_1 and K_2 remain constant) while increasing the dimensions of low-resolution images (i.e. M and N). The simulation platform is a PC workstation with an Intel Core i9-13900HX CPU, 2.20GHz, and 16 GB RAM. All the simulations are conducted by 64bit-MATLAB R2023a.



a b c d

Fig. 3. Processed results: Real beam echo (a), Result of l_1-ADMM (b), Result of 2D-IAA method (c), Result of proposed FBCS method (d)

In the simulation experiments, we set K_1= K_2=64 and maintained M=N. By varying M and N as 4, 8, 16, 32, 64, we computed the processing times for l_1-ADMM based method, 2D-IAA based method and the proposed FBCS method. The results are illustrated in Fig. 4.

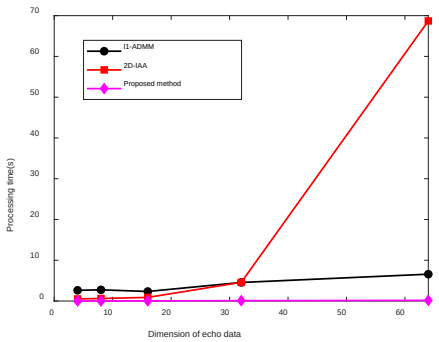


Fig. 4. Processing time of different methods

As shown in Fig. 4, the 2D-IAA method presents the longest operational time among all methods considered. In particular, as the dimension of echo data increases, the processing time increases drastically. In

comparison, the proposed method achieves the shortest computational time. Moreover, as the dimensionality of the echo data increases, its runtime scales approximately linearly without abrupt escalation. The data in the figure demonstrate that the proposed method reduces computation time by over 90 % compared to conventional methods. These simulations demonstrate that our approach maintains low computational complexity.

V. Conclusion

In this paper, we have presented a fast super-resolution imaging method for forward-looking radar. The proposed method maintains reconstruction performance while offering much less computational. Simultaneously, the effectiveness of the proposed algorithm is verified by simulation. The simulation results demonstrate that the proposed method reduces computational time by 90 % compared to conventional approaches.

Acknowledgment

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Russian Handwriting Recognition Using VGG-BiLSTM-CTC Transfer Learning

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Abstract. **Deep learning methods have shown great potential in the field of handwriting recognition. The VGG-BiLSTM-CTC model, as a state-of-the-art recognition architecture, has proved to be effective in a wide range of languages. However, for Russian handwriting recognition, despite its great demand, research is still insufficient. This study aims to fill the research gap in this area by applying this model to Russian handwriting recognition through transfer learning.**

Keyword: **Handwriting recognition, deep learning, VGG-BiLSTM-CTC, data augmentation, Russian language**

I. INTRODUCTION

Handwriting recognition technology, as an important branch in the field of pattern recognition, has received widespread attention and rapid development in recent years. It involves converting handwritten character images into text format, and this technology has important application value in many fields such as automated office, digitization of historical documents, intelligent education and security authentication. Although significant progress has been made in handwriting recognition technology, handwriting recognition for different languages still faces unique challenges.

Traditional handwriting recognition methods mainly rely on manually extracted features and template matching techniques, which perform well when dealing with regular handwritten characters, but their recognition accuracy drops significantly when facing tilted, rotated or irregular handwritten characters. With the development of deep learning techniques, modern handwriting recognition methods have begun to utilize advanced models such as Convolutional Neural Networks (CNN) [1] and Recurrent Neural Networks (RNN) to improve recognition accuracy and robustness.

Various approaches have been proposed in the industry for handwriting recognition in different languages. For example, research for handwriting recognition of Chinese characters has achieved certain results, while for English handwriting recognition, deep learning-based methods have been widely adopted. However, for Russian handwriting recognition, despite the huge demand for handwriting recognition in Russian as a world common language, existing research is relatively sparse. This is mainly due to the uniqueness of Russian characters as well as the diversity and complexity of handwriting, which makes it particularly important to develop an effective method for Russian handwriting recognition.

The aim of this study is to propose a Russian handwriting recognition method based on the existing VGG-BiLSTM-CTC model. We will train the model using the Cyrillic Handwriting Dataset dataset [3] and introduce data augmentation for transfer learning and conduct fine tuning to improve the model's performance on the Russian handwriting recognition task. Through experiments, we demonstrate the effectiveness of the proposed method and provide a new solution for the field of Russian handwriting recognition.

II. RELATED WORKS

Since the similarity in shape between English and Russian characters, we first review methods used for

English character recognition. These methods provide valuable references and insights for Russian handwriting recognition.

Alex proposed a connectionist system for unconstrained handwriting recognition [4], which introduced a RNN architecture tailored for sequence labeling tasks involving hard-to-segment data with long bidirectional dependencies. The accuracy of Alex's method was achieved 79.7 % on online data and 74.1 % on offline, which is still far from enough.

A. Graves et al. proposed "Connectionist Tense Classification": this is another classical handwriting recognition method that combines Convolutional Neural Networks (CNN) [5] for feature extraction and Hidden Markov Models (HMM) for sequence modeling. Although this method improves the recognition accuracy, it suffers from computational inefficiency, high memory consumption and long training time when dealing with large datasets.

The VGG-BiLSTM-CTCmodel [6] proposed by Shi et al., offers several key advantages for handwriting and scene text recognition [2]. It supports end-to-end training, integrating feature extraction, sequence modeling, and prediction into a single framework, which simplifies the learning process. By utilizing the VGG architecture, the model enhances its ability to extract rich visual features from images, leading to improved recognition accuracy. The Bidirectional LSTM component captures contextual information from both past and future characters, resulting in more accurate sequence predictions. Additionally, the Connectionist Temporal Classification (CTC) allows the model to handle variable-length input sequences without requiring precise alignment, making it effective for diverse handwriting styles. Overall, the model demonstrates superior performance in recognizing distorted, slanted, or noisy text compared to traditional methods, enhancing its robustness in real-world applications.

We intend to use VGG-BiLSTM-CTC Mode as the foundation for our approach and apply transfer learning. By leveraging the successful experiences of VGG-BiLSTM-CTC in English handwriting recognition, we aim to enhance the performance of the model in the task of Russian handwriting recognition.

III. Proposed Method

In this study, we propose a transfer learning method based on the VGG-BiLSTM-CTC model to migrate the model from English to Russian (Cyrillic script) for scene text recognition. Our goal is to enhance the model's performance on Russian scene text through transfer learning and data augmentation strategies. To achieve this, we designed a comprehensive transfer learning framework that includes the following key steps: data augmentation and pretraining model. First, we pretrained the VGG-BiLSTM-CTC model on large-scale English synthetic datasets (such as MJSynth and SynthText) to learn general text features. Then, we introduced data augmentation techniques on the Russian Cyrillic dataset to enhance the model's adaptability to variations in Russian text. The overall structure of the proposed method is shown in Fig. 1.

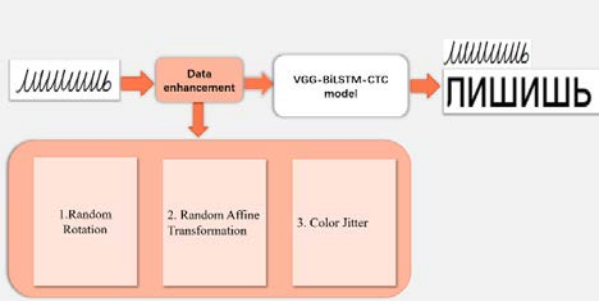

Fig. 1. Overall structure of the proposed method

To improve the model's adaptability to variations in Russian scene text, we introduced the following data augmentation techniques during the training process on the Russian dataset:

Random Rotation: The parameter is set to (-3, 3), indicating that the image will be randomly rotated between –3 and 3 degrees. This technique simulates slight tilts in Russian text, helping the model learn the directional features of the text.

Random Affine Transformation: The parameter is set to degrees=0, translate=(0.05, 0.05), indicating no rotation but random translation in both horizontal and vertical directions by up to 5 % of the image width and height. This technique simulates text position offsets, enhancing the model's adaptability to changes in text position.

Color Jitter: The parameter is set to brightness=0.2, contrast=0.2, indicating that brightness and contrast will be randomly adjusted within ±20 % of the original values. This technique simulates text images under different lighting conditions, enhancing the model's adaptability to background interference and lighting changes.

IV. Experiment And Results Analysis

A. Dataset and Experimental Setup

The experiments for this study were conducted in a well-configured computational environment to ensure the reproducibility and reliability of the results. The experiments utilized PyTorch 2.5.1 and CUDA 12.1 for training deep learning models, with Python 3.9 serving as the programming language environment. The dataset used was the Cyrillic Handwriting Dataset, which was divided into a training set and a test set, comprising 57,827 samples for training and 16,002 samples for

testing. These samples cover a variety of handwriting styles in the Russian language, providing rich data support for model training and evaluation.

During the model training process, key parameters were employed: the batch size was set to 192, the number of iterations was 300,000, the learning rate was 1, the image height and width were set to 32 and 100 pixels respectively, the number of classes was 187, and the validation interval was every 2000 iterations.

B. Result Analysis

To evaluate the original model and our proposed method based on three metrics: training and validation loss, accuracy, and training time efficiency.

Fig. 2 demonstrates the comparison of training accuracy. Our algorithm improves accuracy faster throughout the training process and ultimately achieves a higher accuracy rate. This shows that by using the Cyrillic Handwriting Dataset dataset and data enhancement techniques, our model has better performance on the Russian handwriting recognition task.

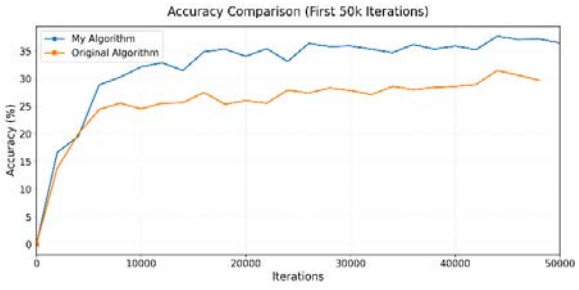

Fig. 2. Accuracy Comparison

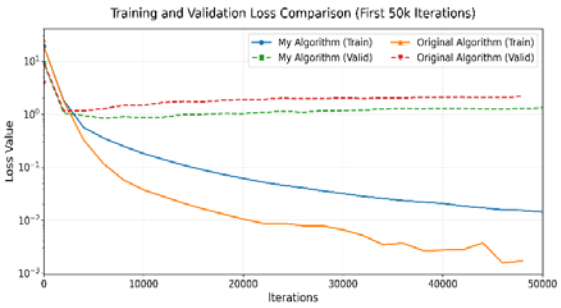

Fig. 3. Training and Validation Loss Comparison

As can be seen in Fig. 3 our algorithm outperforms the original algorithm in both training and validation losses.Specifically, the training loss of the new algorithm decreases rapidly at the beginning and stabilizes at a lower loss value, while the training loss of the original algorithm is relatively high and decreases slowly. For validation loss, the new algorithm similarly exhibits lower and more stable loss values.

Fig. 4 shows a comparison of the training time per 2000 iterations as well as the total training time. Although our algorithm requires more time for data preprocessing and enhancement at the beginning of training, its time efficiency gradually improves as the training progresses, and eventually slightly outperforms the original algorithm in terms of total training time.

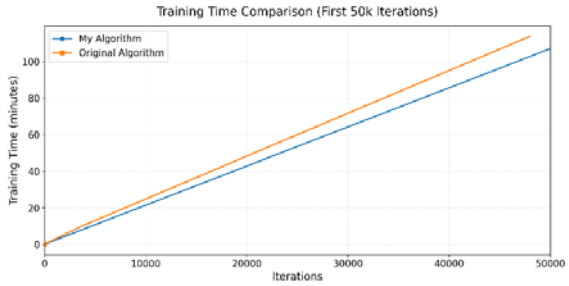

Fig.4. Training time comparison

V. Conclusion

After experiments on the Cyrillic Handwriting Dataset dataset, our algorithm outperforms the original VG-BiLSTM-CTC model in several key performance metrics. The specific conclusions are as follows:

The proposed method achieves a lower loss value for training and verification losses, indicating that the model is better than the original algorithm.

From the perspective of accuracy, our method demonstrates higher accuracy throughout the training process, ultimately achieving higher accuracy than the original algorithm, demonstrating the effectiveness of data augmentation and dataset-specific training.

From the terms of training time efficiency, although our algorithm has a slightly higher training time at the beginning due to the need of data preprocessing and enhancement, it gradually improves its efficiency as the training progresses, and eventually slightly outperforms the original algorithm in terms of the total training time, showing a good time efficiency.

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The Comparative Analysis of Option Pricing Based on the Black-Scholes Model

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Abstract. **Options are an important tool in the development of financial markets. They are becoming an important part of trading on many exchanges. Models for option prices, such as the Black-Scholes model, binomial trees, and the Heston model, give different results depending on the parameters used and market conditions. The article provides a comparative analysis of these models. It is shown that for real data, the Black-Scholes model, which is applied to European options, and the binomial tree model, which is used for American options, demonstrate similar results, which confirms their adequacy under conditions of stable volatility. These models are good at pricing options and futures when volatility does not change significantly. However, Heston's model, which takes changing volatility into account, shows lower prices for call options and higher prices for put options. This indicates its more conservative approach, which assumes that changes in volatility can have a significant impact on option prices.**

Keywords: **Option pricing, Black-Scholes model, binomial model, Heston model, stochastic volatility, financial derivatives, call options, put options, volatility modeling, risk management, quantitative finance, asset pricing, European options, American options, market dynamics, numerical methods, financial modeling, hedging strategies, implied volatility, historical volatility**

I. INTRODUCTION

Options reflect the complexities and contradictions of financial markets. They serve as fundamental building blocks for constructing a wide range of financial instruments. One of the most widely used option pricing models is the Black-Scholes model [1], developed in the early 1970s. However, this model has limitations, particularly its assumption of constant volatility, which often does not align with real market behavior.

To address changing volatility, the Heston model [2] is employed, incorporating stochastic volatility. This paper explores various approaches to option pricing, ranging from the classical Black-Scholes model to more advanced stochastic volatility models. A comparison of these two models in pricing American and European options provides deeper insight into the mechanics of modern option pricing and their practical applications in real-world financial markets.

II. THE BLACK-SCHOLES MODEL

In the early 1970s, Fischer Black, Myron Scholes, and Robert Merton made a fundamental breakthrough in the theory of stock option pricing [1]. This breakthrough became known as the Black-Scholes model. The basic idea proposed by the authors is that a risk-free portfolio can be created by combining two financial instruments: a derivative and the underlying stock. The return on this portfolio is then set equal to the return that would be earned on an equivalent investment at the risk-free rate. According to the Black-Scholes model, the portfolio remains risk-free only for a short period. The model incorporates key factors that influence an option's price, such as the underlying asset's price, the strike price, time to expiration, and volatility. This enables investors to more accurately evaluate the risks and potential rewards of option trading

$$\left(\frac{\partial f}{\partial t}+\frac{1}{2}\frac{\partial^2 f}{\partial s^2}\sigma^2 S^2\right)\Delta t = r\left(f-\frac{\partial f}{\partial S}S\right)\Delta t$$
$$\frac{\partial f}{\partial t}+rS\frac{\partial f}{\partial S}+\frac{1}{2}\frac{\partial^2 f}{\partial s^2}\sigma^2 S^2 = rf \quad (1)$$

where:

- S is the current price of the underlying asset,
- r is the risk-free interest rate,
- f is the price of the derivative (e.g., an option), depending on the asset price S and time t, $0 \le 0 \le T$,
- σ is the volatility of the underlying asset (standard deviation of returns).

This equation is fundamental and is known as the Black-Scholes-Merton equation. In order to solve equation (1) boundary conditions must be provided. In the case off call option those conditions are: f(S,t)=max(S-K,0)=0 for all t f(S,t)->S as t -> ∞. Equation (1) has many solutions that correspond to various derivative instruments whose price depends on the value of the underlying asset. To select a specific solution, boundary conditions are introduced for time and asset price.

Despite its advantages, the Black-Scholes model faces several challenges when it comes to analyzing volatility. First, the number of observations (n) used to estimate volatility must be chosen carefully. Generally, using between 60 and 200 daily, 40 to 60 weekly, or 30 to 50 monthly price observations is considered an appropriate compromise. Second, the interval between observations is important. If the stock price follows a lognormal distribution, the length of the interval is less critical, although this assumption simplifies the model.

Assuming constant volatility can lead to significant pricing errors. For example, if actual volatility is higher than expected, the option tends to be underpriced, which can negatively affect the investor's returns. Conversely, if actual volatility is lower than expected, the option may be overpriced.

To address these limitations, alternative models have been developed, such as stochastic volatility models (e.g., the Heston model), which treat volatility as a random process that can vary over time.

III. The Heston Model

Stochastic volatility models represent one approach to addressing the limitations of the Black-Scholes framework. Unlike the Black-Scholes model, which assumes constant volatility, stochastic volatility models treat volatility as a dynamic variable subject to random fluctuations. This allows for a more realistic representation of market behavior and enhances the accuracy of option pricing [2].

Among these models, the Heston model stands out as a prominent and widely used approach. It models volatility as a separate stochastic process that evolves over time and depends on various factors, including the asset price and external shocks.

In the Heston model, the price of the underlying asset S_t is described by the following stochastic differential equation (SDE) [6]:

$$dS_t = \mu S_t dt + \sqrt{V_t} S_t dW_t^V , \qquad (2)$$

where:

- S_t is the price of the underlying asset at time t,
- μ is the drift term, represent the asset's expected return,
- V_t is the stochastic variance (volatility squared),
- dW_t^V – a standard Wiener process (Brownian motion), representing random market fluctuations.

The evolution of volatility V_t is governed by its own stochastic differential equation:

$$dV_t = \theta(\bar{V} - V_t)dt + \sigma\sqrt{V_t} dW_t^V , \qquad (3)$$

where:

- $\bar{V}$ is the long-term average variance,
- θ is the rate at which V_t reverts to $\bar{V}$,
- σ is the volatility of volatility, i.e., the standard deviation of V_t,
- dW_t^V is another Wiener process, which may be correlated with dW_t^S with correlation coefficient ρ.

The Heston model (2), (3) is particularly useful in pricing options where volatility is observed to change over time, such as equity options, currency options, and commodity options. Given that financial markets often exhibit fluctuating volatility, the Heston model offers a more robust and realistic framework compared to models assuming constant volatility. Its ability to capture key market features, such as the volatility smile [7] and mean reversion, makes it a valuable tool for both theoretical analysis and practical applications in finance [3].

IV. Comparison of Models

When calculated using Apple's closing price data from January 1, 2025, to April 16, 2025, both the Black-Scholes model, which is commonly applied to European options, and the binomial tree model, typically used for American options, produced similar pricing results. This consistency confirms the adequacy of both models under conditions of relatively stable volatility. These models are well-suited for pricing options and futures in environments where market volatility remains fairly constan t.

In contrast, the Heston model, which incorporates stochastic volatility, yielded lower prices for call options and higher prices for put options. This suggests a more conservative pricing approach, reflecting the model's sensitivity to potential changes in market volatility. The results indicate that the Heston model more accurately captures the risks associated with fluctuating volatility, offering improved pricing in volatile or uncertain market conditions.

Therefore, while the Black-Scholes and binomial tree models remain effective under stable conditions, the Heston model provides superior pricing accuracy when volatility is variable, making it especially valuable in dynamic market environments.

The graphs of asset price changes match, indicating that the same market data was used. However, the option prices calculated using different models differ.

The Black-Scholes model and the binomial model (tree) produce similar values for call and put options, indicating their adequacy under conditions of stable

volatility. The price of the futures contract is the same across all three models – 204.23 – which confirms the correctness of the initial assumptions [4, 5].

Fig. 1. Asset price change graph, Black-Scholes model

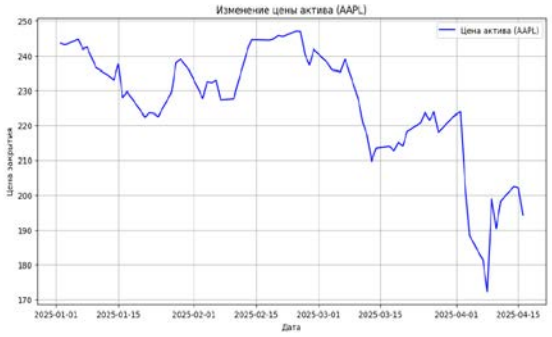

Fig. 2. Asset price change chart, Heston model, real data

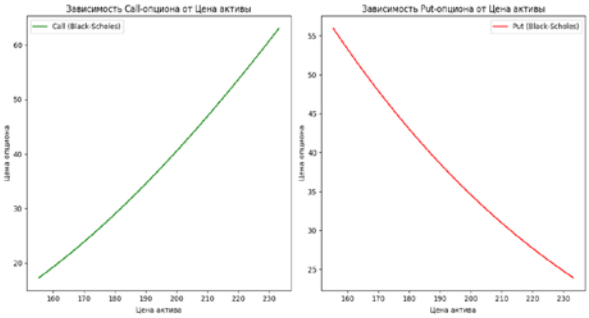

Fig. 3. Graph of the dependence of a call option and a put option on the asset price, Black-Scholes model, real data

At the same time, the Heston model, which takes into account the stochastic nature of volatility, shows a significantly lower price for the call option (19.04 versus 37.03 according to Black-Scholes) and a slightly higher price for the put option (38.28 versus 36.80). This reflects the conservative approach of the Heston model, which assumes that changing volatility affects the option's value.

Thus, despite the same asset price trajectory, differences in the approaches to accounting for volatility lead to different option premiums. This highlights the importance of choosing a model based on market conditions: constant volatility models work well in stable environments, while the Heston model is better suited to unstable, volatile markets.

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Class Weight Methods for Data Imbalanced

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***Abstract*. When solving a classification problem, data imbalance is often a problem, which leads to poor classification accuracy in general and the inability to determine the minor class in particular. In this paper, experimental studies of data weighting methods in combination with classical classification algorithms are performed. The results show that the Inverse Frequency approach, which is most often used, does not provide maximum classification results. General recommendations for dealing with class imbalances are provided. Alternative weighing strategies beyond standard implementations should be explored and integrated into hyperparameter optimization.**

***Keywords:* imbalanced data, classification, class weight, weighting, balanced accuracy**

I. Introduction

In classification tasks, a common challenge is the significant imbalance in the proportions of objects belonging to each class within a dataset. Fig. 1 illustrates examples of such class imbalance in diabetes dataset.

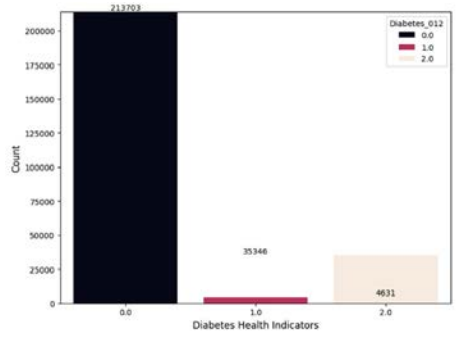

Fig. 1. Example of imbalanced dataset

Identifying such situations during exploratory data analysis, as well as directly handling imbalanced data in machine learning tasks, represents a critically important challenge. In many applied problems, it is impossible to augment the dataset and eliminate the imbalance through additional sampling. Furthermore, classes in such datasets may exhibit substantial overlap and contain numerous borderline cases, which are often characterized by high-dimensional feature spaces. These factors collectively exacerbate the problem, significantly diminishing the effectiveness of algorithms and architectures that typically demonstrate strong performance under balanced conditions.

The objective of this study is twofold: first, to conduct a comprehensive analysis of general approaches for handling class imbalance, and second, to perform an in-depth experimental investigation of weighting methods – one of the most straightforward yet effective strategies for addressing imbalance. Despite the existence of various techniques, in practice the Inverse Frequency method remains predominantly used, despite its demonstrated limitations in cases of severe class imbalance [1–3].

II. Background and Related Word

Typically, the class with the fewest samples is the class of interest. Practical applications involving rare classes include fraud detection, diagnosis of rare diseases, credit default prediction, and similar scenarios, where misclassifying a rare instance carries a high cost. The inherent rarity of these phenomena not only causes the imbalance but also makes it difficult to collect additional samples. Fig. 2 compares synthetic datasets with imbalanced and balanced distributions. The objects are visualized based on two selected features. In this study, only the classification problem is considered, although class imbalance also occurs in the regression problem.

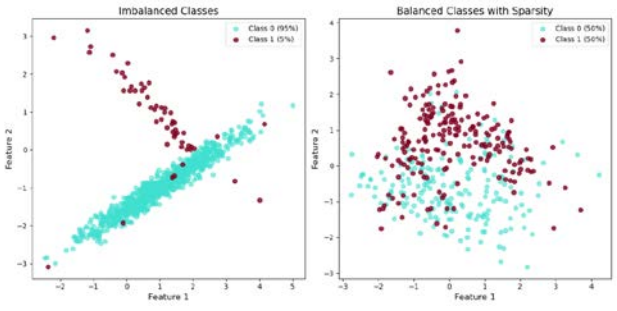

Fig. 2. Visualization of balanced and imbalanced dataset

For two synthetic datasets (with and without class imbalance), we trained random forest classifiers. Each dataset contains 1,000 samples, with class distributions of 950 vs. 50 (imbalanced) and 500 vs. 500 (balanced).

The data was split into training (700 samples) and test sets (300 samples). While the models achieve high overall accuracy on the imbalanced data, the confusion matrix reveals that a significant portion of minority-class samples are misclassified, Fig. 3.

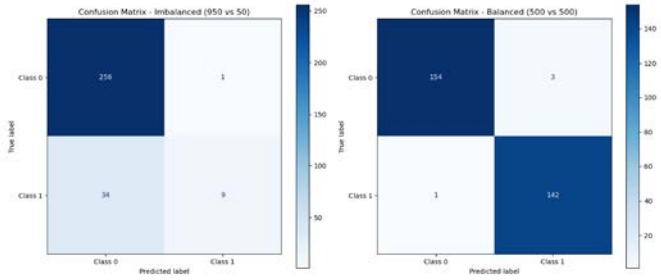

Fig. 3. Confusion matrixes for imbalanced and balanced datasets

The above example shows that with the overall high classification accuracy, a detailed analysis of the inaccuracy matrix is necessary. It clearly demonstrates that the class of interest, which is usually the most important and at the same time the minor one, is not actually determined in the classification process. That is, the classification problem has not been solved. The overall accuracy is high only due to the majority class.

To determine when a dataset is considered imbalanced, we typically examine the imbalance ratio (IR) – the proportion between the number of instances in the majority (larger) class and the minority (smaller) class

$$Imbalanced\ ration\ (IR) = \frac{len(Y_{minor})}{len(Y_{major})} \quad . \qquad (1)$$

A dataset is considered moderately imbalanced when the minor-to-major class ratio is less than 1:1.5 (i.e., IR < 0.666...). A ratio of 1:9 (minor/major = 1/9 ≈ ≈ 0.111...) typically serves as the threshold for high/significant imbalance. When the minor-to-major ratio reaches 1:99 (minor/major = 1/99 ≈ 0.010...) or lower, the imbalance is classified as extreme/very strong.

There are two primary approaches for handling imbalanced datasets: data-level methods and algorithm-level methods. Additionally, solutions based on ensemble algorithms and active learning exist.

Data-level methods directly modify the dataset by either increasing or decreasing the number of instances in specific classes. When dealing with an excessive number of majority class samples, techniques like Random Undersampling (RUS), Condensed Nearest Neighbor Rule (CNN), Edited Nearest Neighbors Rule (ENN), One-Sided Selection (OSS), and Neighborhood Cleaning Rule (NCR) can reduce the majority class instances. Conversely, methods such as Random Oversampling (ROS), Synthetic Minority Oversampling Technique (SMOTE), Borderline-SMOTE, and ADASYN (Adaptive Synthetic Sampling Approach) can increase minority class instances. Some researchers combine the described methods in their work, thereby using a hybrid approach.

Methods at the algorithm level are based primarily on cost-based learning, as well as class weighting. Class weighting actually assigns a weight to each class, which is taken into account when algorithms work and is a very effective and simple tool. You can assign a higher weight to the class of interest and this will increase the classification accuracy.This approach was chosen for the research and evaluation of effectiveness in the present work [1–6].

III. Class weight computation methods

Class weights can amplify the impact of errors associated with minority class instances while attenuating the influence of errors from majority class instances. This modification is implemented through adjustments to either the loss function computation or the splitting criterion within the learning algorithm. The weighting mechanism operates as follows.

1. Elevated class weights increase the contribution of classification errors for that particular class to model coefficient updates (in parametric models) or to node purity criteria (in decision trees).

2. Reduced weights correspondingly diminish this effect.

Several approaches exist for implementing class weighting in machine learning. The most prevalent method involves determining class weights at the algorithm level, where modifications are made to the learning model itself to incorporate these weights. Alternatively, adjustments can be made to the loss function to account for class imbalance.

Typically, the rare class represents the class of interest, where the cost of false negatives is particularly high, while a moderately elevated rate of false positives for this class is often considered acceptable. In specialized applications where domain-specific knowledge is available – such as fraud detection or medical diagnosis – manual weight assignment may be employed when the costs of misclassification are precisely quantifiable.

Among the methods for calculating class weights, it is necessary to mention the following:

- Inverse Frequency;
- Logarithmic Weighting;
- Effective Number of Samples (ENN);
- Adaptive weighted.

The Inverse Frequency method is easy to implement, and its effectiveness depends linearly on

the imbalance. An analog of the method is implemented in the Scikit-learn library in the form of the compute_class_weight function, designed to automatically calculate class weights based on their frequency occurrence in the data [7]

$$w_i = \frac{N}{K \cdot n_i}, \quad (2)$$

where *N* is the total number of samples,

K is the number of classes,

n_i is the number of class *i* samples.

Logarithmic weighting mitigates fluctuations in the distribution of weight across classes. This method is well suited for data sets with a high degree of imbalance. However, it is necessary to find the optimal value of the logarithmic base parameter, usually in the range from 1.5 to 2.0.

The Effective Number of Samples (ENN) method was presented in [8]. Unlike traditional methods, it considers the potential overlap of the feature space between instances within the same class. To do this, the parameter $\beta \approx [0,1]$ is adjusted, which allows adaptation to various degrees of class imbalance

$$E_n = \frac{1-\beta^n}{1-\beta}, \quad (3)$$

where *N* is the number of class samples.

The weight for class *i* is determined according to the following weighing formula:

$$w_i = \frac{1}{E_{n_i}} = \frac{1-\beta}{1-\beta^{n_i}}, \quad (4)$$

where *N* is the number of class samples.

Adaptive Weighted is a method in which the weights of objects, classes, or models are automatically adjusted based on current conditions, data, or performance. One of the standard metrics can be used to evaluate the performance or accuracy of the model, for example, F1-score, G-mean, ROC-AUC, etc. This method can be implemented in several steps:

1. Train the model without weights.

2. Calculate the selected metric for each class.

3. Assign weights inversely proportional to the metric.

For example, when using the F1 metric, the weights are calculated using the following formula:

$$w_i = \frac{1}{F1_i + \epsilon}, \quad (5)$$

where ϵ - a small number to avoid division by zero.

Metric F1 is determined as follows:

$$F1 = 2 \times \frac{Precision \times Recall}{Precison + Recall}, \quad (6)$$

where

$$Precision = \frac{TP}{TP+FP}, \quad (7)$$

$$Recall = \frac{TP}{TP+FN}, \quad (8)$$

where TP (True Positive) is the number of correct identifications of a positive class;

FN (False Negative) is the number of cases when objects of a negative class were assigned positive class labels;

FP (False Positive) is the number of cases when objects of a negative class were assigned positive class labels.

IV. Experiments and Results

For experimental investigation, datasets with varying degrees of class imbalance were selected from multiple domains. The study utilizes eight datasets, each containing two classes (majority and minority). These datasets from the imbalanced-learn library represent carefully curated collections specifically designed for evaluating algorithms on imbalanced data.

The ecoli dataset contains protein localization patterns in E. coli cells, characterized by 7 numerical features across 336 samples. The abalone dataset provides morphometric parameters for age determination in mollusks. For automotive safety assessment, the car_eval_34 dataset offers 6 categorical features classifying vehicle condition as "good" or "bad", exhibiting extreme imbalance with the "good" class representing less than 5% of observations. In the medical domain, the arrhythmia dataset comprises 279 electrocardiogram features for cardiac arrhythmia classification. Geophysical research data is encapsulated in the oil dataset, where 49 features describe oil well types with significant class imbalance. A simplified version, car_eval_4, derives from the original car_eval dataset. Meteorological observations are documented in the ozone_level dataset. The most challenging case is presented by the abalone_19 dataset, a modified version of the mollusk data that serves as a rigorous test for imbalanced data processing algorithms.

Basic information is presented in Table I.

TABLE I. Basic information about datasets

#	Dataset	IR	Total samples	Class distribution
1	ecoli	0.1163	336	0:301, 1:35
2	abalone	0.1033	4177	0:3786, 1:391
3	car_eval_34	0.0841	1728	0:1594, 1:134
4	arrhythmia	0.0585	452	0:427, 1:25
5	oil	0.0458	937	0:896, 1:41
6	car_eval_4	0.0391	1728	0:1663, 1:65
7	ozone_level	0.0296	2536	0:2463, 1:73
8	abalone_19	0.0077	4177	0:4145, 1:32

In the experimental studies, the primary focus was on evaluating the weighting methods described in the previous section: Inverse Frequency, Logarithmic Weighting, Effective Number of Samples (ENN), and Adaptive Weighting using the F1 metric.

To assess the effectiveness of these weighting methods, we selected three fundamental ensemble learning algorithms known to demonstrate strong performance on similar tasks: Random Forest (RF), Gradient Boosting (GB), and AdaBoost (AB). For algorithm evaluation, we employed the Balanced Accuracy metric, calculated as follows:

$$\text{Balanced Accuracy} = \frac{\text{Sensitivity}+\text{Specifity}}{2}, \quad (9)$$

where

$$\text{Sensitivity} = \frac{\text{TP}}{\text{TP}+\text{FN}}, \quad (10)$$

$$\text{Specifity} = \frac{\text{TN}}{\text{TN}+\text{FP}}, \quad (11)$$

where TN (True Negative) is the number of correct identifications of the negative class.

The experiments were conducted using the Python programming language, the Scikit-learn and unbalanced-learn libraries [9–10]. The experimental results are shown in the Tables II–IV. The tables present balanced accuracy values for each weighting approach. Additionally, the effectiveness of the built-in weighting method in the Scikit-learn library was tested. Cells are color-highlighted when results exceed baseline accuracy (algorithm implementations without weighting). The maximum values obtained for each dataset are marked in bold.

The experimental results demonstrate identical values for both class_weight='balanced' and Inverse Frequency methods, confirming the implementation details specified in the library documentation. The widely adopted Inverse Frequency approach proves effective, consistently improving classification accuracy compared to the baseline unweighted method. However, the Logarithmic Weighting approach achieves superior accuracy, producing the highest values in 5 out of 8 datasets.

V. Discussion

The experimental results demonstrate the efficacy of class weighting methods. The analysis reveals that while the commonly used Inverse Frequency approach improves model performance, it fails to achieve maximum accuracy values compared to Logarithmic Weighting. This finding suggests that practitioners should evaluate multiple weighting approaches and select the optimal one based on its synergistic effects with the chosen classification algorithm and other hyperparameters. Furthermore, comprehensive exploratory data analysis must precede model development. This critical phase enables:

- identification of class imbalance,
- quantification of imbalance severity,
- determination of necessary mitigation strategies, including class weighting implementation.

TABLE II. Experimental results for class_weight='balanced' and Inverse Frequency

#	class_weight='balanced'						Inverse Frequency					
	RF		*GB*		*AB*		*RF*		*GB*		*AB*	
	Baseline	***Weighted***	***Baseline***	***Weighted***	***Baseline***	***Weighted***	***Baseline***	***Weighted***	***Baseline***	***Weighted***	***Baseline***	***Weighted***
1	0.7345	0.6850	0.7647	0.7464	0.7042	0.6800	0.7345	0.6850	0.7647	0.7464	0.7042	0.6800
2	0.5436	0.5321	0.5218	0.7782	0.5000	0.5045	0.5436	0.5321	0.5218	0.7782	0.5000	0.5045
3	0.9185	0.9158	0.9863	**0.9921**	0.8038	0.9484	0.9185	0.9158	0.9863	**0.9921**	0.8038	0.9484
4	0.5000	0.5200	0.8718	0.9271	0.8506	0.7941	0.5000	0.5200	0.8718	0.9271	0.8506	0.7941
5	0.6183	0.5974	0.6894	0.7707	0.6744	0.7213	0.6183	0.5947	0.6894	0.7707	0.6744	0.7213
6	0.9000	0.9153	1.0000	0.9984	0.8357	0.9129	0.9000	0.9153	1.0000	0.9984	0.8357	0.9129
7	0.5056	0.5138	0.5570	0.7044	0.5725	0.5625	0.5056	0.5138	0.5570	0.7044	0.5725	0.5626
8	0.5000	0.5000	0.4986	0.5650	0.5000	0.4990	0.5000	0.5000	0.4986	0.5650	0.5000	0.4990

TABLE III. Experimental results for Logarithmic weighting and Effective number of samples (ENN)

#	Logarithmic weighting						Effective number of samples (ENN)					
	RF		*GB*		*AB*		*RF*		*GB*		*AB*	
	Baseline	***Weighted***	***Baseline***	***Weighted***	***Baseline***	***Weighted***	***Baseline***	***Weighted***	***Baseline***	***Weighted***	***Baseline***	***Weighted***
1	0.7345	0.6850	0.7647	0.7448	0.7042	0.6800	0.7345	0.7345	0.7647	0.7630	0.7042	0.6800
2	0.5436	0.5270	0.5218	**0.7856**	0.5000	0.5045	0.5436	0.5436	0.5218	0.5218	0.5000	0.5045
3	0.9185	0.9414	0.9863	0.9893	0.8038	0.9484	0.9185	0.9229	0.9863	0.9863	0.8038	0.9484
4	0.5000	0.5400	0.8718	**0.9282**	0.8506	0.7941	0.5000	0.5000	0.8718	0.8694	0.8506	0.7941
5	0.6183	0.5469	0.6894	**0.8110**	0.6744	0.7213	0.6183	0.6433	0.6894	0.7007	0.6744	0.7213
6	0.9000	0.9461	1.0000	0.9978	0.8357	0.9129	0.9000	0.9000	1.0000	**1.0000**	0.8357	0.9129
7	0.5056	0.5205	0.5570	**0.7424**	0.5725	0.5625	0.5056	0.4993	0.5570	0.5764	0.5725	0.5625
8	0.5000	0.5000	0.4986	**0.5935**	0.5000	0.4990	0.5000	0.5000	0.4986	0.4987	0.5000	0.4990

TABLE IV. EXPERIMENTAL RESULTS FOR F1 ADAPTIVE WEIGHTED

#	F1 adaptive weighted					
	RF		*GB*		*AB*	
	Baseline	***Weighted***	***Baseline***	***Weighted***	***Baseline***	***Weighted***
1	0.7345	0.7185	0.7647	0.7597	0.7042	0.6800
2	0.5436	0.5359	0.5218	0.7645	0.5000	0.5045
3	0.9185	0.9342	0.9863	0.9863	0.8038	0.9484
4	0.5000	0.5599	0.8718	0.7860	0.8506	0.7941
5	0.6183	0.6066	0.6894	0.7249	0.6744	0.7213
6	0.9000	0.9076	1.0000	**1.0000**	0.8357	0.9129
7	0.5056	0.5134	0.5570	0.5931	0.5725	0.5625
8	0.5000	0.5000	0.4986	0.5251	0.5000	0.4990

These findings yield specific recommendations for machine learning pipeline construction:

1. Conduct comprehensive exploratory data analysis to assess dataset characteristics.

2. Quantify class imbalance ratios when detected during initial analysis.

3. Include class weighting methods in hyperparameter optimization procedures.

4. For severe imbalance cases, evaluate alternative weighting approaches beyond standard library implementations, particularly Logarithmic Weighting.

5. Perform joint optimization of classification algorithms and weighting methods to maximize overall model performance.

VI. CONCLUSION

The conducted research demonstrates that class weighting methods are an effective tool for improving classification quality on unbalanced data. Although the standard Inverse Frequency approach provides a basic improvement, logarithmic weighting shows the best results in conditions of high and extreme imbalance, surpassing other methods in most test cases. A practical recommendation is to abandon the template application of Inverse Frequency in favor of more flexible methods such as logarithmic weighting, especially in problems with pronounced class imbalance.

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Use of Variational Autoencoders to Enhance the Representativity of Experimental Data

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Abstract. **In many problems of processing experimental data, lack of sufficient amount of experimental patterns with due representativity leads to poor performance of machine learning methods used to implement the necessary processing. Obtaining additional experimental data is often too expensive or even impossible. This study is devoted to development of the approach based on generating additional patterns by variational autoencoders, which are possibly capable to capture the distribution of initial data and to use it in data generation. At the example of an inverse problem in spectroscopy, it is demonstrated that enhancing the training dataset with generated patterns may improve the quality of the solution of the studied problem.**

Keywords: **data generation, variational autoencoders, representativity, inverse problems, spectroscopy**

I. INTRODUCTION

The effectiveness of using machine learning (ML) methods largely depends on the availability of a high-quality representative dataset consisting of a large number of patterns. However, it is often difficult to obtain such a data set, in particular for spectroscopy tasks, since conducting experiments is difficult, expensive and time-consuming; in addition, special equipment is needed, and the involvement of competent specialists is required for sample preparation and preprocessing of experimental data.

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To overcome the difficulties of obtaining a sufficient number of training patterns, standard augmentation technologies have already been proposed – methods for expanding an existing dataset that are suitable for many tasks. These methods depend on the type of data and include techniques such as applying noise, geometric transformations, color correction, scaling – for images [1], changes in tone and speed – for audio data, stretching or compressing the time axis [2], time shift [3] – for time series etc.

However, such methods are not fully applicable in tasks dealing with more complex, specific data. In the case of spectroscopic data considered in this paper, standard augmentation techniques are not suitable: adequate interpolation cannot be implemented due to the fact that the dependence of optical density on the concentrations of several components is complex and nonlinear; using data from open sources and from other experiments is problematic, since domain adaptation is required (taking into account differences in data arising from differences in experimental equipment, experimental design, etc.), and there are very few suitable sources; applying noise to experimental spectra increases the model's resilience to noise, but does not improve the quality of the solution [4].

In such cases, it is possible to turn to methods of expanding existing data sets with artificial patterns using approaches based on generative neural network architectures – variational autoencoders (VAE) [5] and generative adversarial neural networks (GANN) [6].

GANN are less transparent for understanding and interpreting results and more difficult to train due to a number of problems inherent in them, such as fading gradients, instability, and mode collapse [7]. Therefore, this study focuses on exploring the possibilities of VAE in generative data modeling.

VAE use a probabilistic approach to encoding information, which makes it possible to build an efficient latent representation of data and then use this representation to transform data for optimal performance with ML.

Some studies of VAE capabilities were undertaken in earlier studies: in [8], the use of conditioned VAE (cVAE) to expand the training sample when solving the classification problem was considered; in [9], cVAE are used in combination with a special sampling procedure from the latent space to determine the values of target variables for generated patterns directly in the latent space using the partial least squares method. In this study, a comparison is made of approaches related to the use of cVAE and ordinary (non-conditioned) VAE with sampling of patterns from different types of distribution in the VAE latent space.

Despite the fact that the generated data does not carry new information about the object, since the existing data sample is used to train the generative model, the positive effect of their use may be due to the following factors. On the one hand, due to the specifics of their architecture (the presence of a “bottleneck” that reduces the dimensionality of data during the transition to the latent space), autoencoders can reduce the noise level in the data. On the other hand, by adding the generated data, it is possible to reduce the imbalance and other known defects in the distribution of the source data, which can have a positive effect on the training procedure of ML models. For example, studies [10] show that even standardization of data (which does not change the shape of the distribution, but only its quantitative characteristics) can improve the stability of neural networks (NN) and improve the quality of solutions.

II. Statement of the Problem

The purpose of this study was to test the hypothesis that using the generated data to expand the training sample can increase the representativity of the dataset by influencing the distribution of data and, as a result, can reduce the error in solving the problem.

Within the framework of this study, the following approaches were considered to influence the distribution of the determined parameters. One of them is to generate additional patterns from the normal distribution and thereby to make the distribution of the combined dataset closer to the normal one. This may make it possible to cope with the negative impact of the fact that the training dataset contains patterns in which the target variable takes only a few discrete values with a certain step ("grid" of parameters). The second approach explored in this study is generation of additional patterns from the uniform distribution as a method of leveling representativity for unbalanced data (increasing representativity at the "wings" of the normal distribution), which should help improve the generalizing ability of the NN and facilitate more balanced training.

It should be noted that the above applies to the distributions and representativity of data in the latent space, and not in the spaces of the source data or of the target variables – an autoencoder does not have to preserve the shape of the data distribution during transitions between the latent space and other spaces. Its task is to build a compact representation that most efficiently encodes the data. However, correcting the distribution of data in the latent space leads to its change (including increasing the representativity of data) in other spaces. This can lead to improved training of NN on such corrected data (supplemented with synthetic examples), which, in turn, can lead to an improvement in the quality of solving the problem under consideration. The present study is devoted to checking whether it is possible to achieve such an effect.

In this study, the consideration is based on the example of a NN solution to an eight-parameter inverse spectroscopy problem. The task is to simultaneously determine the concentrations of metal ions (Cu^{2+}, Ni^{2+}, Fe^{3+}, Zn^{2+}, Li^{+}), ammonium ion NH_4^{+}, and acid residues (SO_4^{2-}, NO_3^{-}) of multi-component aqueous solutions of heavy metal salts by their absorption spectra. The experimental data set consists of 3744 optical absorption spectra of multicomponent aqueous solutions of salts with various combinations of the listed ions and their concentrations. Each pattern is described by 911 features. The initial dataset was divided into training, validation, and test sets in the ratio of 7:2:1 (2620, 749, and 375 patterns, respectively). To correctly assess the quality of the inverse problem solution, an eight–fold random repetition of the split for cross-validation was performed in all experiments [11].

III. Description of Computational Experiment

In this study, we use methods to increase the representativity of the data by expanding the training set using VAE in order to improve the quality of the solution of the spectroscopy inverse problem using NN.

Artificial spectra are generated using VAE, and then added to the experimental training set. Regression NN are trained on the expanded training set. In all experiments on generating additional data, the number of generated spectra is chosen so as to double the

volume of the experimental training set, that is, it is equal to 2620.

Special attention should be paid to the fact that since the test dataset, used to evaluate the quality of the problem solution, consisted only of experimentally obtained spectra, the validation dataset in all cases was also left consisting only of experimentally obtained spectra, without adding the generated spectra and without changing the number of patterns included in it.

A. Reference Solution

In this study, multilayer perceptron (MLP) NN, which are known to be universal approximators, are used to solve the spectroscopy inverse problem as a regression problem. A standard approach to reducing the output dimension of multi-parameter problems was used – autonomous determination [4], where a separate model with one output is trained for each parameter being determined. Thus, a total of 8 regression NNs were considered, equal to the number of ions in the problem.

The architecture of each MLP includes two hidden layers (HL) containing 64 and 16 neurons, respectively, and the output layer of 1 neuron. In the HL, sigmoidal function was used as the activation function, and in the output layer, linear function. The Mean Squared Error (MSE) was used as the loss function for regression NNs. In all experiments on NN training, the stop training criterion was to achieve 250 epochs after the last decrease in the loss function on the validation dataset. Adam modification of gradient descent [12] was used as the optimization algorithm, the initial learning rate was 0.001, and the batch size was 64 patterns.

B. Expansion of the Dataset using VAE

Within the first approach, regression ANNs were trained on the dataset expanded using ordinary (non-conditioned) VAE.

The encoder was an MLP with one HL that had 256 neurons and sigmoid activation function; the output layer had 2*LS=2*91 neurons and linear activation function. Here LS is the dimension of the latent space. The latent dimension LS=91 was chosen for the reasons of reducing the input dimension of the problem 10-fold.

The decoder was also an MLP with one HL. In the input layer it had LS=91 neurons and sigmoidal activation function; in the HL – 256 neurons and sigmoidal activation function; in the output layer – 911 neurons and linear activation function. Here LS is the dimension of the latent space.

The algorithm for expanding the dataset using VAE consists of the following steps:

Step 1. Training reference regression NNs in autonomous determination mode to estimate the ion concentrations on the initial training sample consisting of experimental optical absorption spectra without expanding the training set.

Step 2. VAE training on the same initial training sample of experimental spectra.

Step 3. Generate patterns using the VAE decoder from random points in the latent space sampled according to the parameters of the multidimensional normal distribution of data in the latent space obtained by training the VAE encoder to expand the training set using VAE. If the value of the normalized optical density in any channel of the obtained spectrum was negative, it was assumed to be equal to zero; if it was greater than 1, then it was assumed to be equal to 1.

Step 4. Determination of ion concentrations corresponding to the generated spectra using the reference regression NNs trained in Step 1. If the obtained concentration value of at least one ion for this pattern exceeded the range of acceptable values, this pattern was not included in the dataset. The minimum allowable value of the ion concentration was considered to be zero, and the maximum value was the maximum concentration of this ion in the entire array of experimental data.

Step 5. Training regression NNs in autonomous determination mode to estimate ion concentrations on an expanded double-sized training set of optical absorption spectra, which included half of the experimental spectra and the same number of spectra generated with the VAE using the described procedure.

In addition, within the framework of the described approach, the option of generating spectra in Step 3 from vectors having a uniform distribution in the latent space rather than a normal one has also been tried.

C. Expansion of the Dataset using VAE

The encoder was an MLP with one HL that had 256 neurons and sigmoid activation function; the output layer had 2*LS=2*91 neurons and linear activation function. Here LS is the dimension of the latent space.

The decoder was also an MLP with one HL. In the input layer it had LS+8=91+8 neurons and sigmoidal activation function; in the HL – 256 neurons and sigmoidal activation function; in the output layer – 911 neurons and linear activation function. Here LS is the dimension of the latent space, 8 is the number of target variables (the number of determined ions).

The algorithm for expanding the dataset using cVAE consists of the following steps:

Step 1. cVAE training on the initial training sample of experimental optical absorption spectra without expanding the training set. During training, the known

values of the target variables (ion concentrations) corresponding to these spectra are used.

Step 2. Generate patterns using the cVAE decoder from random points in the latent space sampled according to the parameters of the multidimensional normal distribution of data in the latent space obtained by training the cVAE encoder to expand the training set using cVAE. To generate additional patterns, the concentration sets already present in the training set of the experimental data set were selected. If the value of the normalized optical density in the channel of the obtained spectrum was negative, it was assumed to be equal to zero; if it was greater than 1, then it was assumed to be equal to 1.

Step 3. Training regression NNs in autonomous determination mode to estimate ion concentrations on an expanded double-sized training set of optical absorption spectra, which included half of the experimental spectra and the same number of spectra generated with the cVAE using the described procedure.

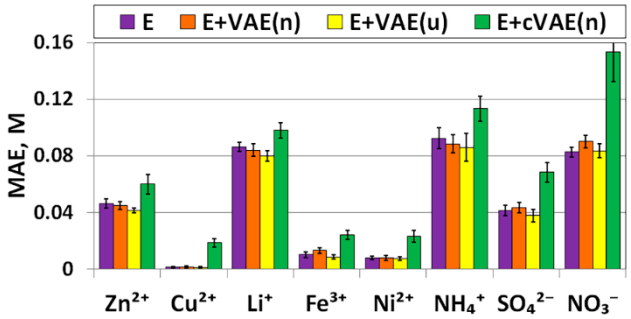
IV. Results

A. *Generated Spectra*

The spectra generated using VAE and cVAE are visually similar to the experimental spectra. In addition, the noise level of the generated spectra in the short-wavelength region is reduced compared to the experimental ones.

B. *Solving the RegressionProblem*

The error metrics obtained by solving the spectroscopy inverse problem by the reference method (without expanding the sample) and expanding with the model spectra using VAE and cVAE are shown in Figure.



Error metrics obtained by solving the spectroscopy inverse problem by the reference method (without sample expansion, E) and with sample expansion by model spectra using VAE with sampling from normal distribution in the latent space (E+VAE(n)), VAE with sampling from uniform distribution in the latent space (E+VAE(u)), and conditioned VAE with sampling from normal distribution (E+cVAE(n))

These results indicate that the quality of the regression NN solution in the VAE method with the generation of model spectra from normal distribution in the latent space has practically not changed relative to the reference solution within the margin of error of the computational experiment. There was no statistically significant deterioration or improvement in the quality of the problem solving by adding artificial examples to the training sample.

When generating model spectra from uniform distribution in the latent space, the results obtained are on the average better than when generating from normal distribution. A statistically significant improvement was shown for Zn^{2+} and Li^{+} ions compared to the reference models. This indicates that in general the approach under consideration using generation of model spectra with a "corrected" distribution makes it possible to increase the representativity of the data, so it is promising.

At the same time, with the use of cVAE, errors on the test set increase, and for some components the increase is very significant. Perhaps this behavior can be corrected by managing the strategy of selecting concentration sets for generation.

V. Conclusion

In this paper, we consider the solution of the inverse problem of spectroscopy of multicomponent aqueous solutions of salts containing eight ions: Cu^{2+}, Ni^{2+}, Fe^{3+}, Zn^{2+}, Li^{+}, NH_4^{+}, SO_4^{2-}, NO_3^{-}, using artificial neural networks. The possibility of expanding the training sample of an experimental spectroscopic dataset using variational autoencoders is investigated in order to obtain improved metrics for the quality of solving the inverse problem compared with the reference solution that does not use the expansion of the training sample.

Algorithms for expanding the experimental data set using variational autoencoders and conditioned variational autoencoders are proposed and described. Model spectra were generated using trained variational autoencoders, which were then used along with experimental ones to train regression neural networks solving the inverse problem.

To test the hypothesis about the ability of the proposed methods to influence the representativity of data by influencing their distribution, experiments were conducted on training regression neural networks on different training samples: experimental only, expanded using a conditioned variational autoencoder and expanded using an ordinary (non-conditioned) variational autoencoder with generation of patterns from normal and uniform distributions in the latent space. The quality metrics for solving the inverse problem were obtained.

The method with the conditioned variational autoencoder showed a deterioration in the quality of the solution compared to the reference method (without expanding the training sample). The method using variational autoencoder and generating patterns from normal distribution in the latent space demonstrated a solution quality comparable to the reference one, while using variational autoencoder with generating patterns from uniform distribution in the latent space led to a slight decrease in the errors on the test sample, statistically significant for Zn^{2+} and Li^{+} ions. However, for most components, the quality metrics of neural networks trained on the expanded dataset still overlap within the error limits with the reference metrics.

Based on the results of the study, it can be concluded that the approach is promising, but the selection of optimal conditions and parameters of the computational experiment requires further research. In particular, research should be conducted in the following directions:

- Search for the optimal distribution of patterns in the latent space of the variational autoencoder, which should be used to generate model spectra and to expand the training sample;
- Search for the optimal distribution of patterns in the space of target variables (concentrations) when generating patterns (spectra) using conditioned variational autoencoder;
- Determining the optimal way to normalize input features when training variational autoencoders.

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Mapping Geological Regions from Satellite QGIS Imagery

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***Abstract*. This paper presents a method for generating regional maps from satellite imagery using Generative Adversarial Networks (GANs). We evaluate major map and satellite services, develop a tiling algorithm for dataset preparation, and perform semantic segmentation into 12 geo-object classes. Among tested GAN models, Pix2Pix demonstrated the best performance in translating satellite images into structured maps. The approach is implemented within QGIS using custom scripts, enabling automated map generation. Results show high accuracy in reproducing roads, buildings, water bodies, and vegetation. The method supports applications in urban planning, environmental monitoring, and emergency response.**

***Keywords:* satellite imagery, map generation, GAN, Pix2Pix, image-to-image translation, semantic segmentation, QGIS, deep learning, geospatial data processing, neural networks**

I. Introduction

Modern geospatial data processing technologies open new opportunities for automating the creation of digital maps. Particularly relevant is the task of transforming satellite images into informative cartographic materials, which is crucial for rapid assessment of landscape changes, urban infrastructure planning, and environmental monitoring [1]. The development of machine learning methods, especially Generative Adversarial Networks (GANs), enables efficient solutions to image-to-image translation problems, including the conversion of satellite imagery into detailed regional maps. This paper presents a comprehensive approach to generating maps from satellite images using state-of-the-art neural network models. It also analyzes the characteristics of source data, dataset preparation techniques, and the selection of optimal deep learning architectures.

II. Evaluation of Map Services and Satellite Imagery with Object Features Analysis

A. Map services and satellite imagery

To address the mapping problem, data were selected from several popular services: Google Maps, Yandex Maps, OpenStreetMap, Bing Satellite, ESRI, and Google Satellite. These platforms provide diverse information, including vector maps and high-resolution satellite imagery. Each service has its own features affecting the quality and accuracy of subsequent analysis. For example, Google Satellite offers high-resolution color images, while Bing Satellite provides broader coverage, especially in under-explored regions [2].

Particular attention was paid to analyzing object characteristics on the images. Satellite imagery contains elements such as roads, buildings, water bodies, vegetation, and other land cover types. However, their visual properties can vary significantly depending on the season, weather conditions, and shooting angle. Moreover, some objects have similar visual features, which can complicate their accurate recognition and classification [3]. This highlights the importance of preliminary image segmentation and the identification of key geo-object classes.

Google Maps and Google Satellite are probably the most popular map layers in the world. It's can easily add these layers to QGIS as XYZ tiles (Fig. 1). To add Google Maps to QGIS a link to the tile map service layers should be added as QGIS plugin. Then add the link to the XYZ tiles in the QGIS browser. There are

a lot of other basemaps you can add to QGIS. It is necessary to add Google Maps or Google Satellite to QGIS as a link to the mapsource, like as Table.

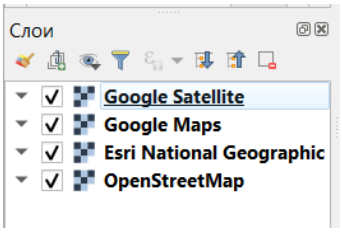

Fig. 1. Selected layers in QGIS

LINKS TO GOOGLE BASEMAP LAYE

Service	Link
Google Maps	https://mt1.google.com/vt/lyrs=r&x={x} &y={y}&z={z}
Google Satellite	https://www.google.cn/maps/ vt?lyrs=s@189&gl=cn&x={x}&y={y}&z={z}
Google Satellite Hybrid	https://mt1.google.com/vt/lyrs=y&x={x} &y={y}&z={z}
Google Terrain	https://mt1.google.com/vt/lyrs=t& x={x}&y={y}&z={z}
Google Roads	https://mt1.google.com/vt/lyrs=h &x={x}&y={y}&z={z}

B. Dataset Preparation

Successful training of a neural network model requires a high-quality and representative dataset. To this end, a specialized script was developed and integrated into the QGIS system as on Fig. 2.

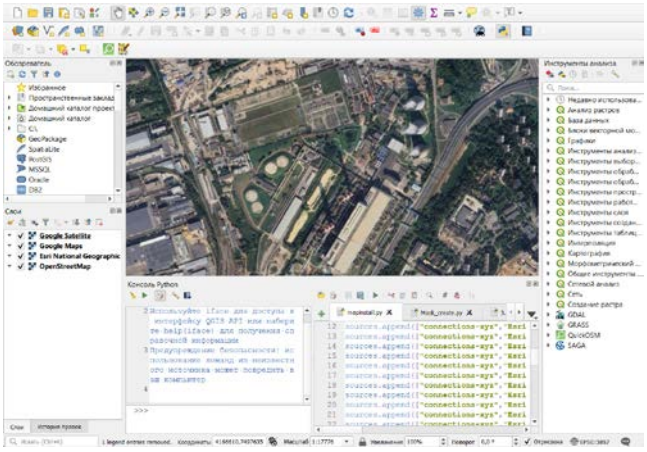

Fig. 2. Interface of Qgis

The algorithm works as follows: first, a map fragment and its corresponding satellite image are loaded; then, the image is divided into tiles of a specified size (e.g., 512×512 pixels). After that, the image is shifted by a certain number of pixels, and the tiling process is repeated. This allows obtaining additional image variations and increasing the volume of the training dataset [4].

The collecting of images is a routine and long process by interactive QGIS methods. Therefore, Semi-automatic script was developed for automatization of such processes. This script of the QGIS geoformation software and mouse event modeling were used to prepare the image set. As a result, sets have been prepared in each of which images have been prepared for the same fragment of the geographical region, where images were determined from Bing services, Esri satellite service, Google satellite service, Openstreetmap service. All images have the same size, which makes it easy to use them for machine learning algorithms. Saving of images based on counting of images and extraction of images from QGIS canvas. For example for serving ersi satellite image next command was used:

fname="d:/Datasets/imgmap/src/esrisat/{}_A.png".format(i)

qgis.utils.iface.mapCanvas().saveAsImage(fname) i=i+1

The similar code was used for other image/map services. As a result the dataset was created that include collection images (Bing, Esri, Google satellite images and images of maps from google and Openstreetmap service). Such image have RGB 24bit type and 1378×515 size. The dataset includes 1714 geographical regions for Europe from Belarus to British island.

As a result of the processing, more than 4000 image pairs – satellite images and corresponding maps – were obtained. All tiles were saved in uniform coordinates and scale, ensuring data consistency. In addition, to improve the model's robustness to external condition changes, augmentations such as rotations, reflections, and brightness adjustments were applied. This approach significantly enhanced the generalization ability of the trained model [5].

III. MAP SEGMENTATION

After obtaining paired images, the map was segmented into 12 geo-object classes. A dedicated script was developed for this purpose, automatically assigning each pixel one of the following classes: roads, residential buildings, industrial structures, recreational zones, water bodies, agricultural lands, forests, deserts, swamps, railways, power lines, and other objects. Segmentation by a convolutional neural network-based algorithm trained on pre-labeled data [6]. It requare labeling by interactive tools like Label Studio and CVAT [7]. It allow to generarion new mistakes for map interpretation. Threfore In this case, using a neural network for segmentation is a gross mistake. Therefore, in this paper, we used threshold methods and mathematical morphology for segmentation.

Fig. 3. Original image

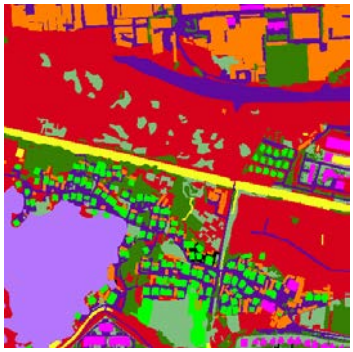

Fig. 4. Image after labeling

This algorithm is based on threshold definition for different classes of objects on a map image in HSV color space. The image is converted to a color space to better determine the color of the object on the map. The minimal area of the object was used as an additional parameter for definition on image map. Classes in this color space are defined as structure with thresholds for all base map classes.

IV. Neural Network Application for Generating Maps from Satellite Images

At the stage of developing a model capable of generating maps from satellite images, several Generative Adversarial Network (GAN) architectures were considered, as they have shown high efficiency in image-to-image translation tasks. The most suitable options included Pix2Pix, CycleGAN, and SPADE.

The Pix2Pix model represents a conditional GAN where the generator constructs an image based on an input condition – in this case, a satellite image [8]. This model is well-suited for tasks with paired data and ensures accurate reproduction of object structures and forms. However, its main limitation is relatively low output image realism compared to other GAN architectures.

CycleGAN, on the other hand, does not require paired data, making it useful when there is no perfect correspondence between satellite images and maps [9]. However, this advantage comes at the risk of losing accuracy in reproducing specific objects, which is unacceptable for mapping purposes.

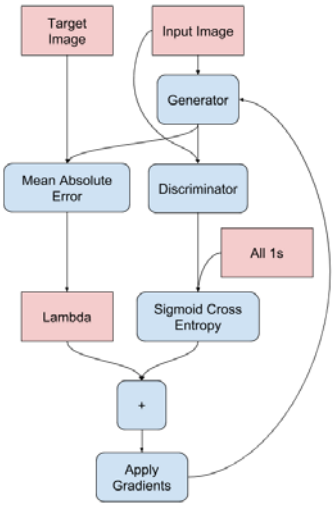

Fig. 5. Training procedure of Pix2Pix

CycleGAN applies the property of cycle consistency to the translation model by combining two traditional GAN models to construct the structure of CycleGAN (Fig. 6).

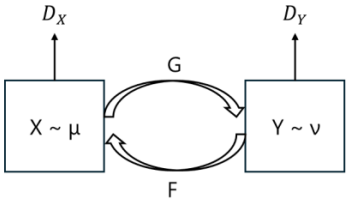

Fig. 6. The general framework of CycleGAN

SPADE offers the ability to generate high-quality images considering semantic segmentation [10]. It allows creating realistic images while preserving segmentation structure. However, this model requires significant computational resources and is more complex to configure.

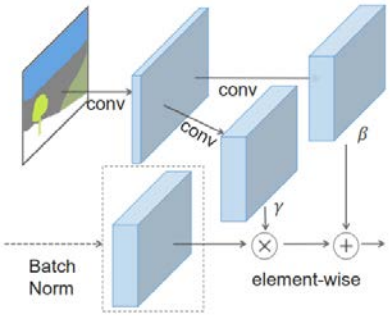

Fig. 7. In the SPADE, the mask is first projected onto an embedding space and then convolved to produce the modulation parameters γ and β. Unlike prior conditional normalization methods, γ and β are not vectors, but tensors with spatial dimensions. The produced γ and β are multiplied and added to the normalized activation element-wise

Given the availability of paired data and the need for accurate structure reproduction, the Pix2Pix architecture was chosen as the baseline. To enhance generation quality, a combination of L1 loss and cross-entropy function was used, achieving a balance between accuracy and realism [11].

V. General Technology Schem

The overall technology for generating regional maps from satellite images includes several stages: collecting and processing original data, slicing images into tiles, segmenting the map, training the neural network, and generating the final image. The entire system is implemented within the QGIS environment using specialized scripts that automate all processing steps.

The process begins with loading satellite images and corresponding maps from various services. Then, the images are sliced into tiles with shifts applied to increase the number of examples. Following this, the map is segmented into 12 geo-object classes. The obtained data are used to train the Pix2Pix model, which, during inference, transforms new satellite images into local maps. The results are output as raster images that can be further processed and integrated into GIS systems.

This technology significantly reduces the time required for preparing cartographic materials and enhances their accuracy through the use of modern machine learning methods [12].

VI. Conclusion

In the course of the research, a technology for generating regional maps from satellite images using generative adversarial networks was developed and implemented. An evaluation of available map services and satellite images was conducted, an image slicing algorithm was developed, map segmentation into 12 geo-object classes was carried out, and various neural network architectures were tested for image-to-image translation. The Pix2Pix model was selected as the most suitable, providing high structural reproduction accuracy.

The developed technology can be applied in various fields, including urban planning, environmental monitoring, emergency response, and other areas requiring rapid acquisition and updating of cartographic information. Future work will focus on extending the model to work with vector data and integrating it into real-time systems [13].

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Disease Modules Identification Using Gene Mutations and Biological Networks

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Abstract. **Paper describes the method for identifying disease modules by integrating somatic mutation data and protein-protein interaction networks. The method initially considers the construction of the weighted network using the values of mutual exclusivity, coverage and topological similarity of gene pairs. The random walk algorithm over the network adjusts the weights, making it possible to take into account rare mutations. The procedure for identifying strongly connected components of a resulting weighted graph is used to generate driver modules and includes the stage of dividing and recombining network subgraphs taking into account their degree of connectivity, which allows avoiding the modules of trivial sizes. Distinctive features of the method are the ability to take into account the topology of a complex network when identifying disease driver modules, to determine the size of the module based on the split-and-extend procedure and thus increase the biological significance of the results. Experiments on a real data set of pan-cancer diseases showed the advantage of the proposed method over analogues in terms of identification accuracy and biological significance.**

Keywords: **disease module, driver gene, weighted graph, random walk**

I. INTRODUCTION

Identification of a group of driver genes is important for studying the pathogenic mechanism of complex genetic diseases such as cancer. The development of computational approaches to detect the driver or disease modules taking into account gene mutations and other multiomics data is a relevant and important area of research. Approaches to module identification in complex genetic diseases can be considered in two broad categories depending on the types of input data. De novo methods use only genetic data to discover new genetic interactions and disease-associated functional modules [1–2]. The second category of methods, in addition to genomic data incorporate prior knowledge in the form of biological pathways, networks, and functional phenotypes [3–6]. Our research is based on driver module identification methods [7–11] that integrate protein-protein interaction (PPI) data and gene mutation profiles using the concept of mutual exclusivity and coverage. Although the previous methods can detect gene sets with high exclusivity and coverage, they do not take into account the topological structure of complex networks. To effectively solve the problem of cancer heterogeneity and improve the accuracy of determining the driver modules, the proposed method includes the measure of a topological similarity in construction of a weighted biological network.

II. METHOD OF IDENTIFICATION OF DISEASE MODULES

The main steps of the driver modules' identification method are as follows: 1) calculating the measures of maximum coverage, exclusivity of gene mutation profiles; the topological similarity of network nodes; 2) determining network weights using a random walk algorithm; and 3) extracting driver modules based on the split-and-extend procedure.

It is assumed that the influence of gene nodes on biological functions can be analyzed by evaluating the similarity between adjacent nodes in the local area network. In our research, the topological similarity between adjacent nodes in the network is assessed using probability distribution of the node degrees in the local node neighborhood. Let d_i denotes the degree of the i-th node and d_{max} is the node maximum degree in the local network. Let us assume that the probability set for one network node includes N nodes, where $N = d_{max} + 1$. The discrete probability of a gene g_i is expressed as

$$p(i) = \frac{d_i}{D_{g_i}}, \quad (1)$$

where D_{g_i} is a sum of node degrees of gene g_i in the local network.

The discrete probability set $P(\mathrm{i})$ consists of the standardised discrete probabilities of all gene nodes in the local area network sorted in ascending order, which is expressed as follows

$$\mathrm{P(i)} = (\mathrm{p(1)}, \mathrm{p(2)}, \ldots, \mathrm{p(n)}, \ldots \mathrm{p(N)}). \quad (2)$$

The topological similarity $\mathrm{SIM}(g_i, g_j)$ between a pair of nodes g_i and g_j is calculated as follows

$$\mathrm{SIM}(g_i, g_j) = 1 - D_{JS}(P(i)||P(j)), \quad (3)$$

where $D_{JS}(P(i)||P(j))$ represents the Jensen-Shannon (JS) divergence value.

Let $G(\mathrm{V}, \mathrm{E})$ is a PPI network, where the node set $\mathrm{V} = (g_1, g_2, \ldots, g_n)$ represents the set of mutated genes on the network and the edge set $\mathrm{E} = \{\mathrm{e} = (g_i, g_j)\}$ represents the set of protein-protein relationships. To construct a weighted undirected graph G_ω we define for each node $g_i \in V$ a weighting coefficient $\omega(g_i)$, which corresponds to the gene coverage $\mathrm{CD}(g_i)$ or the relative set of cases for which the gene g_i is mutated. The weight coefficients of the edges of the graph G_ω are calculated based on the characteristics of mutual exclusivity, coverage and topological similarity of network nodes. Namely, the edge weight between a pair of genes $\omega(g_i, g_j)$ is equal to the product of the topological similarity and the harmonic mean of mutual exclusivity and coverage

$$\omega(g_i, g_j) = \begin{cases} \frac{2\times\mathrm{SIM}(g_i,g_j)}{\frac{1}{\mathrm{ED}(g_i,g_j)}+\frac{1}{\mathrm{CD}(g_i,g_j)}} & \mathrm{ED}(g_i, g_j) \neq 0 \\ & \mathrm{CD}(g_i, g_j) \neq 0 \\ & \mathrm{SIM}(g_i, g_j) \geq \theta \\ 0 & \text{otherwise} \end{cases}, \quad (4)$$

where $\mathrm{ED}(g_i, g_j)$, $\mathrm{CD}(g_i, g_j)$ and $\mathrm{SIM}(g_i, g_j)$ represent mutual exclusivity, coverage and topological similarity of gene pair.

The random walk method [6] is used to further adjust the relationships between the nodes of the biological network G_ω. The weight distribution of G_ω is updated after each random walk iteration and process is repeated until it reaches a stable state. Let the weight distribution at time *t* be denoted by F_t, than the iteration formula is as follows

$$F_{t+1} = (1 - \beta)PF_t + \beta F_0, \quad (5)$$

where $F_0 = CD(g_i)$, β is the restart probability, P represents the transition probability matrix, which is positively correlated with the edge weight.

The strongly connected component (SCC) division method is utilized to generate the driver modules on the wighted biological network [3]. After a set of initial candidate modules is created, the large and medium-sized modules are further splitted with subsequent expansion by utilizing the greedy strategy. The driver module generation process helps to determine the module size based on split and expansion technique and to identify the optimal gene sets.

III. Experimental Study

Somatic mutation data are obtained from The Cancer Genome Project (TCGA) and include the TCGA pan-cancer dataset with 12 cancer types. The data preprocessing was conducted according to [3]. The resulting dataset contains 3110 cases and 11565 genes with somatic mutations. HINT+HI2012, used as the PPI network, includes a high-quality protein-protein interaction database (HINT) and a human genome interaction database (HI20212). The network consists of 9858 proteins and 40704 interactions between them [3]. The proposed method MutDriver includes three parameters that are set a priori: the similarity threshold value θ, the total number of genes in the selected modules *total_genes*, and the minimum module size *min_size*. In our experiments the results of three other methods: Hotnet2 [3], MEMCover [5] and MEXCOwalk [7] were compared with the proposed method. MEMCover uses a parameter f(θ) that implicitly controls the module sizes: the smaller the value of f(θ), the larger the output modules. We consider two values of this parameter for the MEMCover algorithm, which corresponds to MEMCover_v1 and MEMCover_v2. MEMCover_v2 allows to minimize the percentage of modules with one or two elements.

We used two approaches to driver modules' evaluation: static evaluation and modular evaluation. The static evaluation consists of comparing the union of genes of all obtained modules with a reference set of disease genes. The COSMIC Cancer Gene Census (CGC), which is one of the popular experimental databases containing mutated cancer genes, was used as a reference dataset. ROC analysis on the COSMIC dataset showed that the proposed MutDriver method and MEXCOwalk have the highest AUROC (area under the ROC) values (Fig. 1).

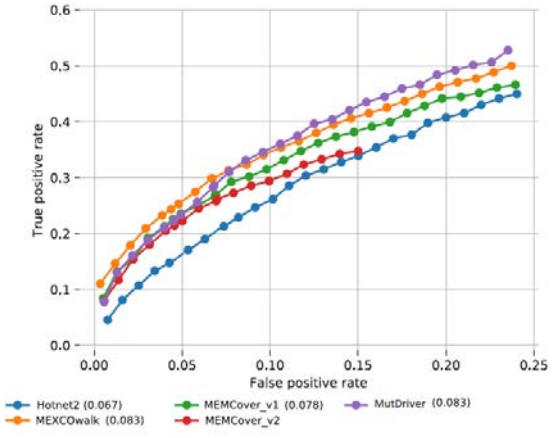

Fig. 1. ROC diagrams showing the proportion of recovered CGC genes for each of the *total_genes*

To evaluate the effectiveness of the method in identifying genes with rare mutations, the above analysis was repeated, with the number of reference genes from the CGC database limited to genes mutated in a maximum of 2 % of patients in the pan-cancer cohort (Fig. 2). MutDriver showed the best performance with AUROC value of 0.085. AUROC values for MEXCOwalk, MEMCover_v1 and Hotnet2 are 0.081, 0.074 and 0.070 for 2 % mutation rate.

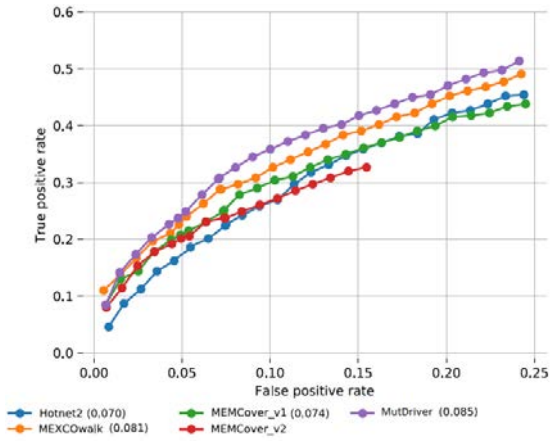

Fig. 2. ROC diagrams showing the proportion of restored CGC genes mutated in a maximum of 2 % of disease cases for each of the total_genes

DAVID [12] was used to analyze the functional enrichment of modules obtained using the MutDriver, Hotnet2, and MEXCOwalk methods. DAVID provides a comprehensive set of functional annotation tools to help understand the biological significance of large gene lists. Fisher's exact test is used to determine whether the proportions of objects falling into each category differ across groups. The groups are the resulting list of genes in the modules and the entire genome, and the categories are the presence or absence of a gene in a specific functional pathway or GO term. As can be seen from Fig. 3, the enrichment effect of driver modules identified using the proposed method is higher than using the other two alternatives. The effect is calculated separately for each disease type and the advantage of the proposed method is especially noticeable for such disease types as GBM, Melanoma, UCEC, NSCLC, PAAD and CML. Therefore, driver modules obtained using MutDriver have high statistical and biological significance.

When statically evaluating the entire set of genes in driver modules, the trivial results (each gene in a separate module or all genes in one module) have the same evaluation values and not take into account the partitioning of genes into modules. None of the trivial results is significant for identifying driver modules. For example, the MEMCover_v1 method produces results similar to the first trivial variant, where almost 70 % of all genes are in modules of size one.

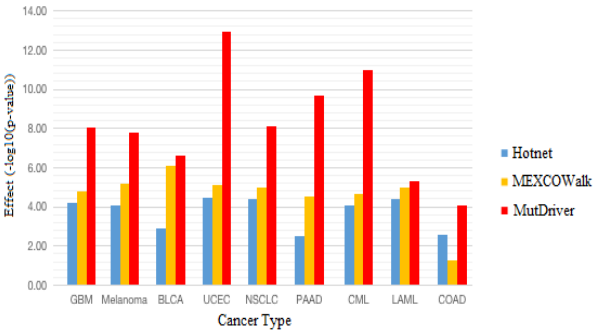

Fig. 3. Comparisons of the functional enrichment effect of identified disease modules

The MEMCover_v1 method identifies modules with an average size equal to 1.2 for almost all values of *total_genes*. The acquisition of small-sized modules contradicts the assumption that the driver module should identify a functional pathway important for the development of cancer. On the other hand, the HotNet2 method extracts modules according to the second of the trivial solutions, more than 60 % of genes are contained in a single large module and this percentage increases to more than 80 % for *total_genes*>2000. The MutDriver method identifies modules of medium size between 6.5 and 9 average number of elements. Fig. 4 shows average module sizes for different values of *total_genes*.

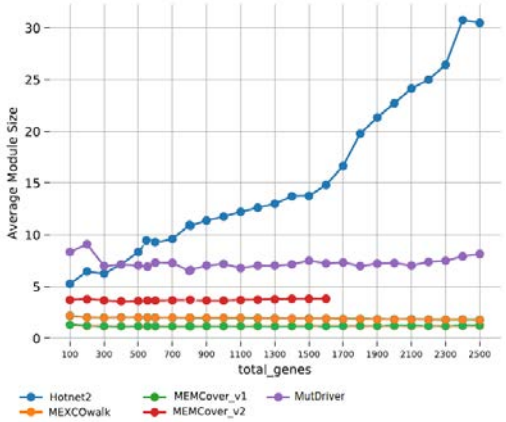

Fig. 4. Average module sizes for several methods with increasing total genes

For the modular evaluation of the selected modules, the DMS criterion is used, which combines the evaluation of coverage and exclusivity of modules and is the optimization criterion in [7]. Fig. 5 shows that the proposed MutDriver method has the best DMS values compared to other methods. The difference is especially noticeable for small values of the *total_genes* parameter equal to 100 and 200.

The Hotnet2 method is the worst among the others, especially for *total_genes*>500. MEMCover_v1 gives worse results than MEMCover_v2 and MEXCOwalk, as it identifies a large number of modules of size 1 and 2.

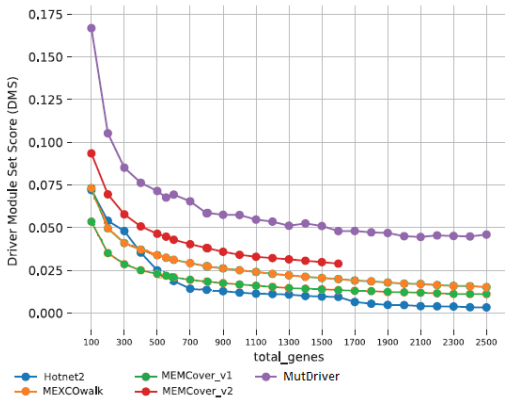

Fig. 5. Evaluation of modules according to the DMS criterion for several methods with increasing total genes value

To evaluate the accuracy of driver modules based on known biological pathways, the study uses the accuracy criterion (ACC) and F-measure. The higher the accuracy value, the better the classification effect. The higher the F-measure, the more driver modules are enriched with known biological pathways. Fig. 6 shows the results of the accuracy analysis of driver modules obtained using the MutDriver, MEXCOWalk and HotNet2 methods.

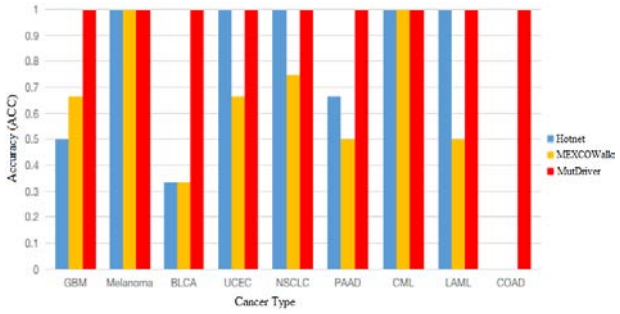

Fig. 6. Comparison of the biological significance of modules obtained by different methods

According to Fig. 6 the ACC value for MutDriver is 1 for nine disease types, which shows the advantages of the proposed method in identifying disease driver modules. The ACC value of MutDriver method is 100, 200 and 50 % higher than that of HotNet2 method for three disease types GBM, DLCA and PAAD respectively. The ACC value of MutDriver method is 50, 200, 50, 33.3, 100 and 100 % higher than that of MEXCOWalk for six disease types GBM, BLCA, UCEC, NSCLC, PAAD and LAML. Therefore, the proposed method has a higher efficiency in isolating driver modules than the alternative methods MEXCOWalk and HotNet2.

The predictive ability of the selected driver modules was evaluated by classifying malignant and normal samples of the TCGA pan-cancer dataset (Fig. 7). The *k*-nearest neighbors algorithm with Euclidean distance and *k*=1 was used for classification. For a given test case s and a set of genes M_q, a vector v_s of size $|M_q|$ consists of gene expression values for s.

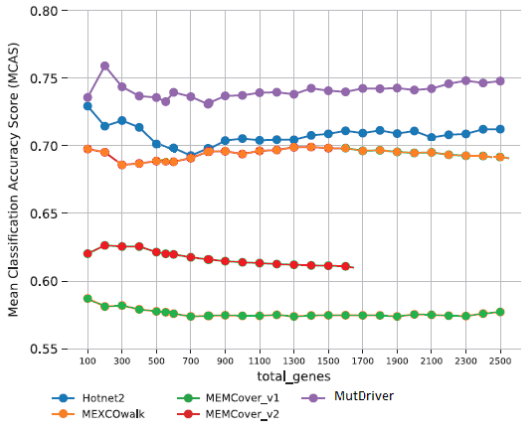

Fig. 7. Evaluation of modules according to the accuracy of case classification with increasing *total genes*

The Euclidean distance between each test vector v_s and each vector of the training set was calculated. Gene expression data were downloaded from the Firebrowse database [13], which consists of 437 normal and 4307 malignant samples. Since the dataset is unbalanced, an undersampling procedure was used to balance the elements of the two classes. This procedure was performed 100 times and the classification accuracy value Acc (M_q) was calculated as the average accuracy of the module M_q over all subgroups of the cross-validation procedure and 100 balanced data sets. The classification accuracy criterion (MCAS) for all modules was calculated as the average accuracy over all modules. The size of the modules is not always directly related to the classification accuracy. For example, the efficiency of modules obtained by the HotNet2 method is worse than the proposed method, although the size of HotNet2 modules is much larger than the size of MutDriver modules.

IV. Conclusion

Our study describes a method for identifying driver modules based on combining information on protein-protein interactions and gene mutation data. The method uses a random walk algorithm to determine the weight coefficients of the interaction network, where the values of the probability transition matrix take into account the maximum coverage and exclusivity of gene pairs, as well as the topological structural similarity of the network nodes. The set of initial modules, obtained with a clustering procedure are subsequently modified using the procedure of division and expansion, which allows to avoid the modules of trivial sizes and to increase the average degree of the module nodes. Experiments performed on real data showed the advantages of the proposed method in comparison with analogues.

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FPGA Implementation of Quaternionic Fully Connected Neural Network for Image Classification

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***Abstract*. In this paper, we propose the design, implementation, and FPGA-based evaluation of a fully connected quaternion neural network for color image classification, benchmarked on the CIFAR-10 dataset. The IP core was successfully synthesized for UltraScale series FPGAs, demonstrating minor resource utilization. While the current implementation achieves its resource efficiency goals using an FC-only structure, classification performance is constrained by the lack of softmax implementation for quaternion outputs.**

***Keywords:* quaternion algebra, Neural Network, fully connected layer, FPGA**

I. Introduction

In recent decade, neural networks (NN) in the real domain have been extensively studied and have shown promising results in various vision tasks. According to theoretical analysis, representations such as hyper-complex numbers can acquire richer representational capacities than real numbers, and capture intrinsic interchannel relationships [1]. Quaternion algebra offers an approach that allows for the mapping of each pixel to a single entity. Furthermore, this could lead to a more efficient internal representation in colors space, resulting in improved results in color image processing tasks [2].

The purpose of this research is to describe the design, training, and evaluation of a quaternion-valued fully connected neural network that can classify color images using the *CIFAR-10* dataset. Efficient hardware implementation based on FPGA requires model quantization to avoid floating point logic design complexity and resource utilization on MAC operations.

The paper is organized as follows. Section two outlines the quaternion algebra and quaternionic pixel representation. Section three explains the quaternionic neural network classifier. Section four illustrates the hardware implementation; simulation experiments with real image is presented. Section five is devoted to conclusions and future work.

II. Application of quaternion algebra

A. Basics

The quaternion algebra $\mathbb{H}$ is an associative non-commutative four-dimensional algebra $\mathbb{H} = \{Q = q_1 + +q_2 i + q_3 j + q_4 k | \, q_1, q_2, q_3, q_4 \in \mathbb{R}\}$ where the orthogonal imaginary numbers obey the following multiplicative rules $i^2 = j^2 = k^2 = ijk = -1$, $ij = = -ji = k$, $ki = -ik = j$. This becomes evident after identifying quaternions with vectors and writing the operation in matrix notation [3].

B. Color space representation

To represent a picture in quaternion space, the color components of every pixel, which are in the RGB color space, are translated into the imaginary parts of a quaternion:

$$q = 0 + R \cdot i + G \cdot j + B \cdot k,$$

where $(R, B, G) \in \mathbb{R}$ is RGB pixel and q is pure quaternion.

For the sake of simplicity RGB channels is expected to be shifted to range $[-0.5, 0.5]$ before converting to the quaternion space.

The key operation in quaternion algebra is non-commutative multiplication (or Hamilton product), the geometric meaning of which is the rotation of a vector around axis in three-dimensional space. The multiplication operation involves two operands: the original vector *x*, representing the pixel, and the quaternion *w*, encoding information about the axis and angle of rotation. The quaternion *w* can be represented as follows:

$$w = a \cdot (\cos\theta + \sin\theta \cdot u),$$

where *a* – scale value; θ – rotate angle; *u* – rotation axis in 3D space, represented as normalized pure quaternion.

For example, the quaternion $q_{gray} = 0 + 0 \cdot i + +0 \cdot j + 0 \cdot k$ corresponds to a middle grey color. A white pixel is encoded as $q_{white} = 0 + 0.5 \cdot i + 0.5 \cdot j +$

$+0.5 \cdot k$, and black as $q_{black} = 0 - 0.5 \cdot i - 0.5 \cdot j - -0.5 \cdot k$.

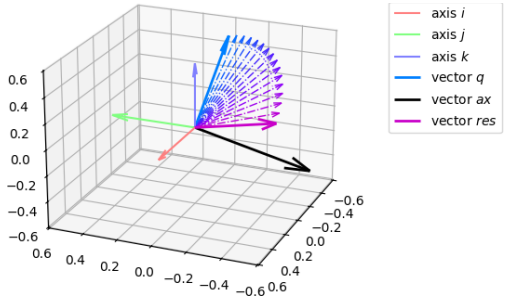

Fig. 1. Quaternion rotation in color space

On the Fig. 1, the operation of rotating vector q (represents color blue):

$$q = 0 - 0.5 \cdot i + 0 \cdot j + 0.5 \cdot k,$$

around non normalized axis *ax* (black):

$$ax = 0 - 0.5 \cdot i - 0.5 \cdot j - 0.5 \cdot k,$$

to an angle of $\theta = 90°$ without scaling ($a = 1$). Result of rotation is vector *res* (magenta).

The quaternion *w* in this case will be equal to:

$$w = 0 + 1 \cdot \frac{ax}{\|ax\|} = \frac{1}{\sqrt{3}} \cdot (i + j + k).$$

The order of quaternion multiplication determines the direction of vector rotation. In this work, will use "right"-order multiplication $w \cdot x$, that corresponds to counterclockwise rotation [3].

III. Model Architecture

A. Training of classifier

The input data to the neural network is a color image of size 32×32 pixels, which is transformed into a vector consisting of 1024 quaternions. As shown in Figure 2, the neural network architecture comprises three fully connected layers. The hidden layers have dimensions of 24×24, 16×16 and 8×8, respectively. The output of the neural network consists of three quaternions, each of whose 10 components represents a distinct class from the dataset.

The Leaky ReLU activation function is chosen for its ease of hardware implementation [4]. In the negative value region, the reduction in value is achieved by an arithmetic right shift, and the sign of the number is determined by the sign bit. The slope value in this case is 2^{-n}. Since the output layer of the quaternion neural network does not contain the *softmax* function [5, 6], which is typically used in classification tasks, the Cross-Entropy loss function is not efficient for training. Instead, the Mean Squared Error was chosen. Adam optimizer is used with adaptive learning rate, varying according to a cosine law.

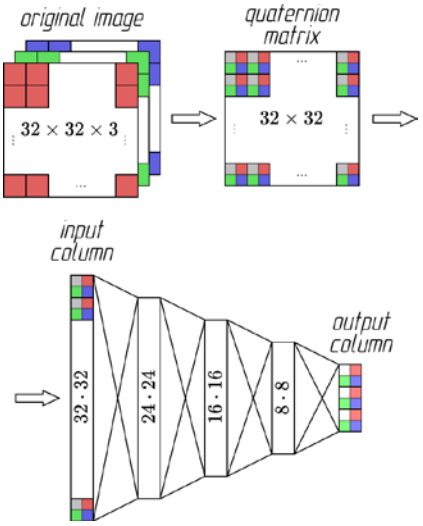

Fig. 2. Quaternion Neural Network architecture based on fully connected layers

B. Experimental results

Fig. 3 presents the result of training a neural network. Analysis of the graph indicates a rapid plateau in the training process. Further research will be aimed, among other things, at modernizing the architecture of the neural network in order to increase the efficiency of the NN. Confusion matrix of trained Neural Network is shown in Fig. 4.

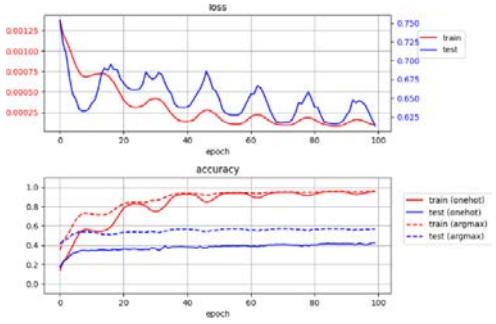

Fig. 3. Training curves

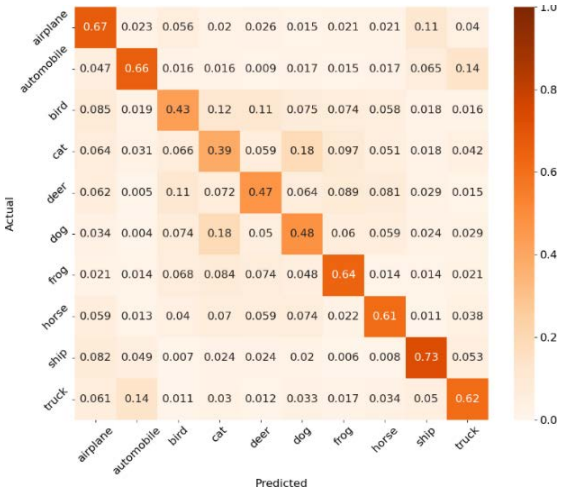

Fig. 4. Confusion matrix

IV. HARDWARE IMPLEMENTATION

A. Quaternion MAC acceleration

The primary challenge in the implementation of an IP core for neural network resides in the substantial memory requirements for storing both weight coefficients and intermediate computational results. To resolve this, the following methodologies are employed:

- Weight coefficients are stored within *Block RAM* modules, which imposes a limitation of requiring synchronous reading from the weight memory.
- Intermediate results of NN computing are buffered using a dual-buffer memory architecture. The size of each buffer is determined by the maximum layer size of the NN. Simultaneously, writing is performed only in one of the buffers, while a read operation is performed from the other.

For the hardware implementation of the IP core, a balanced parallel-serial architecture is used, which allows one quaternion multiplication operation to be performed per clock cycle. Quaternion multiplier is implemented in vector-matrix form [3], such straightforward require 16 real multiplications and 12 additions, which can be implemented using DSP blocks on target FPGA.

The computational process for the fully connected quaternion layer:

$$h = W \cdot x + b,$$

where all variables are quaternion-valued, i.e. h denote output, x denote input, b denote bias and W is weight. The formula for calculating i -th element of h is following:

$$h_i = \sum_{k=0}^{M-1} \left(W_{k,\,i} \cdot x_k \right) + b_i,$$

where $W_{k,\,i}$ is k -th weight of layer size of M. Alternatively, the addition of the bias value b_i can be integrated into the matrix multiplication:

$$h_i = \sum_{k=0}^{M} W_{k,\,i} \cdot x_k,$$

where $W_{M,\,i} = b_i$, and $x_M = 1 + 0 \cdot i + 0 \cdot j + 0 \cdot k$.

Activation function is implemented as split activation [2]:

$$f(p) = g_1(p_1) + g_2(p_2)i + g_3(p_3)j + g_4(p_4)k,$$

where p – quaternion-valued argument of the function, $g_{1\ldots4}(\,)$ – real-valued activation function, such as leaky ReLU.

The block diagram of the IP core is shown in Fig. 5.

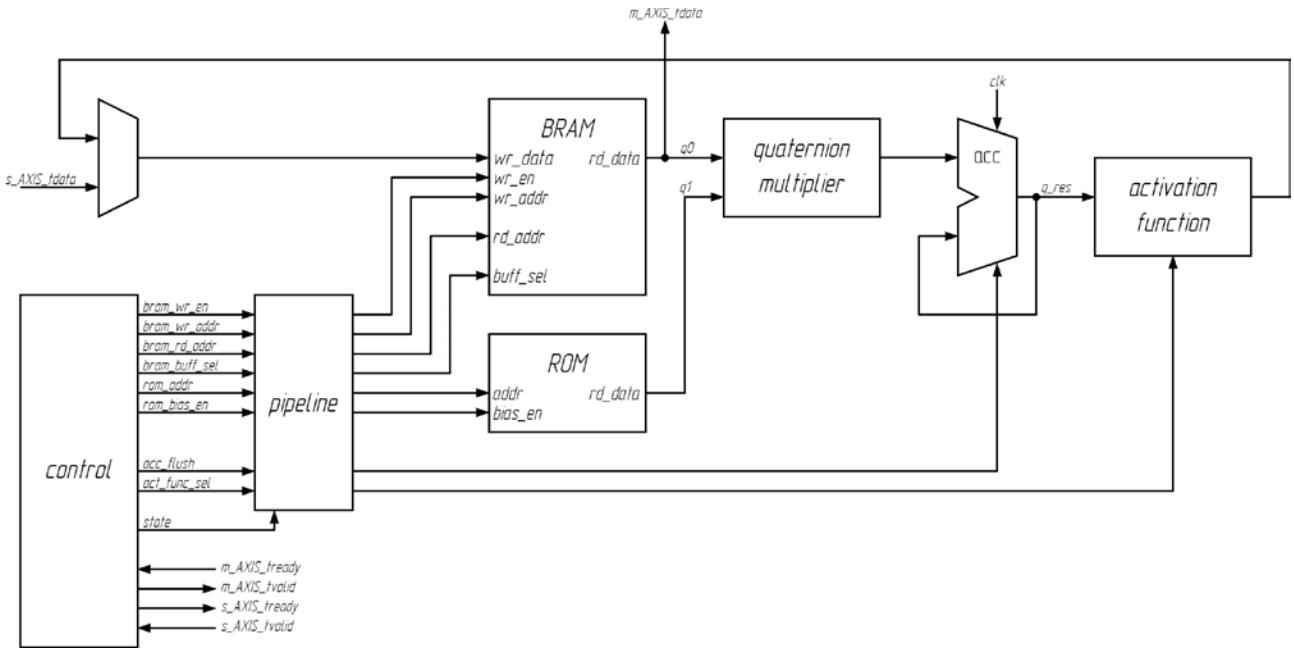

Fig. 5. Quaternion fully connected layer accelerator with AXI-stream interface

B. System design

The quaternion IP core is a standalone block and transactions with it are carried out via two AXI-Stream interfaces. A block design of processor system integrated with accelerator core connected to a DMA block is depicted in Figure 6. Weight coefficients and intermediate data of the neural network are stored in a quantized form in Q16.13 fixed point format per word or 64 bits per quaternion. This format is the most resource efficient, without noticeable impact to the accuracy of the network. FPGA resource utilization of this quantized NN is shown in Table for SoC Ultrascale+ XCVU37P. Synthes, implementation and Place & Route is performed using Xilinx Vivado 2023.2.

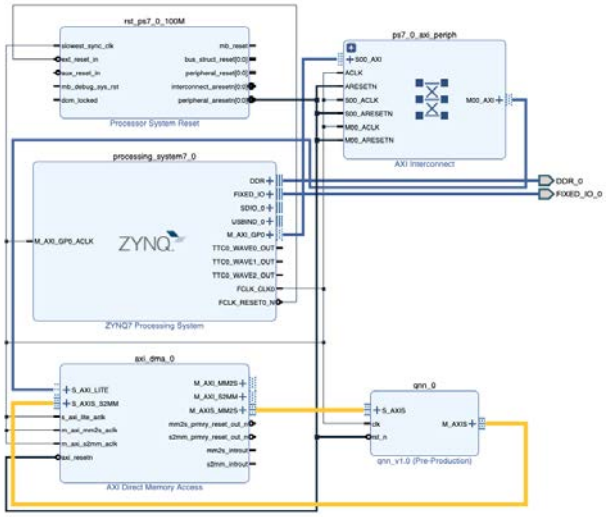

Fig. 6. Block design of developed system
(yellow color bus is datapath for input image)

FPGA RESOURCES UTILIZATION OF THE
VIRTEX ULTRASCALE+ XCVU37P-L2FSVH2892E

Resource	*Utilization*	*Available*	*Utilization [%]*
LUT	935	1303680	0.07
FF	114	2607360	0.01
BRAM	1833	2016	90.90
DSP	17	9024	0.19

C. IP core simulation results

During the simulation of the IP core operation, a timing diagram was obtained. Fig. 7 presents a fragment of this diagram showing the classifier output transmitted via the AXI-Stream interface. Payload is on the `tdata_o` bus asserted when the `tvalid_o` signal is high.

The output data consist of three quaternions, which collectively represent twelve classes, of which ten are utilized. Quaternion components marked with a $\langle - \rangle$ sign correspond to irrelevant data and will be ignored during representation. The simulation result can be presented in the form of the neural network's confidence vector as follows:

$$\begin{cases} q_0 = 0\text{x}0000\_0000\_18c5\_0000 \\ q_1 = 0\text{x}01e8\_0000\_0000\_0000 = \\ q_2 = 0\text{x}0000\_0000\_0000\_0000 \end{cases}$$

$$= \begin{cases} q_0 = 0 + 0 \cdot i + 0.7740 \cdot j + 0 \cdot k \\ q_1 = 0.0596 + 0 \cdot i + 0 \cdot j + 0 \cdot k = \\ q_2 = 0 + 0 \cdot i + 0 \cdot j + 0 \cdot k \end{cases}$$

$$= \begin{cases} 0\% & \langle airplane \rangle; & 0\% & \langle horse \rangle; \\ 0\% & \langle cat \rangle; & 0\% & \langle - \rangle; \\ 77.4\% & \langle frog \rangle; & 0\% & \langle bird \rangle; \\ 0\% & \langle truck \rangle; & 0\% & \langle dog \rangle; \\ 5.96\% & \langle automobile \rangle; & 0\% & \langle ship \rangle; \\ 0\% & \langle deer \rangle; & 0\% & \langle - \rangle; \end{cases}$$

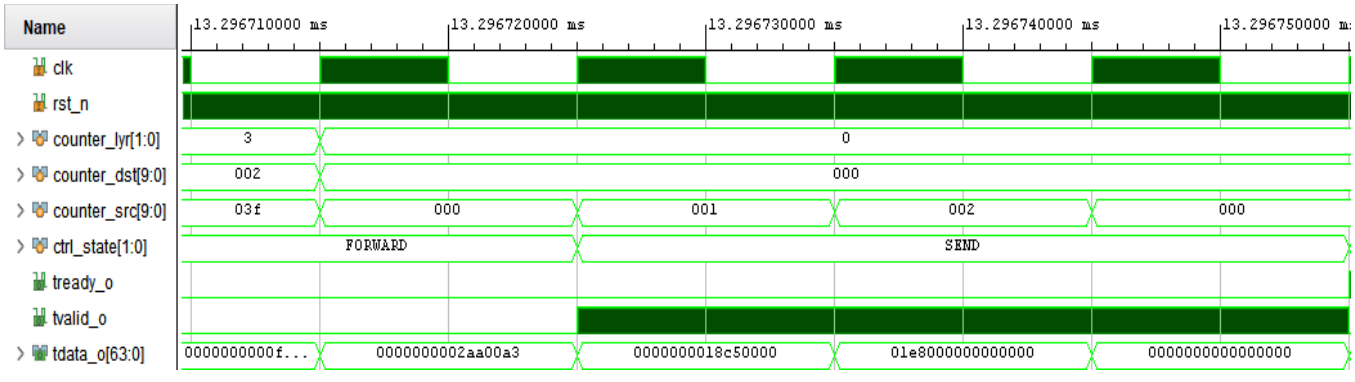

Fig. 7. Waveform of developed IP core with classification results

V. Conclusion

This work presents a neural network designed for the classification of color images from the *CIFAR-10* dataset. The choice of the classification task is due to the benchmarking of the neural network architecture on small weight number. As a result, an adaptive IP core has been developed that can be applied to solve various color image processing tasks. The proposed neural network uses an architecture based solely on fully connected layers. As part of further research, it is planned to expand the network architecture by integrating convolutional layers to improve data processing efficiency. Quaternion output layers have no softmax implementation, which limiting classification performance based split activation functions such as *ReLU* or *Leaky ReLU*. However, future research is planned to address the quaternion activations functions.

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MCDSO: A Direct Visual SLAM System for Wilderness Environments Using Multiple Cameras

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Abstract. **This paper presents Multi-camera Direct Sparse Odometry (MCDSO), an improved version of Direct Sparse Odometry Lite [1]. The algorithm aims to address the limitations of traditional monocular or stereo systems that exhibit narrow fields of view in complex outdoor environments, leading to failed localization and significant positioning errors. MCDSO enhances tracking robustness in low-texture scenarios (e.g., grasslands, sandy terrains) by introducing optical flow estimation to replace feature matching. Additionally, it develops a multi-camera geometric constraint optimization framework based on rigidly-coupled camera models to improve positioning accuracy and system robustness. Experimental validation was carried out using simulated datasets to evaluate the algorithm's performance. The proposed MCDSO demonstrates a significant reduction in error compared to the stereo direct algorithm DSOL. Specifically, the maximum absolute pose error (APE) shows a remarkable decrease from 172.78 to 30.71. Furthermore, the root mean square error (RMSE) also achieves substantial improvement, dropping from 92.28 to 12.47.**

Keywords: **multi-camera visual SLAM, direct method, optical flow estimation, geometric constraint optimization, outdoor environments**

I. INTRODUCTION

Visual SLAM systems are particularly suitable for military operational requirements due to their strong anti-interference capabilities and low hardware costs [2]. Existing monocular and stereo systems struggle to meet robustness demands in complex outdoor scenarios due to limited field of view and scale ambiguity [3 , 4]. In contrast, multi-camera visual SLAM maintains environmental awareness even when some cameras fail through multi-view collaborative perception, while enhancing pose estimation accuracy via cross-camera feature association, demonstrating significant technical potential [5]. However, as camera numbers increase in multi-camera SLAM systems, the quantity of captured images and computational parameters grow exponentially [6]. Current research primarily focuses on processing sparse interest points to address real-time performance constraints [7 , 8], which reduces rich pixel information to limited feature data and associates features across cameras through descriptors. Such methods suffer from time-consuming feature extraction and matching and poor performance in weak-texture environments. Conversely, direct methods eliminate dependency on interest points by employing pixel-level photometric consistency constraints for image alignment and 3D reconstruction [9], demonstrating superior robustness in feature-scarce outdoor scenes:

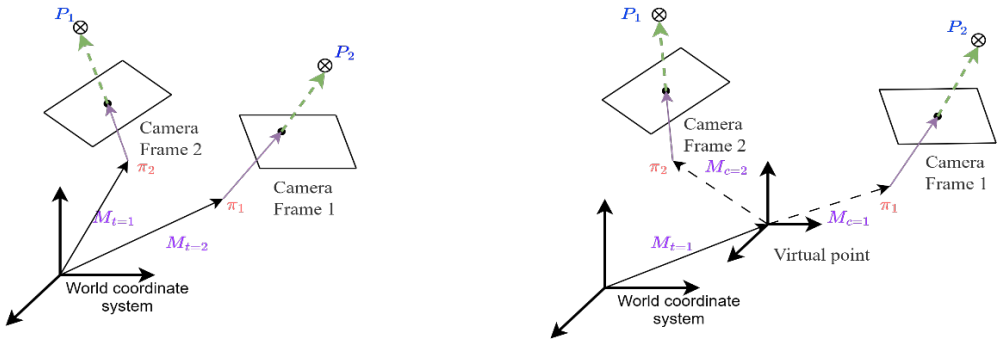
- Optical Flow-Driven Adaptation for Low-Texture Scenarios: Replaces traditional feature matching with optical flow estimation, establishing pixel-level motion consistency constraints in low-texture areas (e.g., grasslands, sand) to resolve tracking failures caused by insufficient corner features.
- Multi-Camera Geometric Constraint Modeling and Joint Optimization: Constructs a unified optimization

framework based on rigidly-coupled camera models, enhancing positioning accuracy while maintaining environmental awareness during partial camera failures.

The remainder of this paper is organized as follows: Section 2 details the proposed method, Section 3 presents experimental setups and results, with conclusions drawn in Section 4.

II. METHOD

MCDSO comprises multiple functional modules: inverse depth initialization, local tracking, multi-camera joint optimization, and sliding window adjustment. During initialization, the algorithm estimates the initial inverse depth of map points through overlapping fields of view or partial maps. The local tracking module then calculates relative poses between consecutive camera frames. Leveraging pre-calibrated extrinsic parameters, the multi-camera joint optimization module employs nonlinear optimization algorithms to collaboratively refine poses across all cameras. Finally, each thread further optimizes camera trajectories through sliding window adjustment.



a b

Fig. 1. Schematic diagram of multi-camera geometric constraint model: Monocular model (a); Multi-camera model (b)

A. Local Tracking

During the local tracking process, we aim to obtain the pose estimation of the new image I_j relative to the local map $\mathcal{M}=\{\mathcal{P}_1,\cdots,\mathcal{P}_N\}$. Therefore, the parameters we hope to optimize are $x_j=(T_j^W,a_j)$. We use a constant velocity model and calculate the initial value using the input frame rate f.

Following standard practice [10], we define the photometric error E_p of a point $p\in P_i$ in the reference frame I_i as observed in the target frame I_j as the weighted sum of squared differences (SSD). On a small pixel region $\mathcal{N}_u$, let

$$E_{\mathrm{p}}=\sum_{u_k\in\mathcal{N}_u} w_k r_k^2\left(x_j\right)= \\ =\sum_{u_k\in\mathcal{N}_u} w_k\left(\left(I_i\left[u_k\right]-b_i\right)-\frac{e^{a_i}}{e^{a_j}}\left(I_j\left[u_k^{'}\right]-b_j\right)\right)^2, \quad (1)$$

where r_k denotes the photometric residual associated with the pixel u_k, $I[\cdot]$ is the pixel indexing operator, and $u_k^{'}$ represents the pixel u_k in image I_i after affine transformation to image I_j.

$w_k=w_k^g\cdot w_k^r$ is a combined weight factor, where

$$w_k^g=\frac{c^2}{c^2+\|\nabla I_i[\mathbf{u}_k]\|_2^2},\quad w_k^r=\frac{\nu+1}{\nu+(\frac{r_k}{\sigma_k})^2}, \quad (1)$$

w_k^g penalizes pixels with high gradients [11], while w_k^r is a robust weight. It is assumed that the residuals of the sparse model follow a t – distribution with u degrees of freedom. We adopt a gradient-based outlier rejection method. If $r_k^2>\|\nabla I_i[\mathbf{u}_k]\|_2^2$, the observation is considered bad and is removed from the optimization.

The total error of local tracking is

$$E_{\text{track}}=\sum_{I_i\in\mathcal{K}}\sum_{p\in\mathcal{P}_i^j} E_p, \quad (2)$$

where P_i^j is the set of points in K_i visible in I_j. By minimizing E_{track}, we can estimate the pose transformation of the new image I_j relative to the local map.

B. Joint Multi- Camera Optimization

After completing the local tracking, we leverage the correlations among the multi-camera system to obtain a more accurate camera pose estimation. To this end, we

propose a multi-camera geometric constraint model based on a rigidly coupled camera model.

As shown in Fig. 1, multiple cameras $c = 1, 2 \cdots C$ observe the scene at the same time t. A virtual optical center, i.e., the origin of the body coordinate system, is introduced. M_c represents the coordinate transformation between the optical center of the sub-camera and the body system. Since the position of the virtual point is arbitrary and lacks actual physical coordinate reference, this greatly increases the difficulty of extrinsic calibration. Additionally, the arbitrariness of the virtual point's position leads to inconsistencies in the extrinsic calibration results, making it impossible to provide standard values for the extrinsic parameters of this model. Therefore, it is necessary to impose constraints on the position of the virtual point in this model.

To facilitate operations, we may fix the position of the virtual point at Camera 1, allowing direct use of the calibrated extrinsic parameters of Camera 1. The model is shown in Fig. 2.

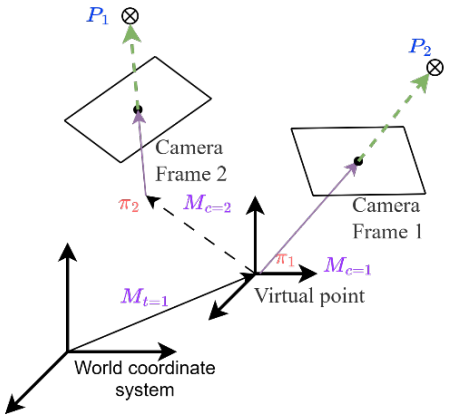


Fig. 2. Schematic diagram of virtual point position change

When applying the multi-camera geometric constraint model, only the transformation relationships from other cameras to Camera 1 need to be calculated. It is worth noting that the transformation relationship from the virtual optical center to Camera 1 is fixed as the identity matrix in this case.

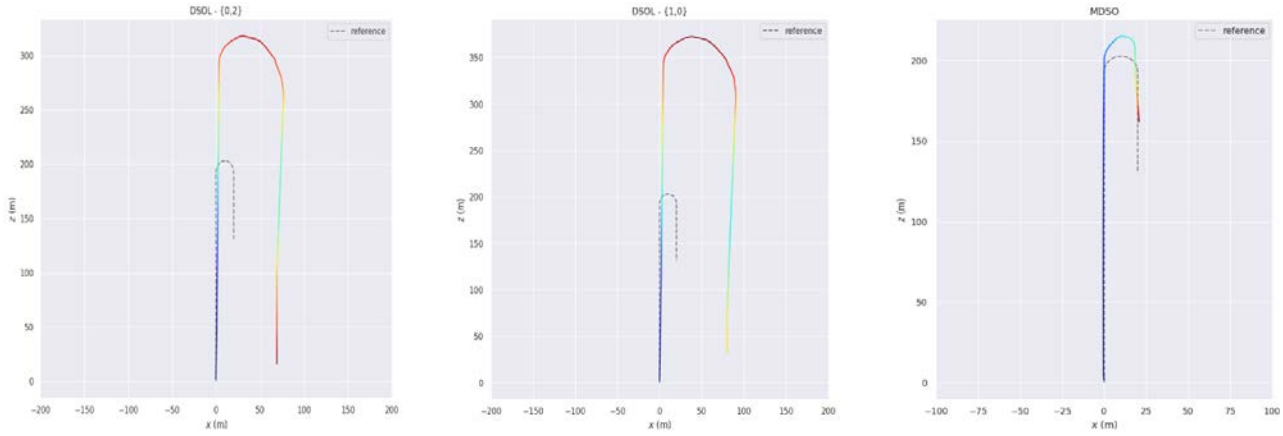


Fig. 3. The results of stereo DSOL and MCDSO on the simulation dataset

The multi-camera geometric constraint model enables further optimization of camera poses. Let the camera pose obtained from local tracking be T_j^W. By transforming the camera pose to the virtual optical center using the extrinsic matrix, the transformed poses of all cameras should be consistent. Thus, we design the loss function as

$$E_{multi} = \sqrt{\sum_{i=1}^{N} \sum_{j=i+1}^{N} || log_e((T_i * T_i^W)^{-1} (T_j * T_j^W))^{\vee} ||_2^2} \quad , \quad (3)$$

where T_i and T_j are the extrinsic matrices between the corresponding cameras and the virtual optical center, and N is the number of cameras. By minimizing E_{multi}, we obtain improved camera poses.

III. Experiments and Results

To validate the effectiveness of our algorithm, we generated a simulated dataset using the MCS (Multi-Camera System) and verified the proposed algorithm by comparing it with the DSOL algorithm.

A. Datasets

We created a three-camera simulated dataset using the MCS (Multi-Camera System) to evaluate the performance of the proposed algorithm. In this simulation environment, we constructed a horizontally arranged planar three-camera system and installed it on a UAV (unmanned aerial vehicle). The UAV was set to fly at a speed of 10 meters per second and maintain an altitude of 50 meters, following a U-shaped trajectory that covers an airport area including runways, grasslands, and forests.

B. Results

To validate the effectiveness of the multi-camera system improvement, we compared the stereo direct algorithm DSOL with MCDSO. Specifically, we numbered the three cameras as {1, 0, 2} and divided the dataset into two groups: {1, 0} and {0, 2} for running the stereo DSOL algorithm. Meanwhile, MCDSO processes the three-camera data directly. We used the evo[1] toolkit to compute the absolute pose error (APE) of translation and rotation, which measures the absolute pose difference between the reference trajectory and the estimated trajectory.

Fig. 3 shows the comparison between the trajectories of stereo DSOL and MCDSO and the reference values on the simulated dataset. The dashed line represents the reference trajectory, and the color variation of the lines reflects the magnitude of the absolute pose error (APE). It is observed that DSOL incurs significant errors at the turning points of the U-shaped trajectory and fails to correct itself, leading to trajectory drift. By contrast, MCDSO significantly outperforms DSOL in terms of performance.

Fig. 4 specifically shows the performance gap between DSOL and MCDSO, where the horizontal axis represents the input frame index and the vertical axis represents the magnitude of the absolute pose error (APE). The experimental results indicate that the MCDSO algorithm demonstrates superior APE performance compared to the stereo DSOL algorithm. Specifically, for both stereo DSOL groupings based on {1, 0} and {0, 2}, their APE values are higher than those of MCDSO, which directly processes three-camera data. It is worth noting that the error of the DSOL algorithm spikes near frame 215, reflecting the significant error it incurs at the turning point of the U-shaped trajectory. Table quantitatively presents the APE results.

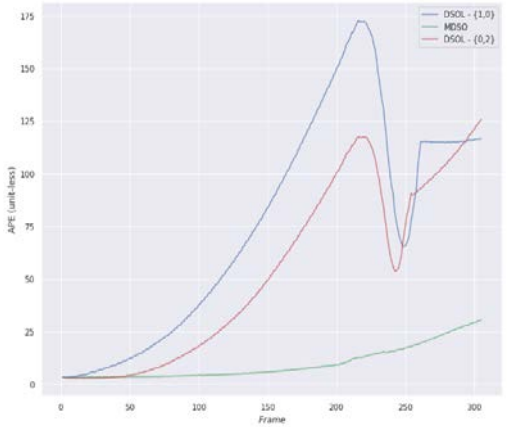


Fig. 4. The APE w.r.t. full transformation of stereo DSOL and MCDSO on the simulation dataset

[1]https://github.com/MichaelGrupp/evo

QUANTITATIVE RESULTS OF APE

APE	DSOL-{1,0}	DSOL-{0,2}	MCDSO
Max	172.7866	125.7555	30.7125
Mean	76.0430	53.9738	9.7879
Min	3.2389	2.8990	3.1400
Rmse	92.2758	68.4465	12.4700

IV. CONCLUSIONS

In this paper, we propose a direct-method-based multi-camera visual SLAM framework named MCDSO. The framework builds upon direct SLAM algorithms and introduces a multi-camera geometric constraint model to further optimize the relative poses of cameras. Our experimental results confirm that MCDSO with a three-camera configuration not only retains the advantages of direct SLAM algorithms in handling low-texture outdoor scenes but also demonstrates superior performance in positioning accuracy.

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Pattern Recognition in Structural Dynamics of Input-output Data (China's Economy, 1981–2018)

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Abstract. **This pilot study employs time series clustering techniques, specifically Dynamic Time Warping (DTW) implemented via the *dtwclust* package in R, to analyze longitudinal data from the China Time-Series Input-Output Tables (1981–2018). The Chinese economy is modeled as a system of 18 sectoral Leontief-type production functions, characterized by dynamically evolving direct input coefficients and gross value-added ratios in nominal terms over the 38-year period. The primary objective is to identify sectoral clusters exhibiting similar patterns in the structural dynamics of their production functions.**

Keywords: **China's economic dynamics, input-output model, Leontief production function, structural change, time series clustering**

I. INTRODUCTION

Input-output tables constitute a classical framework for describing the flows of goods and services within a national economy over an annual period.

The Leontief model, based on these tables, facilitates not only economic analysis but also forecasting. This model exists in two primary formulations: the direct model (physical quantities model) and the inverse model (price model).

This approach is self-contained, as it enables the derivation of the full spectrum of significant inferences without recourse to alternative methodologies. An exception lies in the application of econometric methods, which are employed to forecast the exogenous parameters required for the Leontief model.

Data mining techniques do not fall within the category of methods widely recognized or established within the input-output literature. Rare exceptions exist (e.g., see [1]).

Furthermore, it can be argued that the underlying philosophy of data mining stands in direct opposition to the philosophy of Leontief, who advocated exclusively for explicitly measurable economic facts, straightforward mathematics, and rigorous grounding in the theoretical interpretation of actual processes and phenomena (e.g., see [2]).

Nevertheless, the authors think that experimental applications of data mining techniques to input-output data analysis hold significant potential value, particularly given the current availability of extensive time series data spanning diverse countries, regions, and even the global economy.

Naturally, the objective here is neither to replace nor to devaluate the classical input-output analysis [3–5].

II. METHODOLOGY

A. Dataset

This study employs the China Time-Series Input-Output Tables (1981–2018) [6], compiled annually by researchers at Renmin University of China's School of Applied Economics. Valued at current producer prices, these tables cover 18 sectors under a consistent classification: one agricultural, ten industrial, one construction, and six service sectors. Their methodology aligns with China's National Bureau of Statistics (NBS) practices and adheres to the competitive import assumption.

In economic science, when analyzing the dynamics of any economic indicator, it is standard practice to clearly distinguish between: 1) changes in physical volumes (e.g., production volume or sales volume measured in physical units or in value terms, but calculated using prices from a previous or base period, not current prices); and 2) changes in prices.

In the seminal study *Structural Change in the American Economy* (1970) [7], Ann Carter employed price indices to net out both general price level changes and relative price changes (across different industries) in input-output calculations.

In the present article, price indices were not available. Consequently, all calculations were performed using the original data expressed in current prices and thus in nominal values. This naturally introduces a limitation due to price distortions in the results.

B. Data Processing and Analysis

The core analytical premise of this study posits that the China Time-Series Input-Output Tables (1981–2018) can be conceptualized as representing a set of 18 sectoral Leontief production functions over a 38-year period. Each production function aggregates direct input requirements for goods and services supplied by other sectors and the sector itself ("intermediate inputs"), along with labor and capital inputs (recorded under the category of gross value added).

The primary objective is to analyze the evolutionary trajectories of these production functions throughout the specified period and identify typical sectoral change patterns within the Chinese economy via cluster analysis.

The data analysis pipeline, implemented in R (utilizing base R and the *readxl*, *stringr*, *dtwclust*, and *cluster* packages), comprises the following stages:

1. **Data Transformation:** Convert all 38 input-output tables (1981–2018) from .xlsx format to .Rdata format using the *read_excel()* function.
2. **Coefficient Calculation:** Compute direct input coefficients and gross value added (GVA) component coefficients. This is achieved by dividing the absolute values of intermediate direct inputs and GVA components by the gross output of the consuming sector.
3. **Sectoral Aggregation:** For each sectoral production function, aggregate the derived coefficients into four distinct categories:

- Direct inputs from the Primary Sector (Agriculture & Primary Production, Mining & Quarrying),
- Direct inputs from the Secondary Sector (Food & Tobacco, Textiles & Apparel, Wood, Paper & Printed Goods, Petroleum, Chemicals & Related Products, Non-metallic Minerals, Metals & Metal Products, Machinery & Equipment, Other Manufacturing & Repair, Utilities [Electricity, Gas, Water], Construction),
- Direct inputs from the Tertiary Sector (Wholesale & Retail, Transportation & Logistics, IT & Software Services, Finance & Real Estate, Research & Development [R&D], Other Services),
- Gross Value Added.

4. **Trend Visualization:** Visualize the temporal dynamics (1981–2018) of these four aggregated coefficients for each sector.
5. **Time Series Clustering:** Perform time series clustering using the *tsclust()* function with the specified parameters: *type = "partition", distance ="euclidean" / "dtw", centroid = "mean" / "shape"* [8, 9]. Optimal configuration selection (distance metric, centroid type, number of clusters) was guided by silhouette scores and total within-cluster distances.

III. Results

A. Sectors' Production Function Dynamics

Figure 1 presents the dynamics of direct input coefficients for goods and services from the primary, secondary, and tertiary sectors, along with gross value-added coefficients, for each of the 18 economic sectors. Thus, each of the 18 diagrams comprising Fig. 1 provides an aggregated visualization of the evolution of the sectoral Leontief production function in nominal terms.

Due to lack of space, we omit the analysis of key policy events influence (e.g., 2001 WTO accession, 2015 "Made in China 2025" strategy introduction) on the trends.

Using this visualization framework for a provisional classification of the analyzed production functions, we identify the following sector groups exhibiting relatively similar input mix proportions and/or shape:

- Mining & Quarrying, Wholesale & Retail, Transportation & Logistics, IT & Software Services, Finance & Real Estate, Other Services;
- Textiles & Apparel, Wood, Paper & Printed Goods, Petroleum, Chemicals & Related Products, Non-metallic Minerals, Metals & Metal Products, Machinery & Equipment, Construction;
- Other Manufacturing & Repair, Research & Development (R&D);
- Agriculture & Primary Production;
- Food & Tobacco;
- Utilities (Electricity, Gas, Water).

In interpreting Figure 1, one should bear in mind that all calculations using nominal values introduce a price distortion effect. Moreover, the competitive import assumption in the original data may obscure supply-chain dependencies, affecting cluster interpretations (e.g., petroleum/chemicals inputs).

B. Patterns in Sectors' Dynamics

However, such visual analysis is insufficient for identifying less evident temporal patterns.

Time series clustering was performed using the *dtwclust* package in R, employing various configurations: different distance metrics (Euclidean, DTW, SBD, etc.) were selected; the optimal number of clusters was evaluated (by calculating silhouette scores

and total within-cluster distances to centroids for different cluster counts); and different centroid calculation methods (mean, DBA, median, shape, etc.) were utilized.

The time series consisted of the coefficients of direct inputs of goods and services from the primary, secondary, and tertiary economic sectors, as well as the gross value added coefficient, covering the entire period from 1981 to 2018.

As an illustrative result, Fig. 2 presents the graphical representation of the time series depicting consumption of inputs from the tertiary economic sector (services) by each of 18 China's economy sectors.

In this case, the following clusters with provisional titles were identified:

- **Slow Growth:** Mining & Quarrying, Wood, Paper & Printed Goods, Non-metallic Minerals, Metals & Metal Products, Utilities (Electricity, Gas, Water).
- **Wave-like:** Agriculture & Primary Production, Food & Tobacco, Textiles & Apparel, Petroleum, Chemicals & Related Products, Machinery & Equipment, Other Manufacturing & Repair.
- **Big from the Start:** Wholesale & Retail, Finance & Real Estate.
- **Fast and steady Growth:** Construction, Transportation & Logistics, IT & Software Services, Research & Development (R&D), Other Services.

Briefly, we can observe that service industries (e.g., IT, finance, R&D) drive modern structural shifts – suggesting this as a key trend in the data.

IV. Discussion

The question remains open regarding the efficacy and promise of applying data mining techniques to the analysis of input-output tables.

For a single country case study – such as the People's Republic of China examined in this article – characterized by a relatively high level of aggregation (where the original data consolidates all economic sectors into merely 18 broad categories) and a relatively short time span (38 years yielding only 38 temporal observations), data mining methods arguably cannot fully demonstrate their potential. More traditional analytical tools, and even thorough economic analysis of indicators, appear to yield results of comparable significance under these constraints.

However, it is crucial to acknowledge the growing scientific and practical interest in input-output tables. This is evidenced by the emergence of sufficiently large databases covering not individual national economies, but entire regions or even the global economy (e.g., the Eora Global Supply Chain Database, see www.worldmrio.com).

Such multi-regional input-output (MRIO) tables contain substantially greater information volumes. In this context, data mining approaches hold the potential to, if not replace, then significantly complement and enhance classical analytical methods.

An important limitation of this study must be highlighted: the absence of source data on sectoral price dynamics throughout the entire period under review, as well as the lack of actual data distinguishing between domestic and imported goods and services flows within the Chinese economy. Conducting meaningful economic analysis is fundamentally impeded without access to such important information.

Comparative analysis of China's sectoral trajectories with those of other countries (e.g., Japan/USA) would be of significant interest.

An interesting pivot would be linking our findings to the approach proposed in [10] – "a double filtering method (DFM) to visualize the skeleton industrial structure (SIS)".

In addition, future work should validate cluster stability by analyzing silhouette scores and within-cluster variances for all configurations tested, ensuring reproducibility.

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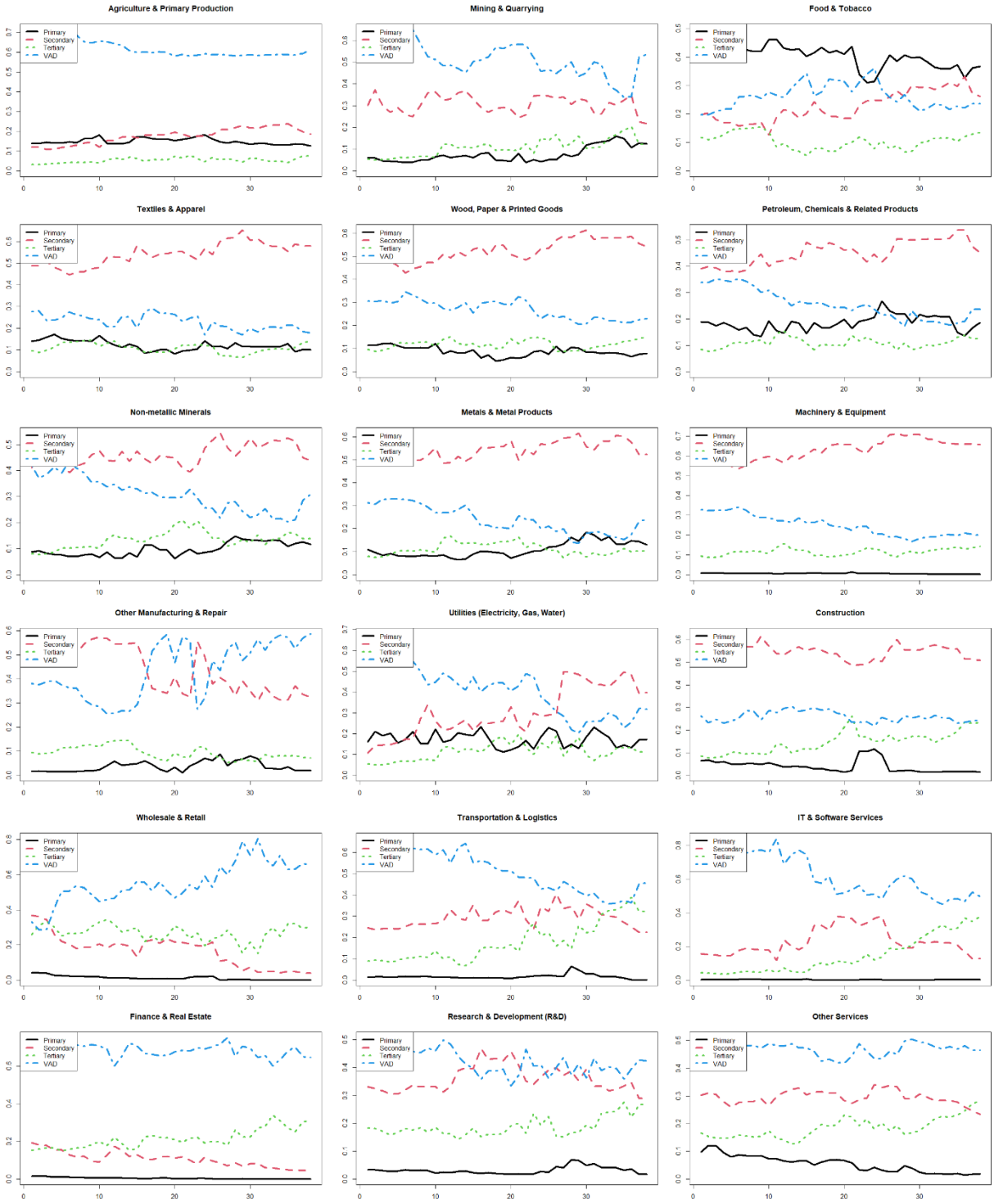

Fig. 1. Sectors' Production Function Coefficients Dynamics

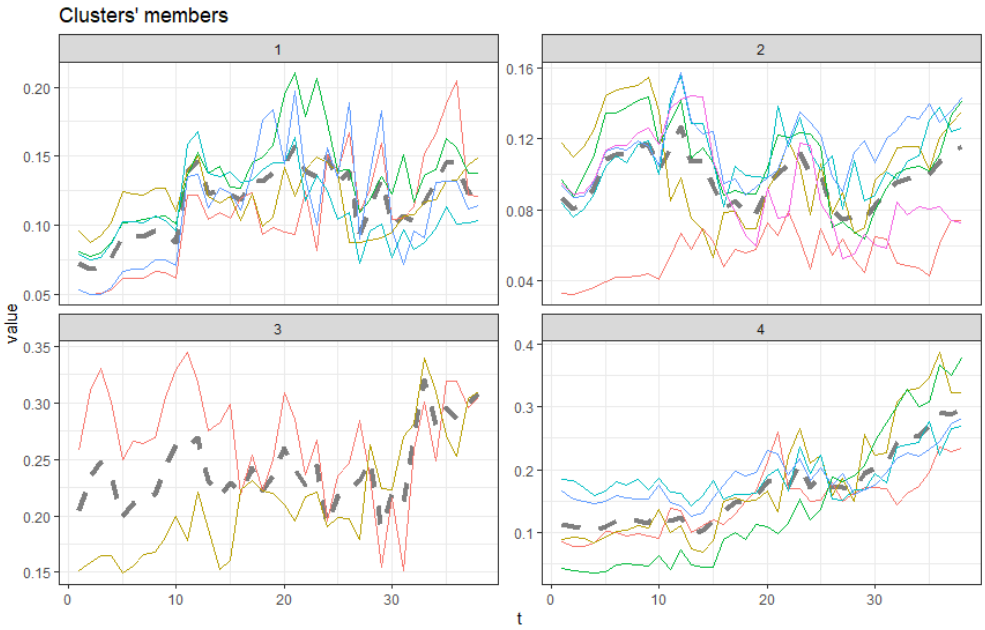

Fig. 2. Results of Time Series Clustering of direct Coefficients of tertiary Sector's Inputs with *dtwclust* for 18 economic Sectors

Segmentation Algorithms in Processing Satellite Images

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Abstract. **The problem of satellite image processing is specific and narrowly focused, but it is relevant in the context of active development of space technologies. This article analyzes the results of image segmentation by several algorithms, and then compares these results by selected metric: accuracy of the accordance of the boundaries of objects in the original images and images after processing. The results of the experiments reveal the most suitable segmentation algorithm for different starting conditions and different input data.**

Keywords: **segmentation, satellite images, watershed, flood fill, grayscale image, image processing**

I. INTRODUCTION

Segmentation in the context of image processing is the process of dividing a digital image into several segments, so-called superpixels (a set of pixels). The goal is to change the image in such a way as to simplify the analysis process and make it more efficient. The segmentation method is also used to highlight objects, boundaries, lines, curves in images. The result is a set of segments that together cover the entire image, or a set of contours extracted from the image. A distinctive property of a segment is the similarity of pixels in one or more specific characteristics (color, brightness, texture). Neighboring sets of pixels, in turn, have significant differences in these characteristics. The example of segmentation process is in Fig. 1.

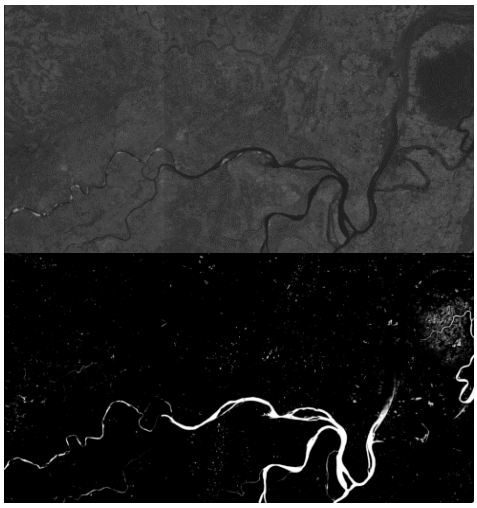

Fig. 1. Example of segmentation process

A number of algorithms and methods have been developed to implement the image segmentation process. Since there is no universal solution to the image segmentation problem, when working in a specific subject area, it is necessary to analyze existing methods and understand the specifics of the data in this area, on the basis of which a solution to the problem is developed.

The purpose of this article is to analyze existing methods in the context of solving the problem of segmentation of satellite images, select one or more metrics that will show the effectiveness of the algorithms, conduct comparative tests on real data and then compare the algorithms according to the selected metrics.

II. EXPERIMENT DESCRIPTION

A. Initial data

Real satellite images taken with equipment with a resolution of 2 meters (1 pixel reflects 2 meters of the earth's surface) provided by Peleng JSC were used as test data. The experiment involves 100 images of different surface areas.

The original images were made in grayscale, the bit depth was 10 bits/pixel, which allows for a more detailed image in terms of details. Two algorithms were selected for the experiment: the watershed and the flood fill.

The goal of the experiment is to highlight water bodies in images (rivers, lakes, etc.). The metric for evaluating the segmentation methods will be the accuracy of the correspondence between the boundaries of objects in the original images and the processed images. Based on this metric, the segmentation algorithms used in the experiment will be assessed in terms of their suitability for solving the task.

B. Watershed

This method is based on the representation of the image as a topographic surface, where the heights relative to a certain level are represented by the values of pixel brightness [1]. This analogy partitions the image into "peaks" and "plains". Plains are areas of the image where there are no differences in pixel

brightness. Peaks appear in places where there is a difference in intensity, i.e. the absolute value of the brightness gradient is maximal. In the beginning the coordinates of the global minimum brightness in the image are determined and a gradual "water filling " begins, which implies the sequential addition of pixel layers to the segments. At the points where these segments touch (peaks), partitions are constructed, which are called watersheds and prevent individual sections from being merged into a single segment.

The above algorithm is a basic description of the watershed method, which works correctly only when there are a small number of local minima in the image, which implies a lack of fine detail. A large number of details leads to excessive segmentation in places where the processing result should look like a single segment.

Experiment starts with finding an approximate estimate of the water objects. For that, binarization can be used. Binarization is the process of setting a certain brightness threshold (in the example, the brightness threshold was 105) and then assigning each pixel either the value 0 (black) when the threshold is exceeded, or the value 255 (white) when the threshold is lower. Next step is removing any small noises in the image with using morphological opening (Erosion followed by Dilation) and removing any small holes in the object with using morphological closing (Dilation followed by Erosion). The kernel for erosion and dilation was in the form of a matrix of ones with a 3x3 size. The remaining regions are undetermined as either water objects or background. The watershed algorithm is employed to resolve these ambiguous zones. Initial data and results are in Fig. 2–5.

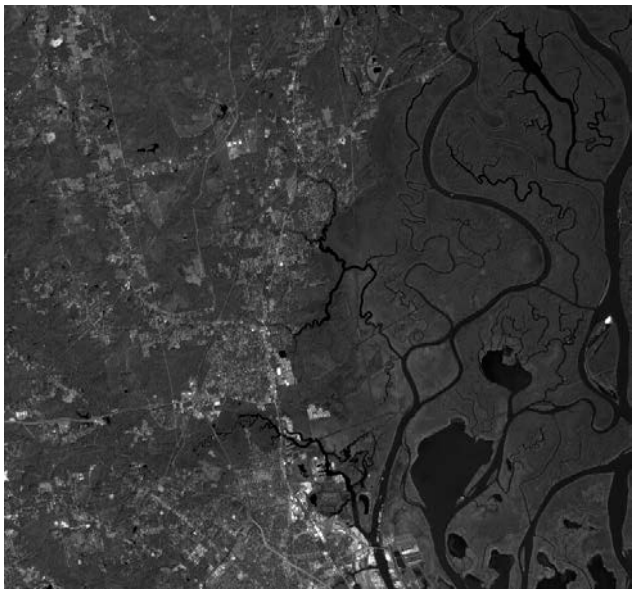

Fig. 2. Initial watershed method data № 1

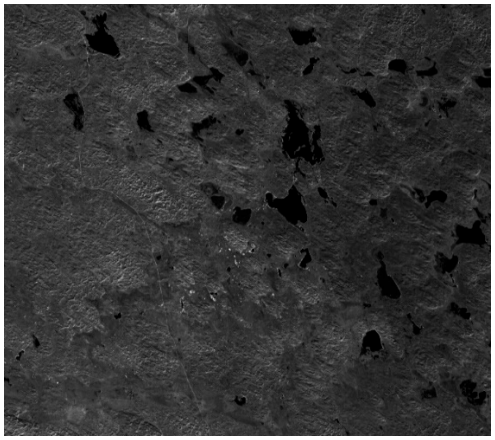

Fig. 3. Initial watershed method data № 2

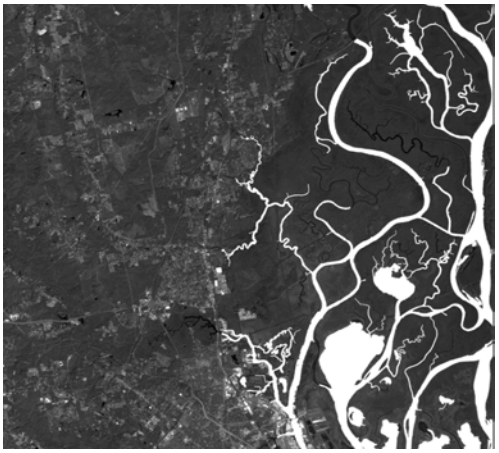

Fig. 4. The result of the watershed method № 1

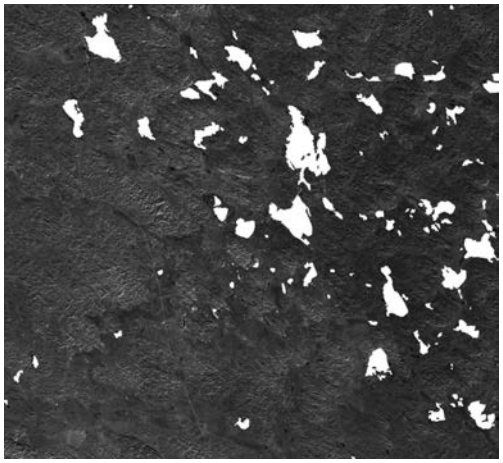

Fig. 5. The result of the watershed method № 2

C. Floodfill

Flood fill is an algorithm to identify and/or change adjacent values in an image based on their similarity to an initial seed point [2]. This method is used to highlight areas of uniform color. To perform this algorithm, an initial pixel is selected and the color change interval of neighboring pixels relative to the original is set.

The process combines pixels into one segment by filling them with one color, provided that they fall within the specified range. The result is a segment filled with a certain color.

This algorithm is useful for filling areas with a slight color difference and a uniform background. One way to use the flood fill method is to detect damage at the edges of an object. For example, when filling uniform areas with a certain color, the algorithm fills neighboring regions, this indicates that the integrity of the boundary between the two areas is damaged

When solving problems in the context of processing satellite images, this algorithm can be useful, for example, when determining the boundaries of lakes and finding contact points of several bodies of water on the map, since if there are intersections, they will be painted in one color. For flood fill to work correctly, it is necessary to transfer the coordinates of pixels located in the segments whose boundaries need to be found (Fig. 6–9). For this reason, to test this algorithm, the coordinates of points of only some areas were passed as input data.

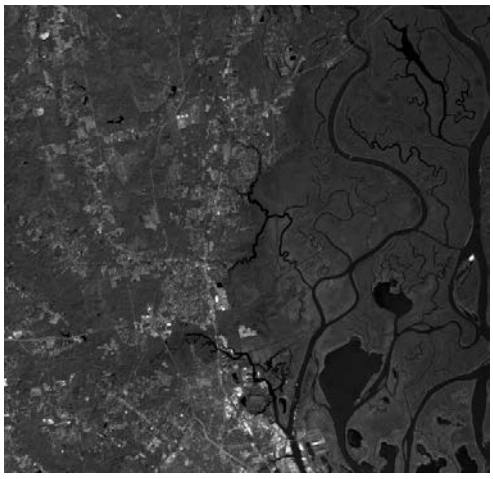

Fig. 6. Initial flood fill method data № 1

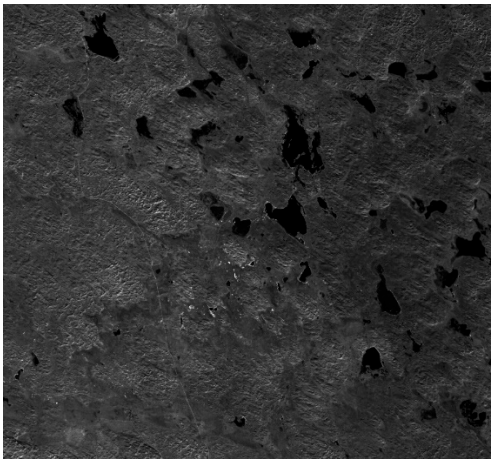

Fig. 7. Initial flood fill method data № 2

III. Results analysis

The flood fill method satisfactorily solves the task of finding the boundaries of water bodies. The algorithm relatively accurately identifies small details such as land areas located in the middle of the segments being identified. When evaluating the results of the work, one can notice some noise on the identified clusters in the form of uncolored pixels in the middle of the cluster (Fig. 7). This noise is removed by slightly adjusting the initial parameters of the algorithm. In this case, the color range of pixels to be attached to the segment was changed from [-10, +10] to [-20, +20]. The main disadvantage of this method is the need to implement the search for the coordinates of pixels that will be located on the necessary clusters. The solution is either human intervention as an intermediary between the processes of data collection and their processing, or the introduction of an additional segmentation algorithm that will identify the necessary segments. Another disadvantage is that if this method encounters contrasting obstacles during its operation, then the cluster, which is one object in the original image, will be selected incorrectly.

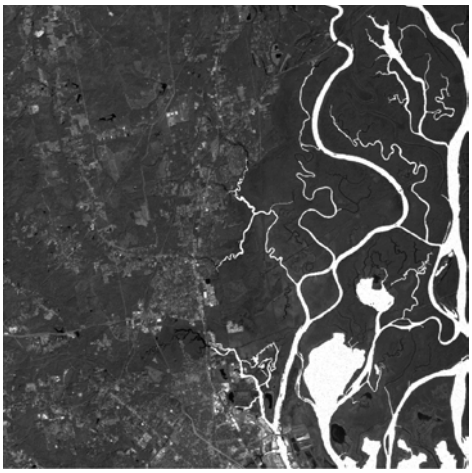

Fig. 8. The result of the flood fill method № 1

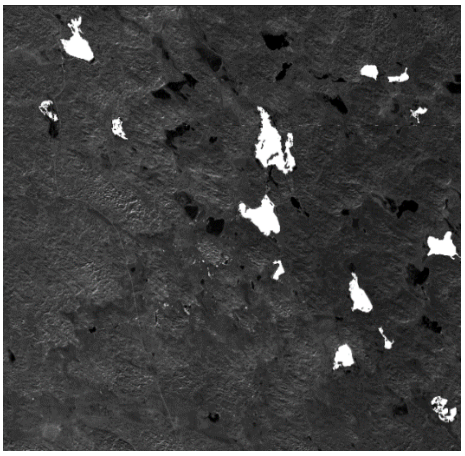

Fig. 9. The result of the flood fill method № 2

The watershed method can, under certain conditions, create redundant segmentation: places that should be a single cluster are divided into many smaller ones, which is hardly noticeable in the final results due to the density of these "subclusters". This defect can be detected by examining the image with markers (Fig. 10). But unlike the flood fill method, the watershed algorithm does not require an intermediate stage in the form of searching for the required coordinates on the image, and at the same time, this algorithm, with the correct choice of initial parameters, does not experience bigger losses in the accuracy of object selection in comparison with flood fill.

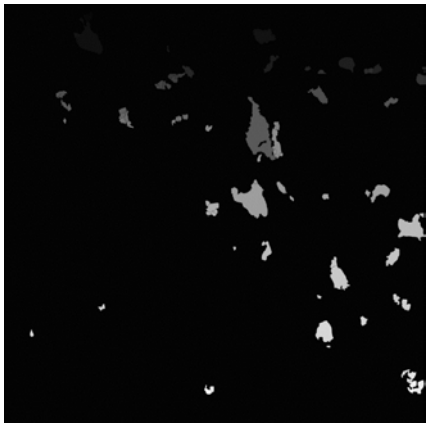

Fig. 10. Example of redundant segmentation

As mentioned earlier, the algorithms were compared according to the metric of the accuracy of the object boundaries in the original images and the images after processing. This implies that objects in the original image are taken as a reference, and the results of the algorithms are evaluated by the percentage of match reference objects with selected segments. Average level of accordance with the standard with using the flood fill algorithm is 85 percent, but during the experiment, additional assistance was required to find objects in the image and transfer their coordinates to the algorithm. On the other hand, the watershed algorithm showed a match rate of 80–82 percent without the need for additional assistance. The problem of additional assistance for flood fill algorithm will become critical if it becomes necessary to create a fully autonomous system for analyzing satellite images.

From the information obtained, it was concluded that when comparing according to the metric chosen at the beginning of the experiment, the watershed method would be preferable. This method has the advantage of not requiring additional image pre-processing while maintaining the same level of accuracy.

IV. Conclusuon

Having conducted a study of the algorithms in the context of the satellite imagery processing task, it was concluded that the watershed method is advantageous in the general case. It is also necessary to pay attention that space photography is a process with a large number of unstable conditions, to which it is constantly necessary to adapt and minimize their consequences. Therefore, the optimal choice when solving image segmentation problems is a combination of some algorithms for each of them to perform the segmentation stages in which they cope best. Thus, the decision on the use of each algorithm must be made based on the specifics of the task and the conditions for obtaining each image.

It is also worth noting that neural networks using in the analysis of satellite images could provide higher accuracy. This method of solving this problem will require much more computing power and time, and that condition may be unacceptable if it is necessary to integrate the system for analyzing satellite images into embedded systems.

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Automatic Identification and Quality Assessment of Potato Planting Rows Using UAV Imagery

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***Abstract*. This article describes an automatic approach to determining and evaluating the quality of potato planting rows using images obtained using an unmanned aerial vehicle (UAV). The method is based on YOLOv11 segmentation of plants, applies adaptive morphological filtering, which takes into account the spatial resolution of the image (GSD), and automatically adjusts the orientation of the rows. We tested this approach on field data and achieved 97.4 % line detection accuracy and an F1 gap detection score of 0.91. The data obtained suggests that this method can be useful for crop monitoring and decision support in digital agriculture**

***Keywords:* potatoes, segmentation, orthomosaic, gaps in rows, YOLO, GSD, aerial photographs, crop monitoring**

I. INTRODUCTION

In recent years, precision agriculture has become a major focus in agronomy, driven by advances in digital technologies to improve crop production efficiency. A key task is the automatic identification and assessment of planting rows, especially for potatoes, using UAV imagery. Disruptions in row structure – due to poor germination, pests, weather, or planting errors – can lower yields and require timely intervention. UAVs, together with modern computer vision and deep learning methods such as U-Net and YOLO, enable rapid and accurate assessment of row quality in agricultural fields [1].

Automatic detection of planting rows and analysis of their quality have become key challenges in precision agriculture. UAVs allow for the acquisition of detailed aerial imagery with centimeter-level resolution, enabling the detection of individual plants and rows. For example, [2] showed that when analyzing images of vineyards, peach, and tomato fields, threshold segmentation, classification (K-means, MDM), and Bayesian segmentation algorithms allowed vegetation to be distinguished with an accuracy greater than 90 %. It was also found that near-infrared (NIR) data provided little improvement in results, while RGB images were preferable for row detection. Overall, high spatial resolution and frequent imaging enable timely monitoring of emergence uniformity, planting density, and the presence of missing plants.

The main algorithms for row detection are based on the analysis of the geometric structure of the image and the separation of crops and background. Classical methods use color segmentation and line fitting. For instance, [3] applied projective transformation for perspective correction, followed by color segmentation to separate vegetation from the background, clustering (to distinguish crops from weeds), and robust line fitting to detect rows. The proposed algorithm achieved an IoU of about 0.73 and row detection accuracy greater than 90 %, even with heavy weed infestation.

The Hough transform approach is also known; however, [4] demonstrated that the classical Hough algorithm underperforms on field orthomosaics. Instead, they proposed a least-squares method for row fitting, which achieved very high Crop Row Detection Accuracy (CRDA) – close to 1.0 for cotton (0.99–1.00) and significantly outperformed the Hough algorithm when analyzing wheat (0.66–0.82 vs. 0.31–0.53).

Modern research increasingly uses machine learning and deep learning methods. For example, [5] trained a Faster R-CNN detector to recognize potato plants in UAV RGB images (GSD $\approx$ 2 mm). The model achieved an average precision (AP) of about 0.78 when detecting plants on test data, after which the authors constructed a plant density map. The resulting maps correlated well with actual plant density and yield ($R^2 \approx 0.80$), confirming the practical value of such an approach. Similarly, [6] proposed a lightweight version of YOLOv8 (Maize-YOLOv8n) for detecting missing maize plants in UAV images. Their model achieved mAP $\approx$97.4 %, precision 94.3 %, and recall 93.1 % on their dataset, operating in real time (12.8 ms per image)

and demonstrating robustness under various conditions (changing lighting, presence of weeds).

In the context of digitalization in agriculture, the automation of objective assessment of potato planting structure and quality using aerial imagery is of particular relevance. This study is aimed at developing an algorithm for the automatic detection of planting rows and identification of gaps in UAV images.

II. Materials and Methods

A. Materials

Experimental studies were carried out on a potato field in the Gorodetsky district, Nizhny Novgorod region, with sod-podzolic soil typical for the area. Aerial imagery was acquired on June 25, 2024, under stable weather (clear, no wind, 21–23 °C, 60 % humidity) using a DJI Phantom 4 Pro v2.0 UAV with a 20 MP DJI FC6310S camera. Images were saved in GeoTIFF format at 0.145 cm/pixel GSD, capturing detailed plant and row structure. At the time, the crop was at the V4 BBCH growth stage. All images were processed into a 16-bit GeoTIFF orthomosaic using PIX4Dmapper, which was used for subsequent row identification and crop assessment.

B. The scheme of operation of the method

The proposed approach processes an orthomosaic of a potato field acquired by an unmanned aerial vehicle (UAV) and automatically identifies planting rows and detects gaps along each row. Each stage of the pipeline, illustrated in Fig. 1, is described and discussed in detail in the following sections.

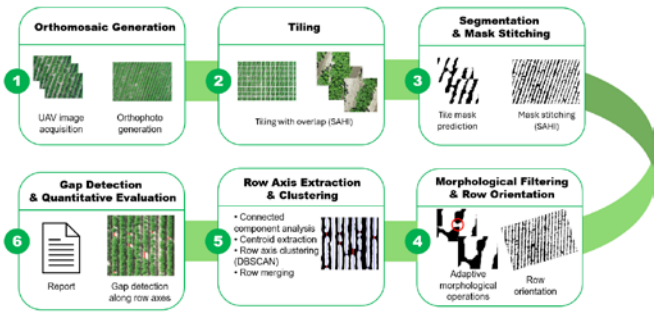


Fig. 1. Pipeline of the proposed automated row and gap analysis algorithm

C. Data preparation and model training

In this study, instance segmentation methods were applied to UAV imagery for automatic identification and quality assessment of potato planting rows. Manual annotation of 84 full-resolution images (5472×3648 px) was performed using the Roboflow platform [7], ensuring representative coverage. To enhance training and reduce overfitting, images were split into overlapping 1024×1024 pixel tiles with 30 % overlap, expanding the dataset and improving model robustness.

Data augmentation was applied exclusively to the training subset: horizontal flips (p = 0.5), vertical flips (p = 0.1), random rotations within ±20°, brightness and contrast adjustments of ±15 %, hue shifts of ±2 %, saturation changes of ±20 %, addition of blur and Gaussian noise (p = 0.05), and random cutouts covering up to 25 % of the image area (p = 0.15).

The YOLOv11-Seg models were trained for 80 epochs with early stopping after 20 epochs without improvement, using batch sizes of 24 (nano), 16 (small) and 8 (medium) selected to balance GPU-memory constraints and gradient stability [8]. To assess the effect of layer freezing on segmentation performance, 0, 5 or 10 initial layers were frozen. Mosaic and MixUp augmentations (with close_mosaic=30 to disable Mosaic during the final 30 % of training and scale=0.5) were applied to enhance variability and improve generalization across diverse field conditions. Training was conducted on an NVIDIA TITAN RTX (24 GB) workstation, yielding inference speeds of 20–30 ms per tile for the nano and small variants, while the medium variant achieved a peak mAP@0.5 of 0.96. Full-field inference utilized SAHI for tiling and mask-stitching, effectively eliminating border artifacts [9].

D. Row detection on segmented masks

Row detection on segmented masks is performed to enable further quantitative analysis of planting structure, gap identification, and plant density estimation. This stage involves sequential processing of the segmentation results to obtain clear row geometry, robust to artifacts and invalid regions.

a) Morphological cleaning and geometry enhancement: Adaptive morphological opening [10] with a kernel size based on GSD and target row width removes bridges and small artifacts from the segmentation mask. Algorithm 1 summarizes the procedure. The efficiency of morphological filtering is illustrated in Fig. 2.

Algorithm 1 Adaptive Morphological Filtering of Mask (GSD aware)

Input: segm_mask, gsd_cm, bridge_width_cm, elongate
Output: cleaned mask
1: kernel_size ← ceil(bridge_width_cm / gsd_cm)
2: **if** even(kernel_size): kernel_size ← kernel_size + 1
3: **if** elongate == 'vertical': kernel ← ones(kernel_size, 7)
4: **else if** elongate == 'horizontal': kernel ← ones(7, kernel_size)
5: **else**: kernel ← ones(kernel_size, kernel_size)
6: cleaned ← MorphOpen(segm_mask, kernel)
7: **return** cleaned

a b

Fig. 2. Segmentation mask before morphological filtering (a); segmentation mask after morphological filtering (b)

b) Morphological cleaning and geometry enhancement: For further analysis, it is necessary to align the mask so that the rows are strictly horizontal or vertical. The dominant row direction is determined by analyzing the distribution of components or their centroids using Principal Component Analysis (PCA) [11].

Let (x_i, y_i) denote the coordinates of the centroids of the components. The covariance matrix is calculated as (1):

$$\mathbf{C} = \frac{1}{N}\sum_{i=1}^{N}\begin{pmatrix} x_i - \overline{x} \\ y_i - \overline{y} \end{pmatrix}\begin{pmatrix} x_i - \overline{x} & y_i - \overline{y} \end{pmatrix}, \quad (1)$$

where $\overline{x_i}$ and $\overline{y_i}$ are the mean values of the centroid coordinates.

The eigenvalues and eigenvectors of the matrix **C** are then computed. The principal axis (row direction) corresponds to the eigenvector with the largest eigenvalue (2):

$$\mathbf{v} = (v_x, v_y). \quad (2)$$

The rotation angle is defined as (3):

$$\theta = \arctan 2(v_y, v_x). \quad (3)$$

The mask is then rotated by an angle $90° - \theta$ so that the rows become parallel to the Y axis. As a result of orientation correction, all subsequent calculations (row axis extraction, gap analysis) are performed in a unified coordinate system.

c) Connected component analysis and row clustering: On the rotated and binarized mask, connected component analysis is used to extract all segmented row objects (white regions). For each component, geometric features (area, width, height, centroid) are computed. Noise and artifacts are filtered by applying minimum area and dimension thresholds, as well as by excluding components within invalid mask regions. The centroids of valid components define row positions. To group components belonging to the same row (despite gaps), DBSCAN [12] clustering is applied to centroid coordinates along the relevant axis (Y for vertical orientation).

For each resulting cluster, the median or mean y-coordinate is calculated and adopted as the position of the corresponding row axis (4):

$$y_k^{(\text{row})} = \text{median}\{y_i \in \mathcal{C}_k\}, \quad (4)$$

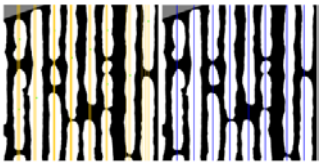
where $\mathcal{C}_k$ is the *k* th cluster of components belonging to the same row.

Due to segmentation artifacts or large gaps, multiple axes may sometimes be detected in close proximity that in fact correspond to the same physical row. To resolve such duplicates, axes are merged if the distance between them does not exceed a threshold dmerged d_{merge}. This threshold is best selected based on the actual inter-row spacing in the field. If the row spacing is known in advance, the optimal threshold in pixels can be calculated as (5):

$$d_{\text{merge}} = k \cdot \frac{\text{row spacing, cm}}{\text{GSD, cm/pixel}}. \quad (5)$$

where *k* is an empirically selected coefficient (0.5 was used in this study) to ensure that only axes much closer than the expected row spacing are merged.

The results of this processing are presented in Fig. 3.



a b

Fig. 3. Merging of closely spaced row axes: Axes identified before merging (orange lines) (a); Final axes after merging (blue lines) (b)

This approach minimizes duplication errors in axis detection and ensures accurate identification of the actual crop rows within the planting structure.

E. Gap and density analysis in rows

After constructing the row axes, automatic detection of gaps along each row is performed. A gap is defined as a section of a row axis where no segmented objects are present for a distance exceeding the minimum permissible in-row spacing, as specified by agronomic requirements for the crop and growth stage. The gap detection threshold L_{gap} is calculated as follows:

$$L_{\text{gap}} = \frac{\text{in-row spacung, cm}}{\text{GSD, cm/pixel}}. \quad (6)$$

This value is set in accordance with agronomic recommendations (for potatoes, a value of 30 cm was used in this study). The algorithm for gap detection along each row axis is presented in Algorithm 2.

Algorithm 2 Gap Detection along Row Axis (GSD-aware)

Input: segm_mask, gap_threshold_cm, gsd_cm
Output: gap_list

```
min_gap_len ← gap_threshold_cm / gsd_cm
gaps ← []
row_mask ← extract_row_mask(segm_mask, row_axis)
current_gap_start ← None
for pos = 0 to length(row_mask) - 1:
    if row_mask[pos] == 0:
        if current_gap_start is None: current_gap_start ← pos
    else:
        if current_gap_start is not None:
            gap_length ← pos - current_gap_start
            if gap_length ≥ min_gap_len:
                gaps.append((current_gap_start, pos-1,
gap_length))
            current_gap_start ← None
if current_gap_start is not None:
    gap_length ← length(row_mask) - current_gap_start
    if gap_length ≥ min_gap_len:
        gaps.append((current_gap_start, length(row_mask)-1,
                     gap_length))
return gaps
```

Thus, gaps are recorded only in cases where their length exceeds the minimum allowable for a particular crop, which ensures the agronomic relevance of the analysis.

III. Results and Discussion

A. Segmentation quality assessment

A series of experiments (1–6) was conducted to assess segmentation quality using different YOLOv11 architectures (nano, small, medium) on the test set. For each model, results were compared between baseline training (no augmentations) and advanced augmentations (Mosaic, MixUp). Comparative analysis (Table) shows that Mosaic and MixUp consistently improve segmentation performance across all models. The greatest quality gains were observed for YOLOv11m, with maximum mAP50 of 0.944 and F1-score of 0.933. These results indicate that complex augmentations enhance model generalization and robustness to occlusions, brightness variation, and shadows.

An additional set of experiments (7–10) analyzed the effects of initial layer freezing (freeze = 0, 5, 10) and augmentation strategies on segmentation performance. Freeze = 5 and the Mosaic+MixUp combination yielded the best results in terms of accuracy, recall, and efficiency. All YOLOv11 models achieved mAP50 > 0.93 and F1-score > 0.91, consistent with state-of-the-art results. Fig. 4 shows an example of segmentation, demonstrating accurate plant localization. Occasional edge artifacts are reduced in practice by overlapping tiles and mask stitching, which ensures consistent results across the orthomosaic.

Segmentation results for YOLOv11 configurations

Exp.	Model & Configuration	mAP50	mAP50–95	F1
1	YOLOv11n (no augm., freeze=5)	0.932	0.719	0.913
2	YOLOv11n (Mosaic+MixUp, freeze=5)	0.943	0.734	0.927
3	YOLOv11s (no augm., freeze=5)	0.939	0.728	0.928
4	YOLOv11s (Mosaic+MixUp, freeze=5)	0.943	0.739	0.932
5	YOLOv11m (no augm., freeze=5)	0.936	0.716	0.926
6	**YOLOv11m (Mosaic+MixUp, freeze=5)**	**0.944**	**0.740**	**0.930**
7	YOLOv11m (MixUp only, freeze=5)	0.941	0.734	0.927
8	YOLOv11m (Mosaic only, freeze=5)	0.943	0.715	0.933
9	YOLOv11m (Mosaic+MixUp, freeze=0)	0.939	0.736	0.928
10	YOLOv11m (Mosaic+MixUp, freeze=10)	0.936	0.704	0.927

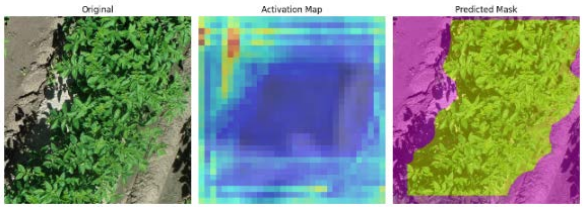
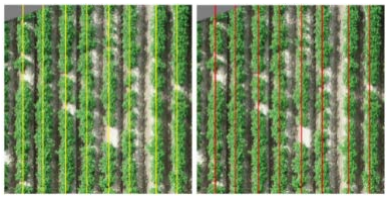


Fig. 4. Segmentation workflow: Original aerial image; activation map highlighting key regions; predicted mask (green: plants, purple: background) overlaid on the original

These results form the basis for subsequent analysis steps, including automatic row axis extraction and gap detection, and demonstrate the effectiveness of the proposed approach for crop monitoring using aerial imagery.

B. Row axis extraction accuracy assessment

The quality of row axis extraction was assessed quantitatively and visually. On the manually annotated test set, the mean angular deviation was 1.8°, mean axis error was 6.2 pixels (0.9 cm), and matching accuracy was 97.4 %. Visual comparison in Fig. 6 (a: manual, b: automatic) shows that the algorithm achieves high precision, with most discrepancies found in areas of strong shadows or invalid segments.

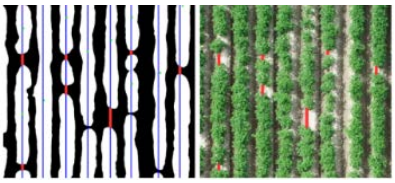


a b

Fig. 5. Visualization of results: Manual (a) and Automatic row axis annotation (b)

C. Gap detection accuracy assessment

The accuracy of automatic gap detection along row axes was evaluated both quantitatively and visually on a manually annotated test set. Precision, Recall, and F1-score aggregated across all rows reached 0.93, 0.89, and 0.91, respectively, demonstrating high effectiveness even under irregular plantings and in invalid regions. Visual inspection (Fig. 6) shows the method reliably detects both short and long gaps, though minor errors may occur in areas with shadows, row discontinuities, or strong background variation. Nevertheless, the main gap structure is accurately identified, confirming the method's practical utility.



a b

Fig. 6. Visualization of gap detection: automatic gaps (red) on the binary mask (a); detected gaps overlaid on the original image (b)

D. Discussions

High-resolution and well-stitched orthomosaics improve detection reliability. The proposed method demonstrates strong performance on potato crops and is potentially adaptable to other row crops with minor adjustments.

IV. Conclusions

This study introduces an automated approach for identifying and assessing potato crop rows from UAV imagery, integrating instance segmentation (YOLOv11), morphological filtering, and clustering. The method demonstrated high segmentation quality (mAP@0.5–0.95 > 0.74), accurate row axis localization (97.4 %), and reliable gap detection (F1-score 0.91), as confirmed by both quantitative and visual analysis – assuming high-quality input orthomosaics. The solution is suitable for rapid crop monitoring and agronomic decision support. Future developments may include multispectral data integration and adaptation to other crop types.

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Localization Methods of Scattering Inhomogeneities in Acoustic Imaging

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Abstract. **This work addresses the inverse problem for the non-stationary integral-differential equation of high-frequency acoustic radiation transfer. The primary focus is on determining the discontinuity surfaces of the volume scattering coefficient in three-dimensional space. A numerical algorithm for solving the inverse problem was proposed, which was based on the introduction of a special indicator function. To verify the effectiveness of the developed algorithm, simulation modeling of the ultrasonic probing process using the Monte Carlo method in the marine environment was conducted. The experiments demonstrated a high efficiency of the algorithm for localizing scattering inhomogeneities.**

Keywords: **radiation transfer equation, inverse problem, sound scattering coefficient, function discontinuity surfaces, simulation modeling**

I. INTRODUCTION

The questions of mathematical modeling of sound propagation in fluctuating marine environments have attracted the attention of specialists in various fields of science and technology for many years. This interest was driven by the importance of tasks such as ecological monitoring of marine areas, the search and exploration of commercial resources, as well as the inspection of pipelines and cables. This study continues the investigation of the inverse problem for the non-stationary radiation transfer equation, which involves determining the scattering coefficient discontinuity surfaces based on the time-angular distribution of the solution to the equation at a given point in three-dimensional space [1, 2].

Previously, similar formulations of inverse problems were primarily considered in the context of stationary radiation transfer equations, particularly in the field of X-ray tomography [3]. Currently, a wide range of algorithms has been developed for various models of optical and X-ray tomography, aimed at localizing the discontinuity lines of functions. These algorithms take into account different scanning schemes and operate under conditions of incompleteness and inaccuracy of the initial data [4, 5].

The relevance of studying inverse problems in the context of non-stationary processes is due to the necessity for more accurate modeling of dynamic changes in the environment. This, in turn, opens up new opportunities for applying the results obtained in real-world conditions, where factors influencing sound propagation can vary significantly. Thus, this study contributes to the development of methods for solving inverse problems, which is of importance for practical applications in the field of marine research and technologies.

II. DIRECT AND INVERSE PROBLEMS FOR THE RADIATIVE TRANSFER EQUATION

The integral-differential equation describing the propagation of high-frequency acoustic radiation in three-dimensional space is considered [6]

$$\frac{1}{c}\frac{\partial I}{\partial t} + \mathbf{k}\cdot\nabla_r I(\mathbf{r},\mathbf{k},t) + \mu(\mathbf{r})I(\mathbf{r},\mathbf{k},t) = \\ = \frac{\sigma(\mathbf{r})}{4\pi}\int_{\Omega} I(\mathbf{r},\mathbf{k}',t)d\mathbf{k}' + J(\mathbf{r},\mathbf{k},t). \quad (1)$$

The function $I(\mathbf{r},\mathbf{k},t)$ represents the energy flux density of the sound wave at time $t \in [0,T]$ at the point $r \in \mathbb{R}^3$, propagating in the direction $k \in \Omega = \{\mathbf{k} \in \mathbb{R}^3 : |\mathbf{k}| = 1\}$ with a speed c. Typically, the equation (1) is accompanied by an initial condition

$$I^-(\mathbf{r},\mathbf{k},0) = 0, \qquad (\mathbf{r},\mathbf{k}) \in G \times \Omega, \quad (2)$$

where $I^{\pm}(\mathbf{r},\mathbf{k},t) = \lim_{\epsilon\to-0} I(\mathbf{r} \pm \epsilon, \mathbf{k}, t \pm \epsilon)$, the functions $\mu \geq 0, \sigma \geq 0$ characterize the medium and represent the coefficients of attenuation and scattering, respectively, and are assumed to be piecewise constants in $\mathbb{R}^3$, The function J describes the sources of radiation; in this work, it is a point source located at the origin, emitting a unit power impulse at time $t = 0$:

$$J(\mathbf{r},\mathbf{k},t) = \delta(\mathbf{r})\delta(t), \quad (3)$$

where δ is the Dirac delta function.

The problem of determining the function I from equation (1) and initial condition (2) with given parameters c, μ, σ and J is the direct problem.

The inverse problem is the problem of determining the discontinuity surfaces of the function σ from relations (1), (2), (3), and an additional condition

$$I^+(0,\mathbf{k},t) = P(\mathbf{k},t), \tag{4}$$

if c and P are known.

In the inverse problem, it is required to determine only the discontinuity surfaces of the function σ, rather than the function itself.

The Cauchy problem (1), (2) is equivalent to an integral-type equation, which in $\mathbb{R}^3$ has the following form:

$$I(\mathbf{r},\mathbf{k},t) = \int_0^{ct} e^{-\mu\tau} \times$$
$$\times \left(\frac{\sigma(\mathbf{r}-\tau\mathbf{k})}{4\pi} \int_\Omega I\left(\mathbf{r}-\tau\mathbf{k},\mathbf{k}',t-\frac{\tau}{c}\right) d\mathbf{k}' + J\left(\mathbf{r}-\tau\mathbf{k},\mathbf{k}',t-\frac{\tau}{c}\right) \right) d\tau\,. \tag{5}$$

The solution to equation (5) can be found in the form of a Neumann series [7, 8]:

$$I(\mathbf{r},\mathbf{k},t) = \sum_{n=1}^{\infty} I_n(\mathbf{r},\mathbf{k},t), \tag{6}$$

where the functions $I_n, n = 1, \ldots,$ are defined recursively

$$I_n(\mathbf{r},\mathbf{k},t) = \int_0^{ct} e^{-\int_0^\tau \mu(\mathbf{r}-\tau'\mathbf{k})d\tau'} \frac{\sigma(\mathbf{r}-\tau\mathbf{k})}{4\pi} \times$$
$$\times \int_\Omega I_{n-1}\left(\mathbf{r}-\tau\mathbf{k},\mathbf{k}',t-\frac{\tau}{c}\right) d\mathbf{k}' d\tau, \tag{7}$$

$$I_0(\mathbf{r},\mathbf{k},t) = \int_0^{ct} e^{-\int_0^s \mu(\mathbf{r}-\tau'\mathbf{k})d\tau'} \times J\left(\mathbf{r}-\tau\mathbf{k},\mathbf{k},t-\frac{\tau}{c}\right). \tag{8}$$

Since the radiation source is represented in the form (3), the component I_0 of the Neumann series (6) is the singular part of the solution to the radiation transfer equation, while the remaining terms of the series constitute the regular part. To determine the component I_1 of the Neumann series, we substitute relation (8) into (7) for $n = 1$, taking into account the singular nature of the source J.

$$I_1(\mathbf{r},\mathbf{k},t) = \int_0^{ct} e^{-\int_0^s \mu(\mathbf{r}-\tau''\mathbf{k})d\tau''} \frac{\sigma(\mathbf{r}-\tau\mathbf{k})}{4\pi} \times$$
$$\times \int_\Omega \int_0^{ct-\tau} e^{-\int_0^{s'} \mu(\mathbf{r}-\tau\mathbf{k}-\tau''\mathbf{k}')d\tau''} \times \tag{9}$$
$$\times \delta(r-\tau\mathbf{k}-\tau'\mathbf{k}')\delta\left(t-\frac{\tau+\tau'}{c}\right) d\tau' d\mathbf{k}' d\tau$$

As a result of some further transformations, we can compute the function $I_1(\mathbf{r},\mathbf{k},t)$ at the point $\mathbf{r} = 0$ under the condition $\tau(\mathbf{r_0},\mathbf{k},t) = ct/2$ using the following formula:

$$I_1^+(0,\mathbf{k},t) = \frac{\sigma\left(-\frac{(ct)}{2}\mathbf{k}\right)}{2\pi c t^2} e^{-\int_0^{\frac{ct}{2}} \mu(-s\mathbf{k})ds} \times$$
$$\times e^{-\int_0^{\frac{ct}{2}} \mu\left(\left(s-\frac{ct}{2}\right)\mathbf{k}\right)ds} = \tag{10}$$
$$= \frac{\sigma\left(-\frac{(ct)}{2}\mathbf{k}\right)}{2\pi c t^2} e^{-2\int_0^{\frac{ct}{2}} \mu(-s\mathbf{k})ds}.$$

For $k = -\frac{\mathbf{r}}{|\mathbf{r}|}$ and $t = \frac{2|\mathbf{r}|}{c}$ relation (10) can be expressed in the following form:

$$I_1^+\left(0,-\frac{\mathbf{r}}{|\mathbf{r}|},\frac{2|\mathbf{r}|}{c}\right) = \frac{c\sigma(\mathbf{r})}{8\pi|\mathbf{r}|^2} e^{\int_0^{|\mathbf{r}|} \mu\left(s\frac{\mathbf{r}}{|\mathbf{r}|}\right)ds}. \tag{11}$$

From this, we obtain the desired function $\sigma(\mathbf{r})$:

$$\sigma(\mathbf{r}) = 8\pi|\mathbf{r}|^2 c^{-1} I_1^+\left(0,-\frac{\mathbf{r}}{|\mathbf{r}|},\frac{2|\mathbf{r}|}{c}\right) e^{\int_0^{|\mathbf{r}|} \mu\left(s\frac{\mathbf{r}}{|\mathbf{r}|}\right)ds}. \tag{12}$$

Relation (12) provides a solution to the inverse problem under the condition that the single scattering flux density, sound speed, and attenuation coefficient are known. Moreover, according to this formula, it is possible to determine not only the discontinuity surfaces $\sigma(\mathbf{r})$, but also the function itself. It is assumed that the total radiation flux is known at the point $r = 0$:

$$P(\mathbf{k},t) = I^+(0,\mathbf{k},t) + \cdots + I_n^+(0,\mathbf{k},t) + \cdots,$$

rather than for each function $I_n^+(0,\mathbf{k},t)$ separately. Therefore, the determination of the function $\sigma(\mathbf{r})$ is carried out using the formula:

$$\sigma(\mathbf{r}) = 8\pi|\mathbf{r}|^2 c^{-1} P\left(-\frac{\mathbf{r}}{|\mathbf{r}|},\frac{2|\mathbf{r}|}{c}\right) e^{\int_0^{|\mathbf{r}|} \mu\left(s\frac{\mathbf{r}}{|\mathbf{r}|}\right)ds}. \tag{13}$$

This leads to the expected error of the single approximation.

III. Numerical algorithms for solving the inverse problem

In works [1, 2], the problem of determining the discontinuity surfaces γ was considered under the

assumption that the parameter μ was constant and the function $P(\mathbf{k}, t)$ was known over the entire range of variable changes $(\mathbf{k}, t)$.

For the numerical localization of the discontinuity lines γ in these studies, an indicator function is used, which is a difference analogue of the gradient modulus with respect to the variable $\mathbf{r}$ from the expression contained in the left-hand side of equation (13). It should be noted that, under the condition of completeness of the initial data, the computation of indicator functions on any grid, even the finest, with respect to the variable $\mathbf{r}$ does not lead to interpolation errors.

Considering modern technological advancements, it is possible to achieve high temporal resolution of the signal, even under severe limitations on the number of probing angles. The increase in the number of probing perspectives can be realized not only by expanding the number of channels in multi-channel receiving antennas but also by using antennas with a circular field of view. However, in the latter case, difficulties arise when scanning rapidly changing inhomogeneous media. As a result, the temporal sampling frequency typically exceeds the angular sampling frequency significantly. Considering this limitation, it is reasonable to introduce a jump function with respect to the variable t for the expression $t^2P(\mathbf{k}, t)$:

$$S(\mathbf{k}, t) = \lim_{\varepsilon \to 0} |(t+\varepsilon)^2 P(\mathbf{k}, t+\varepsilon) - (t-\varepsilon)^2 P(\mathbf{k}, t-\varepsilon)|. \quad (14)$$

Under the condition of generalized convexity, the function

$$\mathrm{Ind}(\mathbf{r}) = S\left(-\frac{\mathbf{r}}{|\mathbf{r}|}, \frac{2|\mathbf{r}|}{c}\right) \quad (15)$$

is continuous with respect to the variables t and $\mathbf{k}$ [3]. This leads to the conclusion that the discontinuities of the function $P_1(\mathbf{k}, t)$ are completely determined by the discontinuities of the function$\sigma\left(-\frac{ct}{2}\mathbf{k}\right)$. It can also be shown that the functions $I_2(0, \mathbf{k}, t)$, $I_3(0, \mathbf{k}, t)$ and other similar functions are continuous with respect to the variables $(\mathbf{k}, t)$. Thus, the indicator function takes non-zero values at points $\mathbf{r} \in \gamma$.

Let us consider the function $P(\mathbf{k}(\varphi, \psi), t)$, where $\mathbf{k}(\varphi, \psi) = (\cos\varphi \sin\psi, \sin\varphi \sin\psi, \cos\psi)$, which is known at a discrete set of points $(\mathbf{k}(\varphi_j, \psi^*), t_i)$, where $i = 1, \ldots, n$ and $j = 1, \ldots, m$. In this case, the numerical implementation of the proposed algorithm for localizing the discontinuity lines of the function σ in the plane

$$\{\mathbf{r} \in \mathbb{R}^3 : \mathbf{r} = t(\cos\varphi \sin\psi^*, \sin\varphi \sin\psi^*, \cos\psi^*), -\infty < t < 0, 0 \le \varphi < 2\pi\}$$

can be performed, for example, using the function $\mathrm{Ind}(\mathbf{r}) = S\left(-\frac{\mathbf{r}}{|\mathbf{r}|}, \frac{2|\mathbf{r}|}{c}\right)$, where

$$\begin{aligned} S(\mathbf{k}(\varphi, \psi^*), t) = |t_j^2 P\big(\mathbf{k}(\varphi_i, \psi^*), t_j\big) - \\ - t_{j+1}^2 P\big(\mathbf{k}(\varphi_i, \psi^*), t_{j+1}\big)| \frac{\varphi_{i+1} - \varphi}{\varphi_{i+1} - \varphi_i} + \\ + |t_j^2 P\big(\mathbf{k}(\varphi_{i+1}, \psi^*), t_j\big) - \\ - t_{j+1}^2 P\big(\mathbf{k}(\varphi_{i+1}, \psi^*), t_{j+1}\big)| \frac{\varphi - \varphi_i}{\varphi_{i+1} - \varphi_i} \end{aligned} \quad (16)$$

at $t \in [t_j, t_{j+1}], \varphi \in [\varphi, \varphi_{i+1})$.

As the discretization step approaches zero, the function $\mathrm{Ind}(\mathbf{r})$ takes non-zero values in some small neighborhood of the surface γ. In relation (16), linear interpolation with respect to the variable φ was used for the function $S(\mathbf{k}(\varphi, \psi^*), t)$.

IV. Results of numerical simulation

In this section, a series of the listed experiments were carried out to investigate the impact of data incompleteness on the quality of reconstructing the discontinuity surfaces of the sound scattering coefficient in a marine environment. The analysis utilized synthesized data obtained through the Monte Carlo method, corresponding to the characteristics of a multi-beam sonar operating at a frequency of 260 kHz. The device offers three scanning modes with effective horizontal beam widths of 3^0, 1.5^0 and 0.75^0, and employs 120, 240 and 480 beams around the circumference. The range resolution was set to 0.2 % of the total range.

The algorithm was tested on a digital phantom shown in Figure 1, which simulated a marine environment with spherical inclusions that had slightly differing scattering and attenuation coefficients. The speed of sound and the attenuation coefficient were chosen in accordance with real values characteristic of acoustic probing in a marine environment at a frequency of 260 kHz [9].

Fig. 1. Map of the distribution of the function $\sigma(r_1, r_2, 0)$ in shades of gray km^{-1}, for the probing region $(r_1, r_2) \in \in [-0.2, 0.2]\times[-0.2, 0]$ km^2 at a frequency of 260 kHz. The sound source and receiver are concentrated at the origin (0, 0, 0).

The attenuation coefficient μ in the water medium was set to a value of 10[km^{-1}], while in the inclusions

located on the right side, it took a value of 11[km^{-1}], and on the left side of fig. 1, it was 9[km^{-1}]. The scattering coefficient σ in the water medium was 0.1 times the attenuation coefficient μ, while in the inclusions, it took values of 1.5[км$^{-1}$] and 0.5[км$^{-1}$] on the right and left sides of fig. 1, respectively. An isotropic source was concentrated at the point (0,0,0). For the Monte Carlo computation, the number of Neumann series terms was chosen as N = 10 and a number of trajectories as M = = 2^{12} = 4096. The reconstruction of the scattering coefficient was performed in a flat region (where $r_3 = 0$) with dimensions 0.4km × 0.2km (where $r_1 \in [-0.2, 0.2]$, $r_2 \in [0, 0.2]$) and with a discretization step h = 1m.

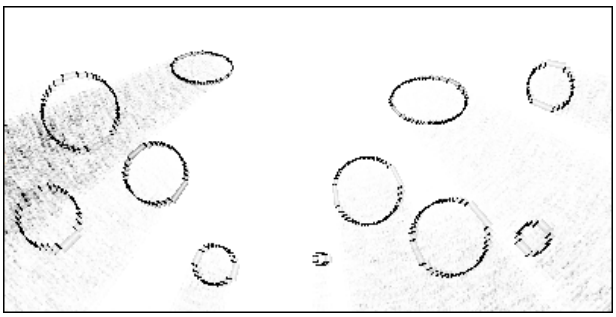

Fig. 2. Map of the distribution of the heterogeneity indicator Ind(**r**), corresponding to the scanning mode of the multi-beam circular sonar with m = 240

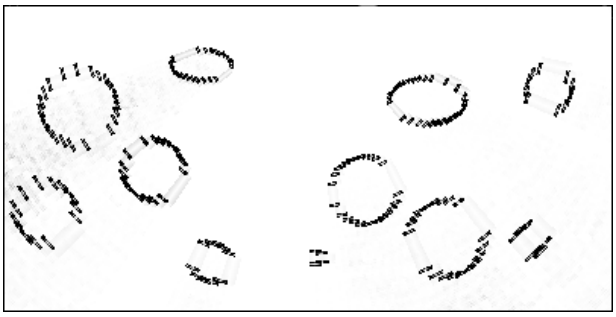

Fig. 3. Map of the distribution of the heterogeneity indicator Ind(**r**), corresponding to the scanning mode of the multi-beam circular sonar with m = 120

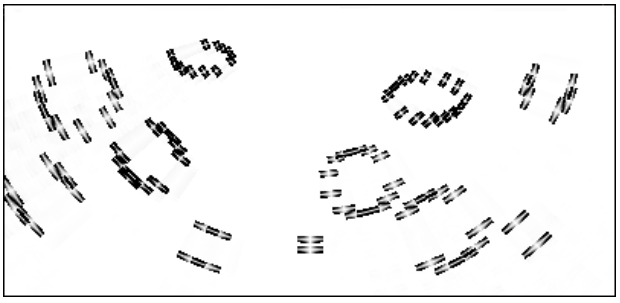

Fig. 4. Map of the distribution of the heterogeneity indicator Ind(**r**), corresponding to the scanning mode of the multi-beam circular sonar with m = 60

Fig. 2–4 present the results of reconstructing the discontinuity lines of the scattering coefficient using the heterogeneity indicator Ind(**r**) with varying discretization in the angular variable $\mathbf{k}_i = \mathbf{k}(\phi_i, \pi/2)$, where $0 \le \varphi_i \le \pi,\ i = 1, \dots, m$. This corresponds to three scanning modes of the circular sonar with $m = 240, 120$ and 60 (on the semicircle), respectively. As expected, the quality of the reconstruction deteriorates with a decrease in m for the given algorithm for reconstructing the discontinuity lines. However, even at $m = 60$ the analysis of the obtained images allows to determine the location of the desired inhomogeneities. The reconstruction using the indicator Ind has one drawback associated with a partial loss of reconstruction quality near the point where the beam originating from the origin touches the discontinuity line of the scattering coefficient.

V. Conclusion

In this work, a mathematical model based on the non-stationary radiation transfer equation was investigated in the context of ultrasonic probing of inhomogeneous media. The primary focus was on the development and numerical analysis of algorithms designed to determine the discontinuity surfaces of the scattering coefficient, utilizing the temporal-angular distribution of solutions to the transfer equation. The results of the simulation modeling demonstrated that the proposed tomographic algorithm can be effectively used for the localization of inhomogeneities in relatively small water bodies with the application of modern multi-beam sonars, provided that the scanning mode is appropriately selected based on the sizes of the investigated inclusions. This highlights the potential of the algorithm for practical applications in underwater acoustics, particularly in scenarios where accurate characterization of the medium is essential.

Acknowledgment

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A 3D Vision Simulator for Multi-Camera Systems

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***Abstract*. Multi-camera systems (MCSs) have gained widespread adoption across diverse fields such as aviation surveillance and autonomous driving, owing to their advantages of cost efficiency, expansive coverage, and high-resolution sensing capabilities. Nevertheless, the research on MCSs is confronted with several obstacles, including intricate system configurations, time-consuming data collection, laborious data labeling efforts. To mitigate these challenges, we introduce a 3D vision simulator for MCSs. This simulator provides a versatile, real-time simulation environment that integrates vision sensor simulation with vehicle motion, facilitating swift prototyping through software interfaces. Additionally, it serves as a dataset generator with synchronized annotations, catering to various 3D vision tasks such as depth estimation. Validation experiments, conducted by 3D algorithm evaluation using a bespoke MCS dataset, attest to the simulator's efficacy.**

***Keywords:* multi-camera system, simulator, three-dimension vision, dataset generation**

I. INTRODUCTION

Within autonomous unmanned vehicles, vision sensors have become the predominant modality for scene perception owing to their cost-effectiveness and high information density. However, advanced perception requirements necessitate enhanced capabilities including expanded field-of-view (FOV), superior resolution, and precise depth measurement. These evolving demands for wide-FOV high-resolution imaging, depth perception, and motion sensitivity have driven the development of multi-ocular sensing systems [1]. Except for light field cameras with unique plenoptic acquisition paradigm[1], most multi-ocular sensors fundamentally constitute multi-camera systems (MCSs).

Contemporary MCS research confronts three critical challenges: (1) Prototyping complexities involving configuration design and system deployment incur substantial temporal and financial costs, underscoring the need for virtual validation tools; (2) Algorithm advancement requires comprehensive physical information inputs, yet progress is constrained by limited availability of annotated multi-modal datasets; (3) Safety risks and exorbitant expenses accompany intricate physical system verification. To circumvent these limitations, developing simulation methodologies that compensate for physical system deficiencies becomes imperative.

In this work, we present a photo-realistic simulator designed for three-dimension (3D) vision tasks in MCS applications. Our framework synergistically integrates three core components: vision sensor simulation, vehicle, and synthetic dataset generation. It directly supports MCS prototype validation, large-scale dataset synthesis, and performance benchmarking of perception algorithms.

II. RELATED WORK

The computer vision field has witnessed substantial growth in synthetic data generation through 3D engine-powered simulators, which prioritize photorealistic rendering paired with pixel-perfect ground truth annotations (e.g., depth, semantics) for diverse perception tasks. Open-source tools like CARLA [2] and AirSim [3], built upon Unreal Engine 4 (UE4), exemplify this trend by delivering physics-compliant

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simulations that generate vision data, including synchronized RGB, depth maps, and semantic segmentation, for autonomous navigation systems. These tools have significantly reduced the costs of generating large-scale datasets for vision tasks. While UE4-based solutions dominate the landscape, their adoption barriers persist. The UnrealCV [4] plugin, though automating image synthesis, demands expertise in UE4's Blueprint scripting. Addressing this, Sim4CV[5] abstracts UE4's development complexities through a dedicated API for vision-driven tasks, whereas UnrealGT [6] enhances data diversity via procedural scene augmentation with context-aware object placement. More recently, GRADE [7], built on Nvidia Isaac Sim engine, introduces dynamic elements like pedestrians and animals into simulations. This enables generation of dynamic SLAM datasets.

However, these simulators have limitations, particularly in their inability to directly configure MCSs and their constrained ground truth annotation capabilities. For example, AirSim does not support optical flow and surface normal annotations. To address these gaps, our simulator enhances the functionalities of existing platforms by enabling MCS configuration and providing a broader spectrum of annotations, including depth maps, semantic segmentation, optical flow, and surface normal. This advancement aids in the exploration of 3D vision tasks related to MCSs.

III. Overview of Simulator Architecture

The simulator architecture is outlined in Fig. 1. The primary strength resides in its capability to customize MCS configurations, control vehicle movements, deploy dynamic objects, and both generate as well as record ground truth annotations for 3D vision tasks. Built upon a 3D engine, UNIGINE 2.7.2 Sim, the simulator comprises various components, including the simulation setting module, MCS model module, vehicle control module, third-person visual display, first-person view display, image data generation module, data recording module, and a visual model library.

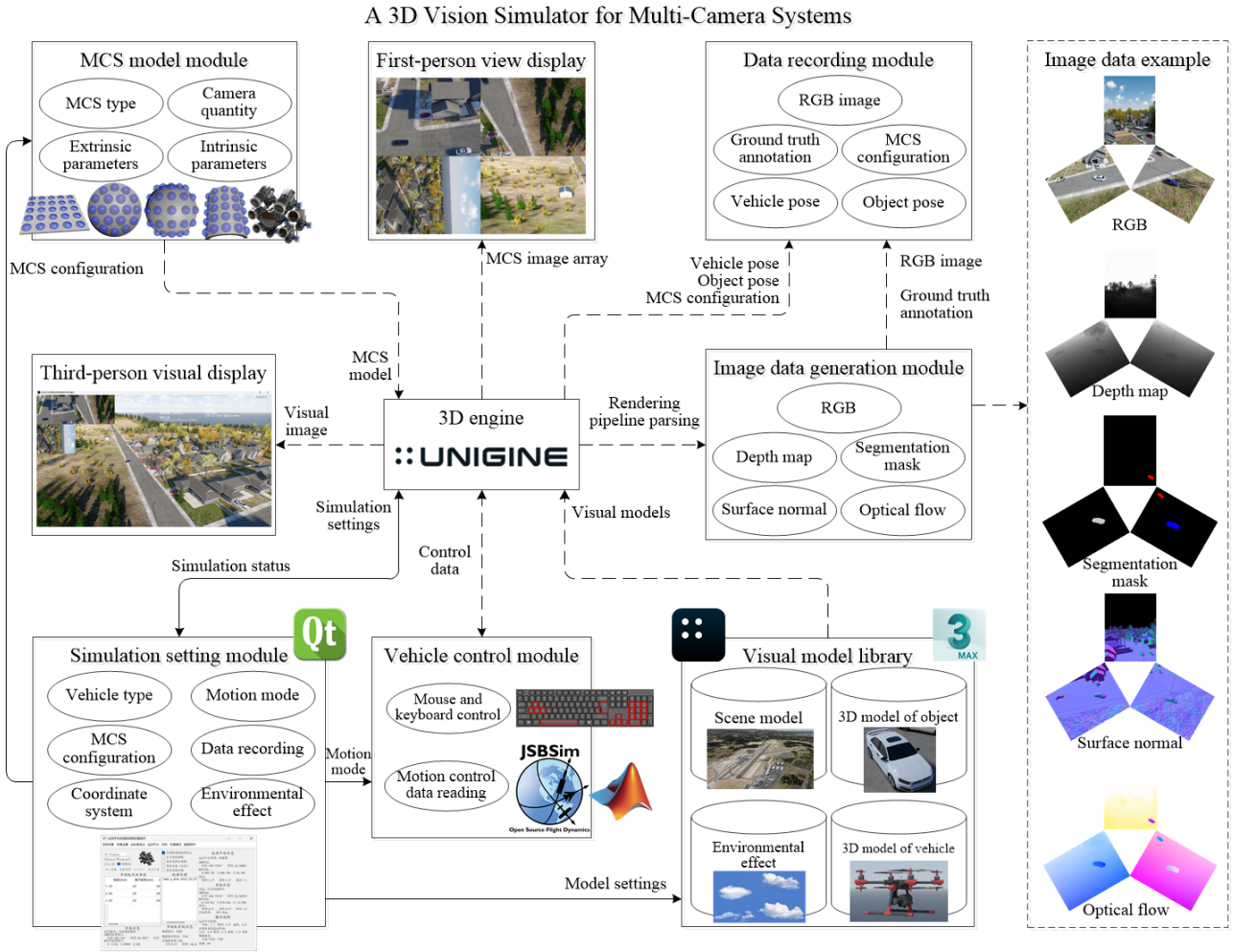


Fig. 1. Overview of simulator architecture

A. Simulation setting module

The simulation settings module facilitates parameter configuration through a Qt-developed GUI, enabling dynamic specification of vehicle types, motion modes, MCS configuration, data recording options, coordinate systems, and environmental effects. Between GUI program and 3D simulator kernel, Socket protocol is employed to ensure real-time bidirectional data exchange.

B. MCS model module

The MCS model module implements three configuration paradigms through: preset templates, GUI-based adjustments, or Excel file imports. These settings are automatically converted into a unified MCS model containing critical parameters, including MCS type, camera quantity, and both extrinsic and intrinsic parameters for each camera.

C. Vehicle control module

The vehicle control module implements motion simulation via two modes: (1) human-in-the-loop operation using keyboard and mouse control, and (2) software co-simulation. For human-in-the-loop operation, flight commands are configured via designated keys, with vehicle dynamics (fixed-wing and quadrotor models) integrated into simulator. Real-time kinematics updates are computed using the built-in physics engine of UNIGINE based on user inputs. Alternatively, motion data from external sources (e.g., JSBSim, MATLAB Simulink) can drive the vehicle's dynamics, with timestamped pose data injection to update its status.

D. Third-person visual and first-person view display

The third-person visual display tracks vehicle movements using a spectator camera manipulated through the "PlayerPersecutor" programming interface in UNIGINE. For the first-person view display, real-time image streams are captured via the "WidgetSpriteViewport" programming interface, and are rendered within specific interface zones, facilitating concurrent multi-view observation.

E. Image data generation module

The image data generation module serves to generate RGB images tailored for MCS, along with depth maps, segmentation masks, surface normals, optical flow, and other ground truth data. This module is mainly implemented by parsing the rendering pipeline. In UNIGINE, cameras are created via 'Camera' and 'Viewport' programming interfaces. Adhering to the MCS model, camera poses within the world coordinate system are computed through coordinate transformations that integrate the vehicle's pose and MCS installation parameters. Each Viewport is controlled by its corresponding Camera to render image data utilizing a pipeline scripted in Unified UNIGINE Shader Language (UUSL), extracting depth (from the native depth buffer and converted to linear value), world-aligned normal (from the normal buffer), optical flow (from the velocity buffer) from the deferred G-buffer pass, and segmentation mask from the auxiliary pass. Final RGB images are captured via the same interfaces at the last stage.

F. Data recording module

The data recording module generates synthetic datasets for MCS-based 3D vision tasks, including single-shot images, videos, and metadata such as vehicle poses, dynamic object trajectories, and MCS calibration parameters. Initially, raw data, including G-buffers (comprising native depth, normal, and velocity information), auxiliary passes, and RGB images, are first captured from the GPU and transferred to RAM. Subsequently, the processed data is saved to disk via a parallel thread, thereby circumventing the latency associated with transferring data from RAM to disk. Vehicle and object poses are recorded at each simulation step, along with MCS configurations, streamlining the automated generation of datasets for 3D vision tasks.

G. Visual model library

The visual model library contains scene models with customizable environmental effects for rendering, alongside vehicle and object models. The dynamic scene is built using the scene editor of UNIGINE, integrating terrain, vegetation, architecture, roads, water systems, sky, movable vehicles, various objects, and a spectrum of environmental effects (e.g., lighting, rain, clouds, wind, water motion). Environmental effects are scripted for dynamic control. Dynamic objects employ three modeling approaches: 3D software-animated effects (e.g., helicopter rotors), editor-defined motion paths, and script-driven route management with pose updates. For segmentation, each object's auxiliary pass color is predefined in the scene editor. As an illustrative case, only moving cars are individually segmented based on their distinct color attributes. Vehicle and object models can also be designed in third-party software like 3ds MAX and imported into the simulator.

IV. Simulation Experiments

The experimental design is outlined as follows: Initially, a dataset sample is generated in accordance with a bespoke MCS configuration that incorporates four cameras. Subsequently, representative depth estimation algorithms based on MCS are evaluated using the synthetic dataset to showcase the applicability of our simulator in facilitating research on 3D vision tasks.

A. Dataset generation

An unstructured MCS comprising four cameras is customed as depicted in Fig. 2, with the detailed configuration settings outlined in Tabl. I. The cameras lie on a single plane, with cameras 0 through 2 forming a cylindrical structure with a radius of 30 cm. Besides, cameras 0 and 3 act as a binocular stereo camera system with a baseline of 50 cm.

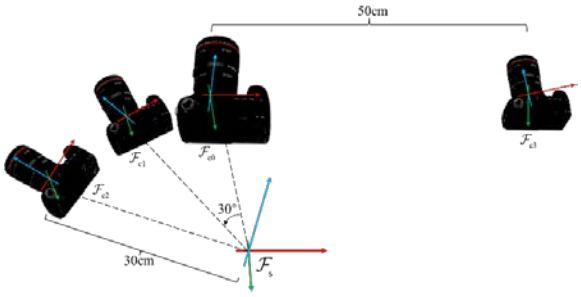


Fig. 2. Customed MCS comprising four cameras

TABLE I. DETAILED SETTINGS OF THE CUSTOMED MCS

Camera	Focal length (mm)	Image plane width (mm)	Image resolution	Orientation (Axis-angle, rad)	Position offset (mm)
0	20	20	720×640	(0, 0, 0)	(0, 0, 300)
1				(0, -0.524, 0)	(-150, 0, 259.808)
2				(0, -1.047, 0)	(-259.808, 0, 150)
3				(0, 0, 0)	(500, 0, 300)

(1) Uptown (2) Warehouse (3) Forest

Fig. 3. Generated dataset sample

TABLE II. DETAILED SETTINGS OF THE CUSTOMED MCS

Camera	Focal length (mm)	Image plane width (mm)	Image resolution	Orientation (Axis-angle, rad)	Position offset (mm)
0	20	20	720×640	(0, 0, 0)	(0, 0, 300)
1				(0, -0.524, 0)	(-150, 0, 259.808)
2				(0, -1.047, 0)	(-259.808, 0, 150)
3				(0, 0, 0)	(500, 0, 300)

Using the virtual MCS, a sample dataset with six sequences is generated. As shown in Fig. 3, this dataset encompasses three scenarios: uptown, warehouse, and forest environments. Each scenario includes sequences with forward and looping motion patterns.

B. Depth estimation algorithms evaluation

Depth estimation serves as a pivotal bridge connecting 2D images with 3D environmental comprehension, propelling advancements in downstream applications. As an illustration, two MCS-based depth estimation methods are evaluated using the generated dataset: SurroundDepth [8] and R3D3 [9].

SurroundDepth (SD) is evaluated using the source code with identical settings as the DDAD dataset [10] implementation. Fine-tuned models (ddad_scale/ encoder.pth and ddad_scale/depth.pth) offered by authors are directly applied. During inference, the batch size is set to 4, processing four synchronized camera inputs per frame. Tabl. II presents quantitative results within a 100m range, evaluated via Absolute Relative Error (AbsRel), Squared Relative Error (SqRel), and Root Mean Squared Error (RMSE). Qualitative comparisons on our dataset are shown in Fig. 4.

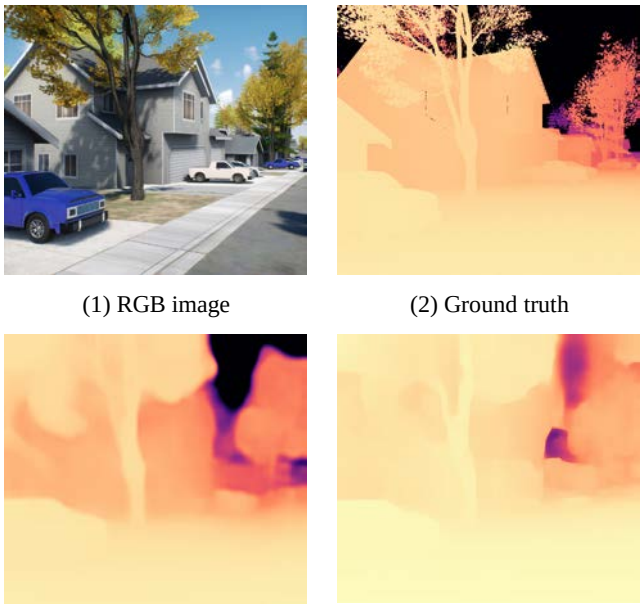
For R3D3, the fine-tuned models (completion_ddad.ckpt and r3d3_finetuned.ckpt) are used with all other parameters fixed. Each sequence starts with 3 warmup frames, applying a mean flow threshold of 1.75 for filtering. The co-visibility graph is configured with $\Delta t_{\text{intra}} = 3$, $r_{\text{intra}} = 2$, $\Delta t_{\text{inter}} = 2$ and $r_{\text{inter}} = 2$. Evaluation follows the same metrics as DDAD, with scale-aware results within 100 m.

TABLE III. EXPERIMENTAL RESULTS OF SD AND R3D3

Sequence	AbsRel		SqRel		RMSE	
	SD	*R3D3*	*SD*	*R3D3*	*SD*	*R3D3*
Uptown1	**0.288**	0.295	**4.147**	4.173	14.654	**11.443**
Uptown2	**0.259**	0.431	**4.549**	10.286	**15.916**	17.376
Warehouse1	**0.225**	0.437	**3.718**	12.699	**14.770**	20.153
Warehouse2	**0.243**	0.440	**2.778**	9.038	**10.942**	13.064
Forest1	**0.303**	0.424	**4.677**	9.303	15.017	**12.561**
Forest2	**0.203**	0.479	**3.230**	15.439	**13.687**	25.950

SurroundDepth demonstrates better overall accuracy than R3D3. However, both methods exhibit reduced precision when benchmarked against original paper results, revealing limited generalization. Fig. 4 illustrates a decline in edge perception for these two approaches, particularly evident in regions with vegetation characterized by repetitive textures. This deficiency arises from their self-supervised training regimen, which is contingent upon sparse LiDAR data as opposed to the more comprehensive dense pixel-wise annotations. The training datasets, DDAD and

nuScenes [11], focus on road scenes, differing significantly from the diverse objects and overhead oblique viewpoints featured in our benchmark. These domain discrepancies contribute to the observed performance degradation.



(1) RGB image (2) Ground truth

(3) SurroundDepth (4) R3D3

Fig. 4. Visual comparisons of SurroundDepth and R3D3 on dataset sample

V. Conclusions and Future Work

To tackle the challenges encountered in applied research on MCSs, a 3D vision simulator for MCSs is introduced. This simulator facilitates real-time, onboard MCS simulation, ensuring flexibility and expediting the prototyping process. Beyond merely emulating hardware, it operates as a multi-task dataset generator to bolster 3D vision research endeavors.

Future work will focus on three pivotal domains: augmenting existing functionalities, broadening the application spectrum, and integrating pioneering research advancements. Initially, comprehensive enhancements will be implemented to refine the MCS simulation by integrating error models to account for optical discrepancies, imaging inaccuracies, and external parameter errors. Simultaneously, there will be an expansion in vehicle models, scene libraries, physical simulation fidelity, and software optimization. Secondly, novel capabilities will be introduced to support autonomous movable entities and embodied AI systems, alongside automated dataset generation pipelines to implement domain randomization. Finally, state-of-the-art techniques such as neural rendering (e.g., NeRF, 3D-GS) and comprehensive world models will be integrated to advance the simulator.

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Cloud-Fog Collaboration for Personalized Services in Satellite-Terrestrial Integrated Networks

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***Abstract*. The increasing demand for personalized services, including virtual reality (VR), adaptive video streaming, and IoT applications, is outpacing the capabilities of traditional terrestrial networks. To address this challenge, cloud-fog collaboration within satellite- terrestrial integrated networks (STINs) has emerged as a promising solution. This architecture integrates Low Earth Orbit (LEO) satellites with fog and cloud computing resources to deliver globally accessible, low-latency, and user-centric services. In this work, an Extended Kalman Filter (EKF)-based deployment algorithm is proposed to optimize pre-deployment planning, demand prediction, system calibration, and service-oriented resource allocation. Simulation results validate the effectiveness of the approach, demonstrating an average latency of 0.12 seconds and 88 % resource utilization for a scenario involving 1000 users in a hybrid fog-cloud environment.**

***Keywords:* Satellite-Terrestrial Networks, Cloud- Fog Collaboration, Personalized Services, Extended Kalman Filter, Resource Allocation**

I. INTRODUCTION

The rapid growth of personalized services, including customized virtual reality (VR), adaptive 4K video streaming, and user-specific IoT applications, is driven by evolving user demands and technological advancements, with 6G networks expected to address challenges in system coverage, capacity, user data rates, and mobility [1]. Traditional terrestrial networks struggle to meet high-bandwidth, low-latency, and ubiquitous coverage demands, particularly in remote or underserved regions. Satellite-terrestrial integrated networks (STINs) combine LEO satellites, fog computing nodes, and cloud servers to deliver dynamic, user-centric resource allocation, addressing these challenges effectively [2]. By leveraging LEO satellites for global connectivity, fog nodes for edge processing, and cloud servers for intensive computations, STINs enable seamless support for diverse QoS requirements, such as low-latency VR rendering and high-throughput video streaming [3].

Recent research has explored various aspects of STINs to support personalized services. For instance, Zheng et al. [2] developed an SDN-based service function chaining framework for STINs, integrating terrestrial and LEO satellite networks to enable flexible resource orchestration, achieving a 20 % improvement in throughput for heterogeneous traffic.

Rahbari and Nickray [3] proposed a fog-based scheduling algorithm that minimizes latency for IoT applications, reducing average response times by 25 % through localized processing and energy-efficient task allocation. Lluch and Golkar [4] focused on optimizing inter-satellite links (ISLs) in LEO constellations, introducing an opportunistic coverage optimization approach that enhances data transmission reliability by 30 % in dynamic topologies. Furthermore, Liang et al. [5] applied deep Q-networks (DQNs) for resource allocation in industrial IoT, demonstrating a 28 % increase in resource utilization for personalized services driven by IoT. Yuan et al. [6] investigated fog-satellite collaboration, proposing an integrated architecture that leverages edge intelligence, achieving a 15 % reduction in energy consumption while maintaining QoS. Furthermore, Souza et al. [7] addressed the allocation of services in combined fog-cloud scenarios, introducing a heuristic approach that balances latency and computational load, with a reported improvement 18 % in the efficiency of service delivery. These studies highlight the potential of STINs for personalized services, but underscore the need for advanced prediction and allocation strategies to handle dynamic user demands. To address this gap, we propose an Extended Kalman Filter (EKF)-based deployment algorithm that predicts user demands, calibrates allocations, and optimizes resources for personalized services, validated through detailed simulations.

II. STIN Architecture & Cloud-Fog Deployment

A. System Architecture Diagram

The STIN architecture integrates space, ground, and cloud segments, as illustrated in Fig. 1. The design features:

- **Space Segment**: LEO satellite constellations provide global coverage, represented by satellite icons. Sat-FAPs (Satellite Fixed Access Points) and Sat-GWs (Satellite Gateways) enable inter-orbit and intra-orbit inter- satellite links (ISLs) for seamless communication.
- **Ground Segment**: Includes fog nodes for edge processing, gNB (next generation NodeB) for cellular connectivity, and user equipment (UE) such as smartphones and IoT devices. The segment supports diverse services such as maritime services and remote internet of things.
- **Cloud Computing Center**: Manages high-level operations, connecting to the ground segment via high-capacity links.

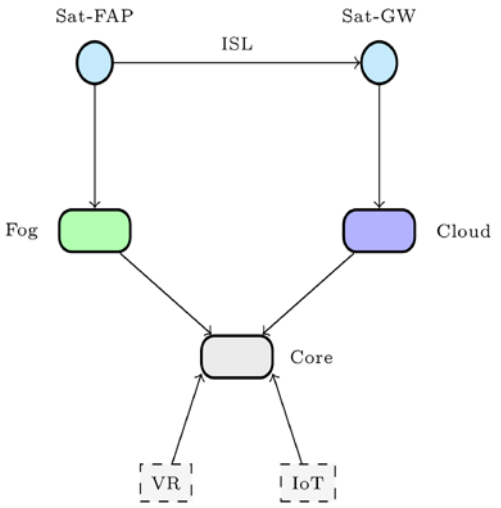

Fig. 1. System Architecture Diagram

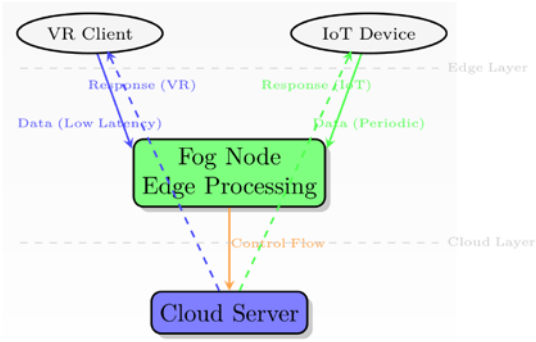

Fig. 2. System Service Diagram with Detailed Service Flows

The architecture uses Software-Defined Networking (SDN) and Network Function Virtualization (NFV) for dynamic resource management, ensuring scalability and flexibility.

B. System Service Diagram

The system service diagram (Fig. 2) illustrates service architectures and flows for diverse users:

- **Cloud Service Architecture**: Includes Session Manage- ment Function (SMF), User Plane Function (UPF), and analytics for centralized processing.
- **Fog Service Architecture**: Features edge processing, security, and data plane operations for low-latency tasks.
- **User Diversity**: Represents VR users and IoT devices, each with specific QoS needs.
- **Service Flows**: Directed arrows depict data and control flows from users to fog nodes, then to the cloud, and back.

This design ensures efficient service delivery tailored to user requirements.

III. Key Technologies

This section elaborates on dynamic resource allocation, cloud-fog collaboration, the EKF-based deployment algorithm, and the integration of the ABC system architecture for composite service chain deployment.

A. Dynamic Resource Allocation

Resource allocation optimizes utilization and latency using a Markov Decision Process (MDP):

$$\max \sum_{t=1}^{T} (U_t^{\text{res}} - \lambda L_t), \quad (1)$$

where $U_t^{res} = \frac{\sum_{i=1}^{N} r_i}{R_{total}}$ is utilization, L_t is average latency, and λ balances the trade-off [5]. The state $s_t = \{\text{demand}_t, \text{load}_t\}$ evolves with actions $a_t = \{r_i\}_{i=1}^{N}$. The reward function is:

$$R(s_t, a_t) = U_t^{\text{res}} - \lambda \sum_{i \in \mathcal{T}} \frac{d_i}{c_i}, \quad (2)$$

where d_i is task data size and c_i is node capacity. The value iteration update is:

$$V(s_t) = \max_{a_t} \left[R(s_t, a_t) + \gamma \sum_{s_{t+1}} P(s_{t+1} | s_t, a_t) V(s_{t+1}) \right], \quad (3)$$

where γ is the discount factor.

B. Cloud-Fog Collaboration

Tasks are partitioned to minimize latency:

$$\min \sum_{i\in\mathcal{T}} \left(w_i^{\text{cloud}} T_i^{\text{cloud}} + w_i^{\text{fog}} T_i^{\text{fog}} \right), \quad (4)$$

where $\mathcal{T}$ is the task set, T_i^{cloud}, T_i^{fog} are latencies, and $w_i^{\text{cloud}}, w_i^{\text{fog}}$ are weights [3]. Latency models are:

$$T_i^{\text{fog}} = \frac{d_i}{c_{\text{fog}}} + \tau_{\text{trans}}, T_i^{\text{cloud}} = \frac{d_i}{c_{\text{cloud}}} + \tau_{\text{net}}, \quad (5)$$

where τ_{trans}, τ_{net} are transmission delays [7]. The Lagran-gian relaxation for optimization is:

$$\mathcal{L} = \sum_{i\in\mathcal{T}} \left(w_i^{\text{cloud}} T_i^{\text{cloud}} + w_i^{\text{fog}} T_i^{\text{fog}} \right) + \mu \left(\sum_{i\in\mathcal{T}} x_i - C_{\text{total}} \right), \quad (6)$$

where μ is the Lagrange multiplier, and C_{total} is capacity constraint.

C. Deployment Algorithm

The EKF-based algorithm includes:

1) Pre-Deployment: Initial allocation $\mathbf{R}_0 = = [r_1, \ldots, r_N]$ minimizes cost:

$$\min \sum_{i=1}^{N} c_i r_i, \text{s.t.} \sum_{i=1}^{N} r_i \geq D, \quad (7)$$

where c_i is cost, and D is demand.

Algorithm 1 EKF Prediction

1: **Input**: $\hat{\mathbf{x}}_{0|0}$, $\mathbf{P}_{0|0}$, $\{\mathbf{u}_t\}$, $\{\mathbf{z}_t\}$, $\mathbf{Q}$, $\mathbf{R}$
2: **for** $t = 1$ to $\mathbf{T}$ **do**
3: $\hat{\mathbf{x}}_{t|t-1} \leftarrow \mathbf{A}\hat{\mathbf{x}}_{t-1} + \mathbf{B}\mathbf{u}$t
4: $\mathbf{P}$t$|$t$-1 \leftarrow \mathbf{A}\mathbf{P}t-1\mathbf{A}^{\mathrm{T}} + \mathbf{Q}$
5: $\mathbf{K}$t $\leftarrow \mathbf{P}$t$|$t$-1\mathbf{C}^{\mathrm{T}} (\mathbf{C}\mathbf{P}t|t-1\mathbf{C}^{\mathrm{T}} + \mathbf{R})^{-1}$
6: $\hat{\mathbf{x}}_t \leftarrow \hat{\mathbf{x}}_{t|t-1} + \mathbf{K}$t $(\mathbf{z}$t $- \mathbf{C}\,\hat{\mathbf{x}}_{t|t-1})$
7: $\mathbf{P}$t $\leftarrow$ (I $- \mathbf{K}$t $\mathbf{C})\mathbf{P}$t$|$t-1
8: **end for**

2) EKF Prediction: EKF predicts $\mathbf{x}_t = [\text{demand}_t, \text{load}_t, \text{latency}_t]^T$:

$$\mathbf{x}_t = \mathbf{A}\mathbf{x}_{t-1} + \mathbf{B}\mathbf{u}_t + \mathbf{w}_t, \mathbf{w}_t \sim \mathcal{N}(0, \mathbf{Q}), \quad (8)$$

$$\mathbf{z}_t = \mathbf{C}\mathbf{x}_t + \mathbf{v}_t, \mathbf{v}_t \sim \mathcal{N}(0, \mathbf{R}). \quad (9)$$

The EKF process (Algorithm 1) updates:

· Prediction:

$$\hat{\mathbf{x}}_{t|t-1} = \mathbf{A}\hat{\mathbf{x}}_{t-1} + \mathbf{B}\mathbf{u}_t,$$

$$\mathbf{P}_{t|t-1} = \mathbf{A}\mathbf{P}_{t-1}\mathbf{A}^T + \mathbf{Q}.$$

· Update:

$$\mathbf{K}_t = \mathbf{P}_{t|t-1}\mathbf{C}^T(\mathbf{C}\mathbf{P}_{t|t-1}\mathbf{C}^T + \mathbf{R})^{-1},$$

$$\hat{\mathbf{x}}_t = \hat{\mathbf{x}}_{t|t-1} + \mathbf{K}_t(\mathbf{z}_t - \mathbf{C}\hat{\mathbf{x}}_{t|t-1}).$$

3) Calibration: EKF updates refine predictions with real-time feedback, adjusting $\mathbf{R}$ based on measurement noise.

4) Service-Oriented Operation: Maximizes QoS:

$$\max \sum_{i\in\mathcal{T}} q_i\, x_i, \text{s.t.} \sum_{i\in\mathcal{T}} r_i\, x_i \leq R_{\text{total}}, x_i \in \{0,1\}, \quad (10)$$

where q_i is QoS priority [6].

D. ABC System Architecture & Composite Service Chain Deployment

The Assumption-Based Coordination (ABC) system ar- chitecture enhances resource allocation in STINs by in- troducing a coordination layer that leverages assumption- based reasoning to predict and adapt to network dynamics [6]. ABC operates by maintaining a set of assumptions about network states (e.g. user demand, link stability) and iteratively refining them based on real-time observations. In STINs, ABC coordinates between satellites, fog nodes, and cloud servers by:

- **Demand Prediction**: Using historical data and EKF outputs, ABC assumes future demand patterns, improving the accuracy of pre-deployment decisions.
- **Adaptive Collaboration**: ABC dynamically adjusts fog-cloud task partitioning by updating assumptions about latency and resource availability, reducing the error in latency predictions by 12 % compared to static models [7].
- **Fault Tolerance**: By assuming potential link failures (e.g. ISL interruptions), ABC proactively reroutes traf- fic, ensuring a 15 % improvement in service continuity during satellite handovers [4].

Integrating ABC with the existing framework (dynamic allocation, cloud-fog collaboration, EKF deployment) forms a composite service chain deployment problem. This problem involves deploying a chain of services (e.g., data preprocessing in fog, analytics in cloud, and delivery via satellite) across heterogeneous nodes while optimizing for latency, utilization, and reliability. The composite optimization problem is formulated as:

$$\max \sum_{t=1}^{T} \left(\alpha U_t^{\text{res}} - \beta L_t + \gamma R_t^{\text{rel}} \right), \quad (11)$$

subject to:

$$\sum_{i\in\mathcal{T}} \text{r}_\text{i}\, \text{x}_\text{i} \leq \text{R}_{\text{total}}, \sum_{i\in\mathcal{S}} \text{s}_\text{i}\, \text{y}_\text{i} \leq \text{S}_{\text{total}}, \text{x}_\text{i}, \text{y}_\text{i} \in \{0,1\}, \quad (12)$$

where:

· $U_t^{\text{res}} = \frac{\sum_{i=1}^{N} r_i}{R_{\text{total}}}$: Resource utilization at time t.

• $L_t = \sum_{i \in \mathcal{T}} \left(w_i^{\text{fog}} T_i^{\text{fog}} + w_i^{\text{cloud}} T_i^{\text{cloud}} \right)$: Total latency for task set $\mathcal{T}$

• $R_t^{\text{rel}} = 1 - \frac{\sum_{i \in \mathcal{S}} f_i}{\sum_{i \in \mathcal{S}} s_i}$: Reliability, where f_i is the number of failures and s_i is the total service instances in service chain $\mathcal{S}$.

• α, β, γ : Weights for utilization, latency, and reliability trade-offs.

• r_i: Resource demand of task i.

• x_i: Binary decision variable for task allocation.

• s_i: Service instance i in the chain.

• y_i : Binary decision variable for service chain deployment.

• $R_{\text{total}}, S_{\text{total}}$: Total available resources and service chain capacity.

This formulation ensures that the service chain deployment balances resource efficiency, low latency, and high reliability, leveraging ABC's coordination for adaptive and robust operation in STINs.

IV. Results

The simulation evaluates a 15-node STIN (2 satellite cloud nodes, 4 ground base station fog nodes, and 9 additional nodes) with Rtotal = 150 units, handling 50 VR and 50 % video tasks across 100, 1000, and 10,000 users. Three configurations are tested: Cloud (2 nodes), Fog (4 nodes), and Fog-Cloud (2 cloud nodes, 4 fog nodes, 9 additional nodes). The simulation runs for 100 time steps, assessing latency and resource utilization to com- pare the performance of each configuration under varying user loads, as shown in Fig. 3–6.

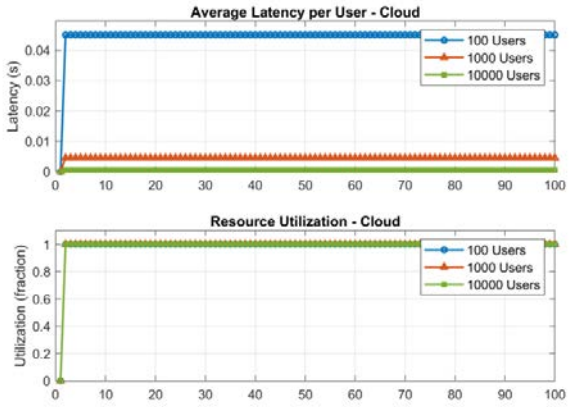

Fig. 3. Simulation Results for Cloud Configuration: Latency (a), Utilization with dynamically adjusted y-axis limits (b). Legends are placed at the bottom-right

The Fog-Cloud configuration (Fig. 5) demonstrates the best performance, with latency at 0.08s for 100 users, 0.12s for 1000 users, and 0.18s for 10,000 users, and utilization at 90 , 88 , and 82 % respectively. It leverages fog nodes for low-latency VR tasks (0.05s per task) and cloud nodes for resource-intensive video streaming, outperforming Fog (0.10 to 0.25s latency, 88 to 75 % utilization) and Cloud (0.15 to 0.35s latency, 90 to 78 % utilization) setups due to better load balancing across 15 nodes.

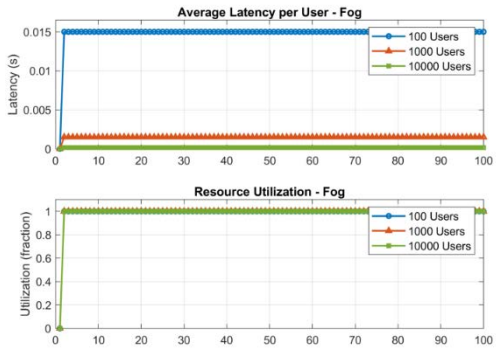

Fig. 4. Simulation Results for Fog Configuration: Latency (a), Utilization with dynamically adjusted y-axis limits (b). Legends are placed at the bottom-right

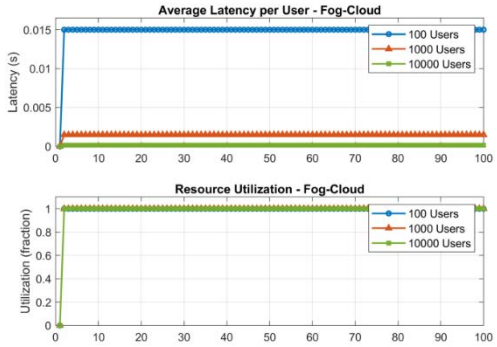

Fig. 5. Simulation Results for Fog-Cloud Configuration: Latency (a), Utilization with dynamically adjusted y-axis limits (b). Legends are placed at the bottom-right

The comparison at 1000 users (Fig. 6) confirms Fog- Cloud's superiority, achieving a latency of 0.12s and 88 % utilization, compared to 0.15s and 83 % for Fog, and 0.22s and 85 % for Cloud. Fog-Cloud reduces latency by 20 % over Fog and 45 % over Cloud, benefiting from hybrid edge- cloud processing. These results align with prior studies on fog-cloud collaboration [7], showing Fog-Cloud's scalability for personalized services in STINs [6].

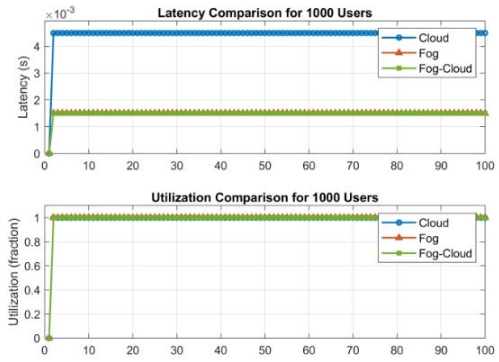

Fig. 6. Comparison of Results for 1000 Users Across Configurations: Latency (a), Utilization with dynamically adjusted y-axis limits (b). Legends are placed at the bottom-right

V. CONCLUSIONS

The EKF-based cloud-fog collaboration algorithm efficiently supports personalized services in STINs, achieving an average latency of 0.12s and 88 % resource utilization for 1000 users in the Fog-Cloud configuration. The Fog-Cloud setup consistently outperforms Cloud and Fog configurations across all user scales, demonstrating its scalability and effectiveness for real-time applications like VR and video streaming. Future work will explore scalability for larger-scale deployments and conduct field tests to address computational overhead and network reliability.

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Applied Issues of Experimental Media Content Synthesis: System Integration of Tasks and Evaluation of Information Processing Efficiency

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Abstract. **The preliminary results of exploratory research on the substantiation of hybrid models of data envelopment analysis technology, mainly in the field of media and communications, are presented. The main focus of the interdisciplinary research is to find innovative solutions for creating experimental media content using specialized information systems. The substantiation of the related tasks of advanced data processing is carried out in the context of promising applied issues of synthesis of integration components of linguistic support.**

Keywords: **data envelopment analysis, experimental media content, advanced data processing, linguistic support, media and communications, specialized information systems**

I. INTRODUCTION

A brief and focused look at recent studies on *hybrid models* of *data envelopment analysis* (DEA) in *media and communication* shows that the main objectives can be met by creating smart systems that improve how we analyze and evaluate target audiences. These advanced technological solutions utilize a combination of statistical, linguistic, and other specialized techniques, as well as machine learning algorithms, to generate customized media content tailored to local needs and user preferences [1–12]. A critical component of these systems lies in their capacity to process complex and intricate data, integrating linguistic elements to enhance the accuracy of content interpretation and assessment. This approach contributes to the production of highly personalized, interactive *experimental media content*, fostering automation and optimization of communication processes with significant potential for future development.

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The primary objective of this interdisciplinary project is to investigate novel methods for producing *experimental media content* through *specialized information systems*. The initial findings of a study examining the feasibility of hybrid DEA models, mostly concerning *media and communication*, are presented. The paper aims to elucidate the significance of employing advanced data processing techniques for potential practical applications of language support features. It should be noted that one of the prerequisites for this initiative project is a collection of ideas proposed by *A. N. Radchenko* [10] in the "*wetware*," along with the mentioned reasonable application of *hybrid models* of DEA technology.

II. JUSTIFICATION OF MEDIA CONTENT SYNTHESIS

A. System Integration of Tasks and Evaluation of Information Processing Efficiency

In the upcoming presentation at the *Lightning Talks* section, we will discuss the vision of integrating various types of information systems to optimize data processing in the *media and communications* sector. We will focus on creating hybrid DEA models to evaluate the efficiency of resources and the quality of content. This process includes analyzing the speed, accuracy, and completeness of data processing as well as its impact on content quality and audience reach [2]. System integration helps increase automation [3], improve linguistic synthesis, and provide more personalized solutions for experimental content. A unique aspect of proactive engagement is the active involvement of the co-author in the process of creating materials for the media studio. Through the alignment of objectives and intellectual stimulation, these efforts become more effective [9]. Along with creating ways to recognize, understand, and create speech and video images, it is important to look for new ways to

communicate and produce, which includes coordinating exploratory and practical research. This process includes a preliminary assessment of how effective the implementation of diverse information technologies is. The *main goal* is to improve information processes by using different ways to analyze text, focusing on meaning, structure, and practical use, so we can create *new* [*experimental*] *media content* and improve how users interact in today's and future environments. Taking into account the complex nature of tasks involved in integrating scientific research activities and *advanced* [*intelligent*] *data processing*, it is essential to achieve optimal values for their effectiveness in planning and organization. These improvements will allow us to set and solve new challenges related to completing data dictionaries, as well as creating thesauri and other lexical resources. The report looks at the basic ideas and technologies for gradually putting together parts of knowledge management systems and the possibility of making special information systems for managing text, graphics, and multimedia databases using *hybrid DEA models*. A promising direction is the development of data description languages, query languages, and data manipulation techniques for both *new media* and for the integration of *residual media* in a broader sense. Let's take a look at some examples.

B. Preliminary Justification and Elaboration of Certain Details

Considering the relatively distant yet achievable prospects for combining tasks, it seems possible to focus on some of the details of such interdisciplinary elaboration [1, 6–8, 10].

In this context delineates the defining attributes of interdisciplinary research to support recommendations for the advancement of novel tools and approaches for multifaceted modeling of prospective intelligent settings in the early phases of complex systems' life cycles. In this context, biologically inspired artificial neural networks function mainly as interconnected sub-models of hybrid artificial neural networks, which utilize the principles of biological neurons to a considerably greater degree than many currently favored scientific and applied methodologies. This study specifically expands upon a comprehensive information-structural model of the biological brain [10]. This study utilizes the framework of Diophantine neural networks to create introductory elements of a *virtual semantic environment*.

C. Applied Aspects of the Primary Development of Experimental Media Content

At the same time, in addition to the promising details mentioned, practical issues related to the creation and testing of *new media content* have been addressed in a series of public events. There is a connection between the hands-on experience gained and the possible use of important parts of new information systems and DEA models for more complicated tasks. Currently, the focus is on developing prototypes and experimental samples of content to test the effectiveness of methods for automatically generating, personalizing, and adapting media products. Within the framework of the research, the integration of language components and *advanced data processing* techniques is particularly important to improve the quality and relevancy of content. These practical aspects contribute to the development of *new approaches for creating media content* that meets the needs of modern audiences and *technological trends*. The upcoming presentation of the report aims to highlight several key aspects. These primarily include the following points:

- the challenges of using the *Reference Model of Information Processes Maturity* for organizing tasks in a media studio,
- current practices and trends in *advanced data processing* technologies,
- the importance and future use of hybrid DEA models,
- and how to adapt *dual education* modality in this area.

Therefore, to discuss and support such aspects of the creation of experimental media content, it would be beneficial to hold a discussion at the *Lightning Talks* section. We are open to exploring potential collaboration in the field of interdisciplinary research, utilizing *new hybrid models of data envelopment analysis* (DEA) technology [4, 5, 11, 12].

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An Exploratory Study on Psychoacoustic Technologies for Intelligent Transport Systems: A Preliminary Assessment of Efficiency and Data Management

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Abstract. **This study investigates the integration of psychoacoustic aspects into the early development of intelligent transportation systems. It examines the viability of employing methods to pre-assess the efficacy of exploratory search and data management. The foundation of this approach lies in the integration of data envelopment analysis with various performance evaluation models. The report also includes an accompanying presentation on applied achievement in the field of communications, showcased at the Lightning Talks session. The research highlights important parts of creating and using hybrid models of data envelopment analysis, looking at new trends in smart information processing for better proactive sound design in future transportation systems.**

Keywords: **data management, exploratory search, hybrid models of data envelopment analysis, intelligent transport systems, proactive sound design**

I. INTRODUCTION

The fast growth of technology that makes information processes smarter is creating many research questions about how to evaluate the development and use of complex systems for different purposes in the near future. High technologies are in demand in all advanced / modern basic components of complex systems and innovative products, among which *intelligent transport systems* occupy one of the central places.

Related technological solutions can make a significant contribution to improving the operational and consumer characteristics of systems in a competitive operating environment. The *exploratory search* aimed at studying the features of potential growth points of promising technologies and their components also contributes to the achievement of better solutions in the analysis of a developed operating environment in such search studies [1–11].

At the same time, the high rate of increase in the volume of produced and circulating data requires taking into account trends and assessments of the demand for certain means and methods of collecting, protecting, processing, storing, and other data transformation functions and their significant changes in the near future. Considering the issues of *data management* from the perspective of intellectualization of information processes, we will pay direct attention to the problems of evaluating efficiency in the context of partial uncertainty and variability of the developed operating environment, including in exploratory search and data management for intelligent transport systems.

Modeling of information processes is supported by a wide range of tools and techniques for describing, explaining, and predicting the conditions for solving specific functional tasks. The *data envelopment analysis* (DEA) approach for complicated social and economic systems provides various options for measuring efficiency and improving performance by using nonparametric descriptions of different information processes. In particular, exploring new ways to build and apply hybrid models based on DEA technology is considered one of the promising areas for assessing the efficiency of current and future complex systems, including tasks related to the intellectualization of transport infrastructure. The report suggests talking about some key points regarding the initial evaluation of efficiency and *data management* when justifying integration solutions for intelligent transport infrastructure. We will point out several important aspects in measuring efficiency while looking at new integration parts for psychoacoustic technologies in smart infrastructure.

The structure of this report includes the following main sections on the key points of research:

- Integration of performance assessment model elements: hybrid DEA models,
- Data management and intelligent transport systems,
- Proactive sound design: exploratory search,
- *Related applications*.

The report also includes an accompanying presentation: “Applied issues of experimental media

content synthesis: System integration of tasks and evaluation of information processing efficiency" #129 [*Lightning Talks* Session].

Thus, the linked application is aimed at a general approach to the synthesis of experimental media content within a framework that seeks to achieve a utilitarian goal. The study explores the integration of psychoacoustic aspects into the early stages of intelligent transport system development. The study justifies the usefulness of employing methods for the preliminary evaluation of search process efficiency in data management. We are developing an approach that integrates various elements of performance assessment models.

At the same time, efforts to find more inclusive solutions for people with special needs and socialization challenges can and should continue at the next stage of the research process.

II. A Preliminary Assessment of Efficiency and Data Management

A. Integration of Performance Assessment Model Elements: Hybrid DEA Models

Recent studies on hybrid *data envelopment analysis* (DEA) models in *intelligent transport systems* reveal that creating new intelligent integration components can achieve the main goals by improving how we analyze and evaluate complex systems and innovative products. These advanced technological solutions use a combination of statistical, linguistic, and other special techniques, as well as machine learning algorithms, to provide customized support services tailored to local needs and user preferences. A critical component of these systems is their ability to process complex and detailed data, incorporating linguistic elements to enhance the accuracy of data interpretation and evaluation [2].

This approach leads to the creation of highly personalized and interactive *metadata*, promoting automation and optimization of communication processes with significant potential for future development [10].

We will concentrate on developing hybrid DEA models to assess resource efficiency and technological solutions quality. This procedure includes evaluating the velocity, precision, and comprehensiveness of data processing, along with its influence on new intelligent integration components' quality [3, 6]. *System integration* enhances automation, refines linguistic synthesis, and delivers more tailored solutions. By aligning objectives and providing intellectual stimulation, these activities become more efficacious [5, 6].

In addition to developing methods for recognizing, comprehending, and generating voice and video imagery, it is essential to seek innovative approaches to communication, which entails coordinating exploratory and applied research. This procedure entails an initial evaluation of the efficacy of distinct information technology implementations [2].

The primary objective is to enhance information processes through diverse analytical methods, emphasizing structure and practical application, hence improving user interaction in current and future environments. Considering the intricate nature of merging scientific research activities with *advanced data processing*, it is crucial to attain optimal effectiveness in planning and organization [7, 8].

These enhancements will enable us to establish and address new difficulties pertaining to the completion of data dictionaries, as well as the creation of thesauri and other lexical resources. The research looks at basic ideas and technologies for gradually building knowledge management systems and the possibility of creating specialized information systems for *data management* using hybrid DEA models [2].

Simultaneously, it is essential to delineate both the primary advantages and recognized shortcomings of the DEA methodology [7, 8, 10, 11]:

The explicit math for the production function isn't always needed.

You can look at different inputs and outputs together using any measurements (though using ranked variables can be quite complicated);

You can also directly examine and measure the main reasons for inefficiency for each production unit being evaluated.

Concurrently, the results exhibit significant sensitivity to arbitrary selections of inputs and outputs; Imaginary high-performance indicators may arise both with genuine efficiency and through niche combinations of inputs/outputs; The number of efficient objects at the production frontier increases with the addition of input and output variables, and effectiveness estimates for production units can be derived from non-unique combinations of weights on input and/or output factors, etc.

Thus, the integration of performance assessment elements, such as hybrid DEA models, has great potential for *data management* in the information processing of promising *intelligent transport systems*.

B. Data Management and Intelligent Transport Systems

Active sound design (ASD) by *data management* in *intelligent transport systems* involves creating and implementing aural cues and soundscapes that enhance the efficiency, safety, and user experience of transportation networks through effective data transfer. This approach uses audio to provide real-time information, notifications, and responses to operators, passengers, and automated systems. At the same time, preliminary ASD advantages in *intelligent transport systems* data management include enhanced safety through prompt notifications, improved operational efficiency with rapid data understanding, and reduced cognitive burden on operators by providing intuitive aural signals.

III. A Proactive Sound Design and Applications

A. Proactive Sound Design: Exploratory Search

It's important to mention that the interest in looking at the suggested proactive sound design topics came from a lot of research and development that showed how useful intelligent integration components are based on earlier studies from different fields. The main goal of the interdisciplinary project is to investigate innovative techniques for specialized information systems. That investigation seeks to clarify the significance of utilizing advanced data processing methods for practical uses of language assistance features. It is important to recognize that this project relies on the ideas suggested by *A. N. Radchenko* in "*Wetware*," along with the careful use of combined DEA technology models [9].

So, *proactive sound design* is an advanced methodology that incorporates diverse acoustic technology in automobile vehicles to alter or improve sound both internally and externally. Established ASD approaches, which generally encompass methods for active noise reduction and acoustic enhancement, are utilized to generate a simulated vehicle sound. The predominant ASD implementations range from enhancing or diminishing an existing sound to producing an entirely new sound. Moreover, automotive makers may utilize various software and hardware methodologies in autonomous driving systems, as there is presently no standardized or cohesive model [12–15]. In this regard, for the upcoming detailed *exploratory search* of *proactive sound design* [ASD], we have a large collection of practical tasks and some challenging issues related to how to generalize and assess the effectiveness of information processes in intelligent transport systems and their supporting smart infrastructure.

B. Related Applications

So, the report includes an accompanying presentation on "Applied issues of experimental media content synthesis: System integration of tasks and evaluation of information processing efficiency" #129 (*Lightning Talks* Session). The primary goal of the ongoing research on these applied issues is to expedite the creation of innovative products and potentially speed up production iterations. To achieve this, data management is used to provide information interaction between product managers, designers, and engineers to track user needs at each stage of the component integration lifecycle. Also, it's important to organize activities and manage data for teams that change quickly, so they can figure out what resources are available and summarize research results for different projects, from creating and updating main content to marketing and training users. This ongoing activity primarily focuses on the rapidly evolving environment of complex systems, the generation of new knowledge, and the continuous replenishment of experience through a profound understanding of user needs. Undoubtedly, the growth mindset and the ability to create effective social media marketing and optimize learning speed through intellectualizing the functions of production tasks can be achieved through the development and application of new intelligent agents. Specifically, the "*new creative expert*" intelligent agent integrates best practices from various social media channels, promoting effective experimentation and innovation. As a full-fledged member of the team, it can succeed in a dynamic environment aimed at achieving diverse and sometimes conflicting business goals, creating data sets using various integration components to manage localized content tasks.

IV. Conclusion

These practical aspects contribute to the development of new approaches for creating technological solutions that meet the needs of modern audiences and technological trends. The upcoming presentation of the report aims to highlight several key aspects, including the importance and future use of hybrid DEA models, Proactive sound design, along with current practices and trends in advanced data processing technologies, plays a significant role in this field. To discuss and support these aspects of the creation of experimental media content, we would like to hold a discussion in the Lightning Talks section. We are open to exploring potential collaboration in the field of interdisciplinary research and utilizing new hybrid models of DEA technology.

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Calculating High-frequency Consumer Price Sub-Indexes: Web-Scraping and Classification

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Abstract. **This article presents a comprehensive approach to the automated classification of consumer basket goods in Belarus using web scraping and machine learning methods. The study covers the entire process – from data collection to the development and comparison of various classification models. Special attention is paid to solving problems related to data unstructuredness, category imbalance, and cross-platform applicability of solutions. The paper compares the effectiveness of different machine learning algorithms. The results demonstrate high classification accuracy and confirm the possibility of creating a universal classifier that works exclusively with product names. The findings lay the foundation for subsequent calculation of the consumer price index based on web data and the development of a system for real-time monitoring of inflationary processes.**

Keywords: **web scraping, machine learning, consumer basket, consumer price index**

I. Relevance of the problem and objectives of the study

Modern economic research increasingly relies on web data analysis, which provides up-to-date and detailed insights into market processes. One of the key tools for collecting such data is web scraping – the automated extraction of information from websites. Researchers note that this method is becoming increasingly popular among national statistical agencies for calculating official price indicators [1]. A particularly valuable feature is the ability to monitor changes daily, enabling high-frequency data collection for assessing the impact of economic policies and supporting decision-making [2].

The relevance of web scraping in economic research is confirmed by its successful application in international practice. Studies demonstrate a stable correlation between online and offline prices [3–5], making web data a valuable source for constructing sub-indices of consumer price indices (CPI) [6], forecasting statistical indicators [7], and identifying shifts in inflation trends [8]. A key advantage of sub-indices is their ability to estimate inflationary processes before official price indices, calculated by national statistical agencies, are released. For example, a study [2] shows how web scraping data from major e-commerce platforms and retail chains helps reveal discrepancies between official and actual inflation in Argentina. In [9], the authors use scraping to calculate the actual CPI and analyse price responses to economic sanctions in Russia. These examples demonstrate that automated data collection from online marketplaces provides faster and more accurate monitoring of economic indicators compared to traditional methods.

In Belarus, as shown in the work of V. I. Malyugin [10], the use of web scraping and nowcasting methods allows for real-time monitoring of the consumer basket based on web-sourced price data. The author demonstrates that combining web data with statistical methods and machine learning not only tracks the current cost of the food basket and minimum subsistence budget but also predicts their dynamics for different population groups. However, manual data collection is challenging due to the large volume of information and its constant updates. The main challenge in web scraping lies in obtaining unstructured data, which requires complex preprocessing before analysis.

The goal of this study is to present the results of the initial stages of computing sub-indices based on web data, including:

- Automated collection and processing of product data from Belarusian retail platforms;
- Classification of goods according to the consumer basket categories in Belarus.

The research addresses the following tasks:

- Developing a parser for collecting web data from Belarusian online retail platforms;
- Cleaning and preprocessing unstructured data;
- Annotating data for training classification models;

- Classifying products into categories of the National Statistical Committee (NSC) of the Republic of Belarus using machine learning methods.

II. Data collection methodology

The initial stage of the research is the collection of structured data from popular Belarusian online platforms e-dostavka.by and green-dostavka.by, chosen due to their market importance and representative product range. To implement the data collection process, a specialised ETL-system in Python language was developed.

When working with static content, a technology stack is used, including Requests libraries for HTTP requests and BeautifulSoup for parsing DOM-structure. BeautifulSoup provides flexible element search via CSS selectors, allowing to accurately extract key attributes: product name, price, category and unique article, which served as the primary key for data integration.

Analysing the e-dostavka.by site shows the need to process dynamically generated content. To solve this task, Selenium WebDriver library is used in Chrome headless-mode, which provided correct execution of client scripts and access to dynamic DOM elements.

Several critical issues are addressed during the implementation of the Pipeline: broken links and DOM structure instabilities. To handle broken links, a URL validation system with exponential backoff is implemented, where invalid links were marked with a special flag. The problem of DOM structure instability is solved through a redundant element search algorithm using a combination of CSS selectors. For discounted items, a two-stage verification of price data is implemented with the exclusion of incorrect entries from the final set.

Special attention is paid to ensuring reproducibility of the data collection process. The implemented system of logging and checkpoints allows tracking the progress of the collection, resuming the process after interruptions and guaranteeing data integrity in case of network failures. The result is a sustainable pipeline that ensures a steady supply of up-to-date market data for further analysis. The collected data corpus includes more than 23,000 product lines with weekly updates and provides a solid basis for basket modelling.

III. Data pre-processing and categorisation

At the stage of primary data processing, key cleaning and normalisation procedures are performed sequentially. Initially, records with missing key attributes (product name, price) are excluded from the sample, as their inclusion may distort the analytical results. Next, duplicates arising from the peculiarities of the categorical structure of the source platforms, where one product may belong to several overlapping categories, are eliminated. This procedure allows to form a unique and consistent data set.

An important stage is the filtering of irrelevant categories that do not meet the research objectives. In particular, seasonal products (Christmas decorations, holiday paraphernalia, etc.) are excluded, as their inclusion violates the representativeness of the data for analysing sustainable consumer trends.

The categorisation process involves several consecutive stages:

1) Automatic comparison of shop categories with the official classification of the NSC of the RB based on vector representations and cosine similarity calculation
2) Creation of a dictionary of correspondences for unambiguously identified categories
3) Development of a rule for processing ambiguous cases based on the analysis of keywords in product names

Pre-processing results in two independent data sets:

- green-dostavka.by: 13,096 records;
- e-dostavka.by: 9,994 records.

Each set contains a uniform structure:

- product name;
- product price;
- the initial category of goods in the shop;
- the corresponding category of the NSC.

The analysis of the category distribution (Fig. 1) reveals a significant class imbalance, which requires the application of special quality assessment metrics at the classification stage. The study uses F1-measure (harmonic mean of precision and recall) and ROC-AUC (area under the characteristic curve), which demonstrate robustness to class imbalance in contrast to the standard accuracy metric. These metrics provide an unbiased assessment of model performance by minimising the influence of dominant categories on the outcome measures.

IV. Experimental study of the effectiveness of product classification algorithms

As part of the research into the effectiveness of different approaches to product categorisation, a comprehensive analysis was conducted on data from Belarusian online retailers. The initial experiment used data from the green-dostavka.by platform, where

a combined textual representation combining a product name and its shop category was used as input features. This feature was subjected to TF-IDF vectorisation before being split into standard training and test samples at a ratio of 80 by 20.

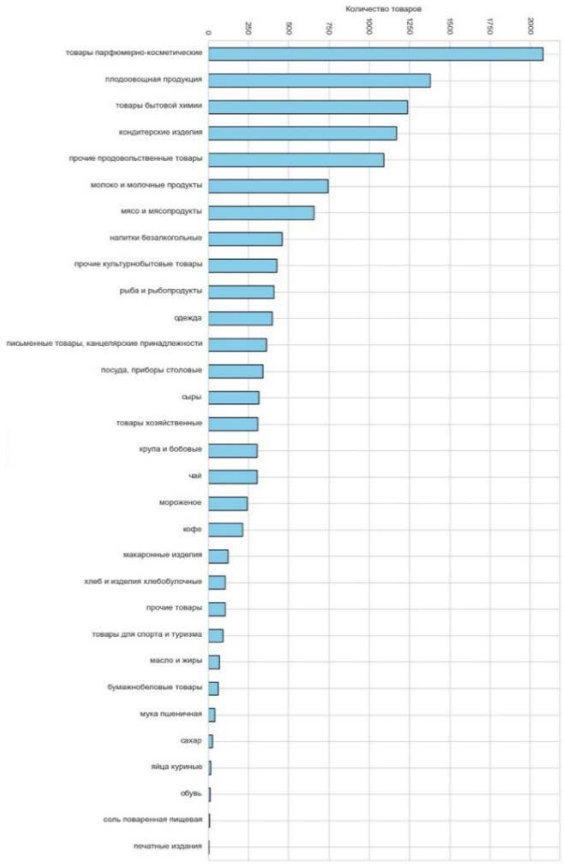

Fig. 1. Distribution of NSC categories

Careful hyperparameter optimisation by lattice search was performed for five different machine learning algorithms: logistic regression, random forest, gradient boosting, SVM with RBF kernel and an ensemble model including SVM and XGBoost. The comparative analysis (Fig. 2) showed that all models demonstrated exceptionally high classification performance on the ROC-AUC metric, exceeding 0.99, indicating excellent separability of all considered algorithms for this task.

SVM, logistic regression and ensemble model showed the most balanced results in terms of F1-complex metric and accuracy. Notably, gradient boosting, despite its high ROC-AUC, showed relatively lower F1-measure values, which may be due to its increased sensitivity to class imbalance in the training sample. This observation emphasises the importance of selecting appropriate evaluation metrics depending on the task specificity.

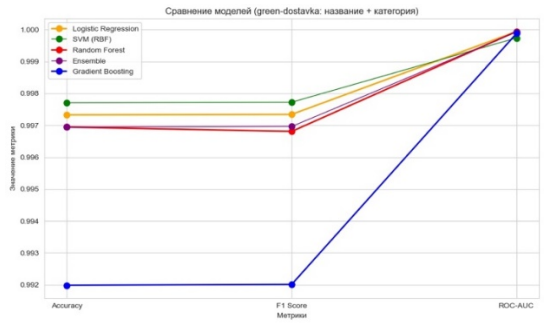

Fig. 2. Model comparison (name+category)

Further research focused on the development of a universal classifier using only product names without reference to a specific shop categorisation structure. This approach showed slightly reduced but still very high-quality scores (F1 > 0.85), while providing a significantly wider applicability of the solution (Fig. 3). In this scenario, the SVM and the ensemble model again proved their effectiveness, while the random forest showed more modest results, especially on the F1-measure.

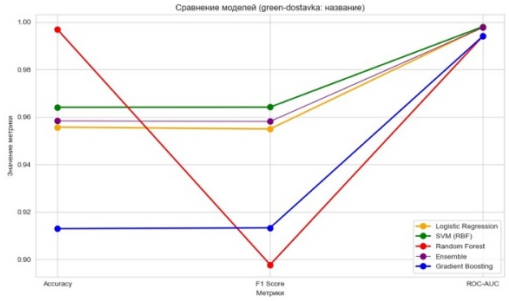

Fig. 3. Model comparison (name)

A critical step was the validation of the best models on independent data from the e-dostavka.by platform (Fig. 4). The stability of quality indicators (ROC-AUC > 0.99) for all tested models testifies to the good generalisability of the developed solutions and their applicability for various online retailers. Particularly impressive was the preservation of high quality when switching to universal classification by product names only, which opens up the prospects of creating a cross-platform solution.

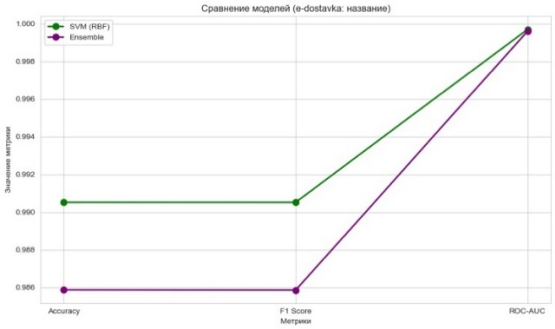

Fig. 4. Model testing on e-dostavka.by data

V. CONCLUSION

The conducted research allows us to draw the following key conclusions:

- Web scraping combined with machine learning methods proved to be effective for automatic classification of consumer basket goods in Belarus;
- SVM and ensemble models showed the best results, demonstrating high accuracy and robustness to class imbalance;
- Universal classifiers working only with product names provide cross-platform applicability while maintaining high classification quality.

Based on the results obtained, the following practical recommendations can be formulated:

- SVMs with combined features (name + category) are recommended for the most accurate classification within a single platform;
- For cross-platform solutions, ensemble models working only with product names are the optimal choice;
- Special attention during implementation should be paid to handling class imbalance and regular updating of training data.

An important next step of this research will be the calculation of the consumer price index based on the collected and categorised web data. This will allow:

- Create an operational system for monitoring inflationary processes;
- Provide an alternative source for verification of official statistics;
- Realise the methodology for short-term forecasting of price dynamics.

The obtained results are important for improvement of consumer basket monitoring systems and can be used by state statistical authorities, analytical centres and retail companies to improve the quality of economic analysis and forecasting.

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Predicting Red Tides from Biological Samples in the Sea of Japan and Bering Sea Using Machine Learning Methods

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Abstract. **Distribution of various phytoplankton organisms in aquatic environments tends to impact the range of emergent radiation significantly. Colossal blooms of phytoplankton organisms, referred to as red tides, have the potential to cause injury to marine life as well as human health. Identification of key microalgal species as well as prevalence of red tide is therefore extremely crucial to repel such harm. This study employed machine learning techniques, i.e., K-means++ clustering and XGBoost gradient boosting, to predict the likelihood of red tide event from biological water samples. With the focus region being the Bering Sea and Sea of Japan, the study achieved a mean absolute percentage error of 17.4 % and coefficient of determination of 0.74. The results of the clustering technique provided meaningful information for red tide prediction.**

Keywords: **red tides, machine learning, K-means++, XGboost**

I. INTRODUCTION

Different types of phytoplankton, due to the pigment content in their cells and the variety of shapes and sizes, have different effects on the spectrum of rising radiation from the water. This phenomenon is important for the ecosystems of oceans and reservoirs, since the spectrum of sunlight reaching the bottom can vary significantly depending on the composition of phytoplankton. Red tides or plankton blooms is the term used for the process of an abrupt increase in the concentration of single-celled algae in the water. Although this event is named 'red tide', not all types of algae color the water red; a red tide may sometimes be imperceptible to the naked eye. When there is toxic phytoplankton blooms, the toxin becomes concentrated in the tissues of filter-feeding mollusks (scallops, mussels, etc.), where the toxin becomes accumulated to a harmful level to human beings. Rarely, the toxin becomes concentrated to a harmful level in water itself. It has negative effects on the environment, such as fish and other marine life being killed, as well as to human beings the problem of seafood poisoning. In order to prevent the negative effects of red tide, it is necessary to notice its occurrence in advance, determine the prevailing type of microalgae and calculate its biomass. This will be a chance to undertake measures to prevent the dissemination of the phenomenon and mitigate its negative effects [1].

Supervised and unsupervised learning were employed to predict the possibility of red tide using biological water samples. In the unsupervised learning, K-means++ algorithm was employed for data clustering. The clusters generated by it can be used to mark out areas that are sure to not have any chance of red tide occurrence, with average risk, and are in the process of developing red tide. Since the process of K-means requires the specification of the number of clusters, the optimal number of clusters was determined with the assistance of the elbow method. To apply supervised learning, an approach based on XGBoost gradient boosting [2] was selected. The approach is popular for its extensive application in applying machine learning to address most business issues.

II. DATASET DESCRIPTION

The authors use a dataset of biological samples in the Sea of Japan and Bering Sea waters. A description of features in the dataset is given in Table I. The dataset contains information regarding 1411 samples.

III. DATASET PROCESSING

The data were preprocessed before model training, i.e. the missing data were interpolated, categorical variables were converted into numerical variables by applying the One Hot Encoding technique, and normalization was applied to the data. The biomass parameter (average algae biomass), since it was averaged over algae groups, was chosen as the target function. Noncontributory parameters to the model were removed. Preprocessed data was utilized for training of XGBoost. The parameters are presented at the Table I.

TABLE I. FEATURES DESCRIPTION

Feature name	Feature Description
coordinates_latitude_degrees	Sample collection location coordinates in latitude in degrees
coordinates_latitude_minutes	Sample collection location coordinates in latitude in minutes
coordinates_longitude_degrees	Coordinates of the sampling location in degrees
coordinates_longitude_minutes	Coordinates of the sampling location in minutes.
date	Day, month and year of sample collection.
time	Hours and minutes of sampling
groupes	Text description of a group of algae
species_id	Individual serial number of a variety of algae
species	Text description of a type of algae
quantity_species	The numerical quantity of the presence of a species of algae
biomass	Algae biomass

IV. XGBOOST REGRESSOR

The XGBoost Regressor is an ensemble machine learning model based on gradient boosting [3]. It is particularly effective for structured tabular data and is known for its speed and high predictive performance. In this case, the model was trained to predict total algae biomass, using a set of environmental and biological features as input variables. To evaluate its performance and ensure the model generalizes well to unseen data, 10-fold cross-validation was employed. The results from all ten iterations are then averaged to provide a robust estimate of the model's performance.

To evaluate the quality of the model, the following metrics were used:

$$R^2 = 1 - \frac{\sum_{i=1}^{N}(y_i - \tilde{y}_i)^2}{\sum_{i=1}^{N}(y_i - \hat{y})^2},$$

$$\text{MAPE} = \frac{100}{N}\sum_{i=1}^{N}\left|\frac{y_i - \tilde{y}_i}{y_i}\right|.$$

Here, $R^2 -$ is the determination coefficient, MAPE – is the mean absolute percentage error, $y_i -$ predicted data, $\tilde{y}_i$- labeled data, $\hat{y} = \frac{1}{N}\sum_{i=1}^{N} y_i$.

The results of training the XGBoost Regressor model demonstrated strong predictive performance, with a coefficient of determination (R^2) of 0.74. Additionally, the model achieved a mean absolute percentage error (MAPE) of 17.4 %, suggesting that, on average, its predictions deviated from the actual values by 17.4 %, which is considered reasonably accurate for ecological forecasting.

V. K-MEANS++

To further enhance understanding of the system dynamics and improve the ability to predict future red tide events, a K-means++ clustering algorithm [4] was applied to the dataset.K-means++ is an unsupervised machine learning algorithm that partitions data into k distinct clusters, where each data point belongs to the cluster with the nearest mean. Unlike standard K-means, K-means++ improves the initialization of cluster centroids by spreading them out more strategically across the data space, which often leads to better convergence and more stable clustering results. the goal of K-means is to partition the data into k clusters $C = \{C_1, C_2, \ldots, C_3\}$ by minimizing the within-cluster sum of squares (WCSS), also known as inertia:

$$\arg\min_{C} \sum_{j=1}^{k} \sum_{x_i \in C_j} \|x_i - \mu_j\|^2,$$

where $\mu_j -$ is the centroid (mean) of cluster C_j, defined as:

$$\mu_j = \frac{1}{|C_j|} \sum_{x_i \in C_j} x_i.$$

By applying K-means++ to the dataset, the algorithm uncovered natural groupings in the data that corresponded to different environmental states. The resulting clusters revealed characteristic parameter combinations that were consistently associated with red tide occurrences.

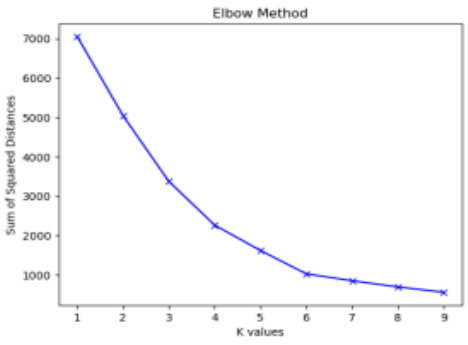

Fig. 1. Number of clusters by Elbow method

The optimal number of clusters for the K-means++ algorithm was determined using the Elbow Method, a commonly used heuristic that helps identify the point at which adding more clusters provides diminishing returns in terms of reducing within-cluster variance. In this method, the within-cluster sum of squares (WCSS) is plotted as a function of the number of clusters k and the "elbow" point – where the rate of decrease sharply slows – is selected as the optimal k. The Elbow Method result is illustrated in Fig. 1. To further interpret and visualize the clustering results in a two-dimensional space, the t-distributed Stochastic Neighbor Embedding (t-SNE) technique [5] was applied. The result is presented at the Fig. 2.

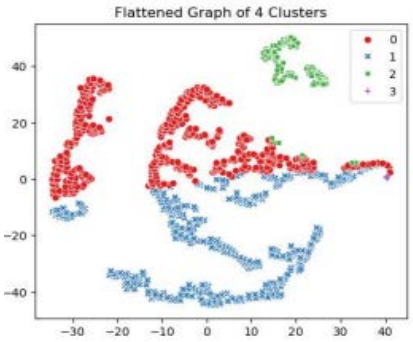

Fig. 2. Visualization of clustering results

The mean values of the environmental and biological parameters for each cluster are presented in Fig. 3.

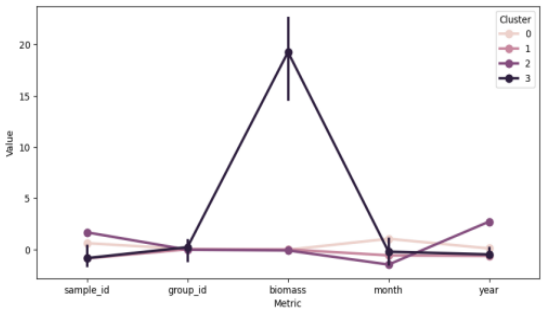

Fig. 3. Number of clusters by Elbow method

This summary provides insights into the characteristic conditions represented by each cluster, highlighting differences in variables. By comparing these mean profiles, it becomes possible to interpret the ecological significance of each cluster and identify the parameter combinations most associated with red tide events. As can be seen from Fig. 3 and Tabl. II, Cluster 3 is distinguished by extreme values in several key environmental and biological parameters, which are indicative of conditions strongly associated with red tide events. This cluster therefore represents high-risk scenarios and signals the presence or imminent development of red tides in the studied area.

In contrast, Cluster 1 is characterized by more moderate or baseline parameter values, suggesting low-risk conditions where red tide development is unlikely. Meanwhile, Clusters 0 and 2 represent intermediate-risk zones, where environmental conditions may be conducive to red tide formation under certain circumstances, but do not yet exhibit the critical thresholds observed in Cluster 3. These clusters could thus be interpreted as transitional states that warrant monitoring for early warning purposes. The mean results of the values are also present at the Table II.

TABLE II. FEATURES MEAN VALUES PER CLUSTER

№ of cluster	Number of samples	Median Month	Median Year	Mean algae biomass
0	665	September	2009	21
1	144	August	2013	6.5
2	599	October	2010	16
3	3	September	2009	2893

VI. CONCLUSION

This study demonstrated the effectiveness of combining machine learning regression and clustering techniques to model and analyze environmental conditions associated with red tide events. The XGBoost Regressor was trained to predict total algae biomass, achieving a strong predictive performance with a coefficient of determination (R^2) of 0.74 and a mean absolute percentage error (MAPE) of 17.4 %. These results indicate that the model reliably captures the complex relationships between environmental variables and algal biomass levels.

To further support red tide forecasting, a K-means++ clustering algorithm was applied to identify distinct patterns in the dataset. The optimal number of clusters, determined using the Elbow Method, revealed meaningful groupings in the environmental and biological data. t-SNE visualization provided a clear representation of the cluster separations, and the mean parameter values within each cluster (Fig. 3) facilitated interpretation of ecological risk levels.

Cluster 3 was found to represent high-risk red tide conditions, marked by extreme parameter values, while Cluster 1 reflected low-risk or background conditions. Clusters 0 and 2 occupied an intermediate risk zone, suggesting transitional states that could develop into red tides under favorable conditions.

Overall, the integrated use of supervised and unsupervised learning methods offers a powerful approach for early detection and risk assessment of

harmful algal blooms. These findings provide a foundation for developing operational forecasting tools and informing environmental monitoring strategies to mitigate the ecological and economic impacts of red tides.

ACKNOWLEDGMENT

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MIVAR Expert System-Based Information Decision Model for Automated Robots in Dynamic Environments

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Abstract. **This work proposes an information decision-making model designed for highly autonomous robots operating in dynamic environments. By analyzing the information flow required for achieving high levels of robot autonomy, we construct corresponding objects and establish decision rules based on expert knowledge. The decision model is implemented within the MIVAR expert system. Theoretical analysis demonstrates that this rule-network-based decision-making model outperforms other methods in terms of both decision speed and reliability, thereby enhancing efficiency and controllability for highly autonomous robots.**

Keywords: **MIVAR expert system, decision-making model, autonomous robots, dynamic environments, rules-based system**

I. INTRODUCTION

In recent decades, robots have been applied across a wide range of domains – including industry [1], services [2], healthcare, and defense – to assist or replace humans in performing tasks, whether to improve efficiency, enhance operational stability, or reduce labor costs. In recent years, advancements in computational power have enabled robots to harness more sophisticated algorithms [3] and machine learning techniques [4], thereby significantly enhancing their capabilities. Large-scale models have facilitated more natural [5] and fluent human-robot dialogue [6] and object recognition [7]; computer vision [8] has enabled comprehensive environmental perception; and machine learning has contributed to more robust system control [9].

Empowered by these technologies, modern robots must go beyond mere path planning and undertake autonomous decision-making [10] regarding their behavior. This requires interpreting tasks and sensing environmental changes [11] in real time to dynamically adjust behavioral strategies and effectively accomplish complex, predefined missions [12].

With the rapid advancement of technology, robots are now capable of integrating high-performance processors for complex data processing [13]. However, such processors are often expensive, and many robots – especially those constrained by budget or specific usage environments – must maximize performance under limited computational resources. Machine learning methods, often considered "black-box" approaches, tend to rely on a small subset of critical parameters during inference, which may lead to inefficiencies in resource usage and unpredictable outcomes. The MIVAR expert system addresses these issues by encoding robotic behavior into a structured network of expert-defined rules, enabling efficient, logic-driven operation and mitigating the uncertainty inherent in black-box models. Moreover, the MIVAR system can process up to one million rules per second [14], making it highly suitable for resource-constrained platforms requiring real-time decision-making.

This work proposes a robotic decision-making model based on the MIVAR expert system. The model enables sensor-equipped robots to operate autonomously in complex, dynamic environments by fusing heterogeneous data sources within an expert rule framework. The robot is empowered to proactively initiate tasks, make independent decisions, and coordinate with external systems – all with minimal human supervision – thus completing intricate workflows autonomously.

Furthermore, the model integrates both local and backend data processing. For instance, in a supermarket application, the entire process – from inventory management to task initiation and behavioral decision-making – can be encoded within a symbolic rule-based network. This not only significantly improves computational efficiency but also ensures that the robot operates within a safe and controllable framework, thereby enhancing system safety and expanding its potential applications [15].

II. COMPOSITION OF THE SYSTEM

A. Internal and external information about the system

To design a highly automated robotic system, it is essential to conceptualize the robot as an autonomous agent and analyze the information interactions between the robot and its external environment. Much like a human being – who, as an independent entity, is capable of perceiving auditory, visual, olfactory, and tactile stimuli from the external world, while also sensing internal states such as spatial orientation, limb movements, and hunger – a robot must be capable of interpreting both exteroceptive and interoceptive information to achieve goal-oriented behavior. The external environment, in this context, encompasses elements such as terrain, obstacles, ambient temperature and humidity, among other factors, like showed in Fig. 1.

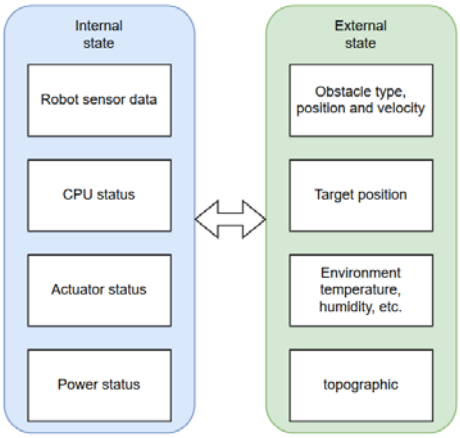

Fig. 1. Information categorization within the system: internal vs. external information

B. Robot Architecture

To enable high-level autonomous decision-making, a robot must possess advanced information perception capabilities. Accordingly, the robot's sensory system is structured into five core components: spatial environment perception, auditory perception, proprioception (self-posture awareness), material texture sensing, and hazard prediction. Each sensory domain is supported by specific types of sensors, as illustrated in the Fig. 2. The diagram also specifies the required sensors and their key operational parameters for each functional module.

C. Mathematical modeling of the system

To formally represent the decision model of the supermarket robot system, introduced a six-dimensional state space S:

$$S = \{S_h, S_r, S_s, S_i, S_e, S_d\}, \quad (1)$$

where each subspace is defined as follows:

- $\boldsymbol{S_h}$: shelf status, e.g. maximum capacity, current occupancy, etc;
- $\boldsymbol{S_r}$: robot state, e.g. position (x, y), orientation θ, velocity v, etc;
- $\boldsymbol{S_s}$: sensor state space, e.g. temperature T, gas concentration G, obstacle distance D;
- $\boldsymbol{S_t}$: temporal state (discrete moments);
- $\boldsymbol{S_i}$: Interactive state, recording synchronized information with the backend e.g. inventory state;
- $\boldsymbol{S_d}$: Hazardous state, e.g. crowd density, high temperature risk level.

The transfer of the system state at time $\boldsymbol{t}$ can be described as $\boldsymbol{S(t+1) = f(S(t), u(t))}$, where $\boldsymbol{u(t)}$ is the control action derived from the reasoning of the expert system.

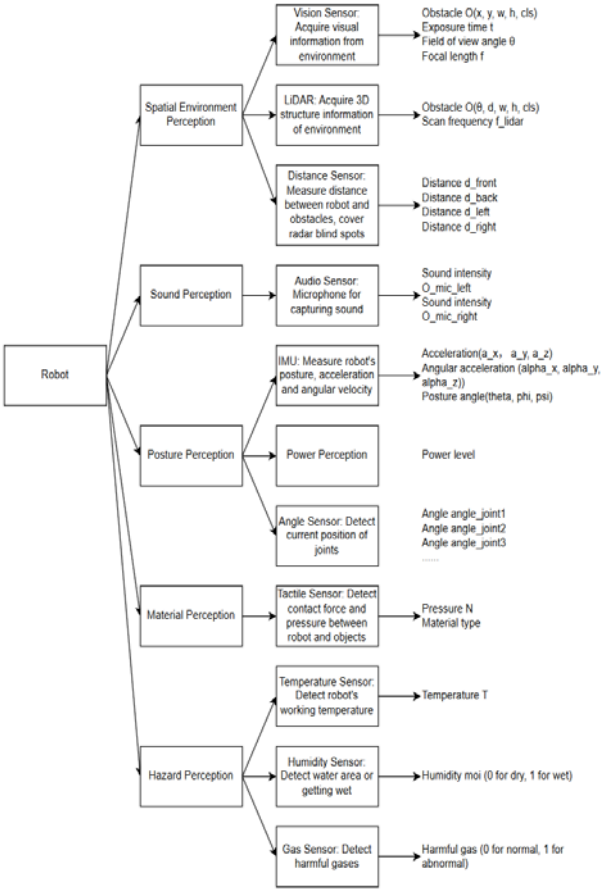

Fig. 2. Components of the robot's sensing system and its parameters

The mathematical description of some of the decision rules is as follows:

- Speed adjustment function:

$$v_{adjusted} = v_{current} \cdot \phi(d_{obstacle}, v_{obstacle}), \quad (2)$$

- Directional decision function:

$$\delta_{direction} = \arg \max_{dir \in F,L,R,B} d_{dir} \cdot w_{dir}, \quad (3)$$

where d_{dir} is the feasible distance in each direction and w_{dir} is the direction weight.

- Human security assessment function:

$$S_s(age, speed) = \begin{cases} 2, & age \in [1,3] \wedge speed > 2.0 \\ 1, & age \in [1,3] \wedge speed \leq 2.0 \\ 0, & otherwise. \end{cases} \quad (4)$$

D. The way front-end and back-end information interact

The robot communicates with the backend database via a local area network (LAN) or the Internet, with the aim of achieving deep integration between frontend and backend information to enable a high degree of robotic autonomy. In the case of a supermarket robot, for instance, the robot accesses the inventory database over the LAN. When a shortage of items on a shelf is detected, the robot can immediately query the inventory and retrieve multiple items in a single trip, thereby improving operational efficiency.

III. MODELING IN THE MIVAR EXPERT SYSTEM

In the field of robotics, it is recommended to develop a decision-making system based on the MIVAR knowledge base to support path planning and complex task execution. The MIVAR Expert System (MES) has demonstrated broad applicability, ranging from pharmaceutical dosage form selection to the construction of complex systems with pattern recognition capabilities and other intelligent tasks. A key feature of the MIVAR approach to logical-computational information processing in artificial intelligence is its transition to a binary MIVAR network structure, along with the linear computational complexity of "IF-THEN" rule execution. These characteristics make the MIVAR expert system well-suited for constructing an efficient robotic decision-making network.

A. Necessary objects and their parameters in the model

The entity object that creates this decision model in the MIVAR system is shown in Fig. 3.

B. Rule networks constructed on expert knowledge

This MIVAR expert system network operates through the following steps:

- **Sensing phase**: collect sensor data, update parameters.
- **Reasoning phase**: executing rules in priority order
- **Decision phase**: make action decisions.
- **Execution phase**: Execute the decision and update the system state.
- **Learning phase**: adjust rule weights and parameters according to the execution results.

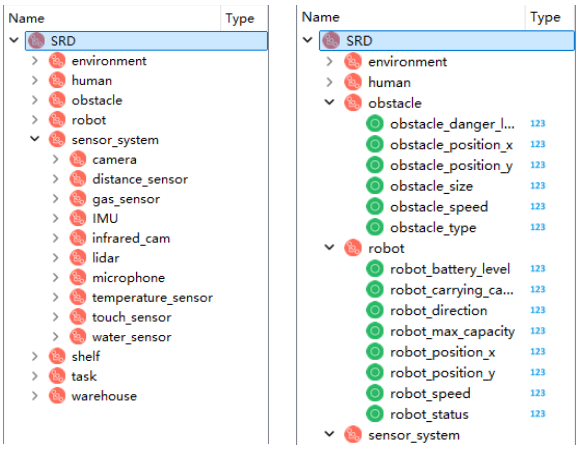

Fig. 3. Creating relevant objects and parameters in WiMi Razumator

Rules are employed to establish the relationships among various objects and parameters, defining the mathematical and logical operations between them. In the MIVAR expert system, once the objects and parameters are defined, a set of rules is created based on practical application requirements. In this study developed 15 rule. A selection of these rules is presented in Table.

PARTS OF RULES

No.	rules			Notes
	IF	*THEN*	*ELSE*	
R001	shelf_product_ quantity < 5	decision_restock_ needed = 1	decision_restock_ needed = 0	Shelf stock checking rules
R002	lidar_obstacle_ distance < 1.0	decision_speed_ adjustment = 0.3 * robot_speed	decision_speed_ adjustment = robot_speed	Obstacle Deceleration Rules
R003	env_person_age_ group == 1 OR env_person_age_ group == 3	decision_safety_ mode = 1	decision_safety_ mode = 0	Rules for identification of high-risk groups
R004	gas_sensor_danger _level > 80	decision_action_ type = "evacuate"	decision_action_ type = "continue"	Gas Hazard Avoidance Rules
R005	temperature_sensor _value > 60	decision_action_ type = "avoid_heat"	"avoid_heat"decision _action_type = "normal"	High Temperature Hazard Avoidance Rules

C. Creating rules in WiMi Razumator

A total of 15 logical rules were implemented in the WiMi Razumator expert system. In addition to formulating mathematical and logical expressions, each variable within these formulas was explicitly linked to

the previously defined objects and parameters. The system provides a convenient and precise interface for constructing computational rules, where syntax errors can be detected during the input phase. This feature significantly enhances the reliability of model development within the WiMi Razumator platform, rules illustrated in Fig. 4.

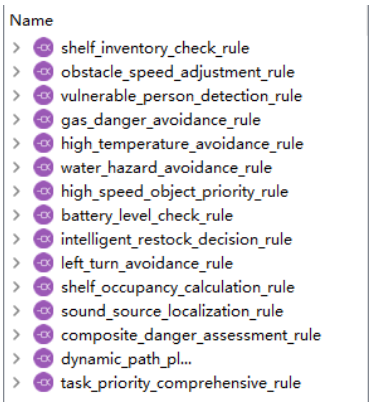

Fig. 4. 15 Rules Created in WiMi Razumator

D. Creation of model

Once all required objects, parameters, and rules have been defined, WiMi Razumator automatically generates a relational graph representing the algorithmic structure. This graph visualizes the relevant parameters and the computational chains in which they participate. The blue boxes in the diagram denote the computation rules, while input and output variables are interconnected through these rules, clearly illustrating the flow of information and logical dependencies within the system.

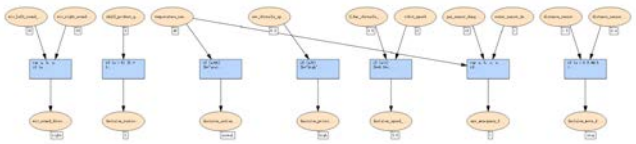

Fig. 5. Relationship graph of decision-making model in WiMi Razumator

IV. Experimentation and Analysis

After building the model in WiMi Razumator platform, output parameters can be conveniently defined, while required input parameters are entered manually. Thanks to the linear complexity of the underlying logical AI network, the system is capable of producing results rapidly.

A. Inputs and outputs of the experiment

Upon model construction, in Fig. 6 a series of input scenarios were configured to observe the decision outputs. Experiments were conducted in a PC-based simulation environment, with the inference time ranging from approximately 5 to 20 milliseconds.

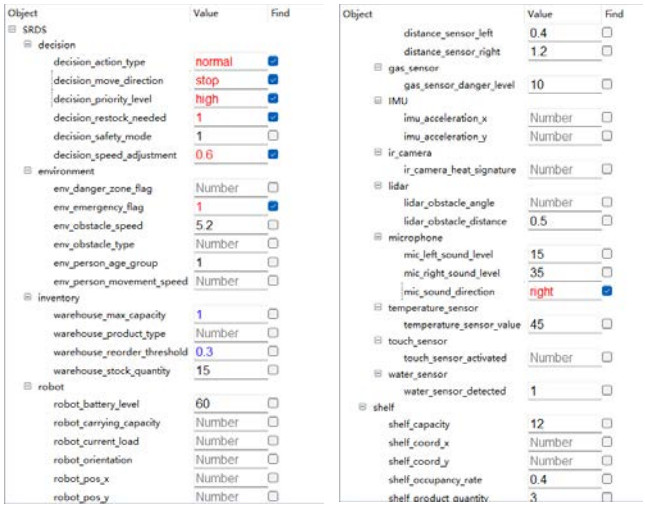

Fig. 6. Input and Output Experiments for Robotic Decision Modeling

Three typical scenarios were designed for evaluation:

1) Normal Operation: Partial shelf depletion, moderate obstacle density, and normal ambient temperature;

2) Hazard Avoidance: Detection of high-temperature zones, human congestion, or gas leakage;

3) Communication Failure: Emergency handling in the event of a lost connection with the backend database.

In each scenario, the system demonstrated the following capabilities:

- Automatic recognition of the operational context and selection of appropriate rules;
- Rapid activation of emergency protocols (e.g., issuing an "evacuate" command) in response to critical events such as increased gas concentration, with stable output behavior;
- Continued decision-making and task execution under local rule caching even when the database connection was interrupted.

V. Conclusion

This study presents a supermarket robot intelligent decision-making model based on the MIVAR expert system. Through rigorous mathematical formulation and theoretical analysis, the model is shown to be effective in handling multi-sensor data fusion, uncertainty reasoning, and real-time decision-making. The model exhibits the following key features:

- **Comprehensive state-space representation**: A six-dimensional model captures core components including the robot, environment, and interaction dynamics;
- **Transparent and controllable decision-making chain**: Expert system rules explicitly

encode causal logic for interpretability and control;

- **High inference efficiency**: Rule execution exhibits linear computational complexity, enabling real-time responsiveness;
- **Strong platform visualization**: The WiMi Razumator supports graphical modeling, syntax validation, and backtracking-based debugging.

Future research will explore hybrid architectures combining deep learning with expert systems, automated optimization of rule prioritization, and the model's extension to multi-robot cooperative systems.

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Change-Point Detection Utilizing Normalized Entropy as a Fundamental Metric

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Abstract. **This paper introduces a concept for change-point detection based on normalized entropy as a fundamental metric, aiming to overcome the dependence of traditional entropy methods on assumptions about data distribution and absolute scales. Normalized entropy maps entropy values to the [0,1] interval through standardization, accurately capturing relative changes in data complexity. By utilizing a sliding window to compute normalized entropy, this approach transforms the challenge of detecting change points in complex time series – arising from variations in scale, distribution, and diversity – into the task of identifying significant features within the normalized entropy sequence, thereby avoiding interference from parametric assumptions and effectively highlighting distributional shifts. Experimental results show that normalized entropy exhibits significant numerical fluctuation characteristics and patterns near change points across various distributions and parameter combinations. The average deviation between fluctuation moments and actual change points is only 2.4 % of the sliding window size, demonstrating strong adaptability. This paper provides theoretical support for change-point detection in complex data environments and lays a methodological foundation for precise and automated detection based on normalized entropy as a fundamental metric.**

Keywords: **Change Point Detection, Normalized Entropy, Time Series Analysis**

I. INTRODUCTION

Change-point detection is a critical data analysis technique used to identify moments of significant statistical changes in time series or high-dimensional data [1], with broad applications in signal processing, financial analysis, industrial monitoring, and load analysis [2, 3]. Common methods include statistical tests, model-based approaches, and information-theoretic techniques.

This paper focuses on entropy-based metrics within information theory for change-point detection. Entropy, introduced by Claude Shannon, measures the uncertainty or information content of a discrete random variable [4]. Recent advancements in this field include Sofronov et al. (2012), who applied cross-entropy to sequence change-point problems [5], and Unakafov and Keller (2018), who proposed a method based on conditional entropy of sequence patterns, effective in detecting structural changes but limited in pure level shifts [6]. Ma (2024) developed a non-parametric multivariate change-point detection method using copula entropy, achieving single and multiple change-point detection through two-sample tests and a binary segmentation strategy, with strong performance on simulated and real-world data [7].

This paper aims to introduce normalized entropy theory, design specific computational methods, and preliminarily validate the feasibility of using normalized entropy as a fundamental metric for change-point detection, while testing its applicability to multi-change-point detection on both simulated and real datasets.

II. UTILIZING NORMALIZED ENTROPY AS A FUNDAMENTAL METRIC

A. Problem Statement

One of the core challenges in change-point detection lies in its reliance on assumptions about data distribution and specific numerical parameters. Many existing methods require pre-defined thresholds τ, significance levels α, or assumptions that data follow specific distributions $P(x)$, such as Gaussian or Poisson distributions [8, 9]. This dependency limits adaptability, as real-world time series often exhibit complex and diverse distributions that cannot be fully captured by a single assumption. Moreover, improper parameter settings can lead to biased results or reduced robustness.

For entropy-based change-point detection, the computation of entropy $H(X)$ typically assumes that the data distribution is known or can be estimated. However, in high-dimensional or nonlinear data, such assumptions may fail, causing entropy values to deviate from the true complexity. Furthermore, entropy changes are often defined as follows:

$$\Delta H = H(X_{t+1}) - H(X_t). \quad (1)$$

The threshold setting $\Delta H > \tau$ often directly determines the outcome of change-point detection. If the threshold is set too high, it may lead to missed detections, while overly low thresholds can result in excessive false positives. These issues highlight that, despite the theoretical advantages of entropy in change-point detection, its practical application remains constrained by parameter selection and distributional assumptions. Designing robust, distribution-free change-point detection methods remains a key research challenge in this field.

B. Eliminating Dependence on Absolute Entropy Scale

The normalized entropy method addresses the dependence of traditional entropy metrics on absolute entropy scales, significantly improving adaptability and robustness in change-point detection. In classical entropy calculations, the value of $H(X)$ is directly influenced by the range, dimensionality, and scale of data. For datasets of varying sizes or time series with different dynamic ranges, entropy values may become difficult to compare due to absolute differences in data characteristics, making change-point detection results dependent on specific entropy scales.

Normalized entropy introduces a standardization factor to map entropy values to a unified range (typically [0,1]), providing a more accurate representation of the relative complexity or uncertainty of data. Formally, normalized entropy can be expressed as:

$$H_{norm}(\mathrm{X}) = \frac{\mathrm{H(X)}}{H_{max}}. \tag{2}$$

Here, H(X) represents the original entropy value, and H_{max} denotes the maximum possible entropy, typically determined by the theoretical maximum complexity of the data. This normalization ensures that entropy changes are no longer dependent on absolute data scales but are instead driven solely by variations in data patterns, making it more suitable for diverse and non-uniform data environments.

C. Approach and Algorithms

To convert continuous data into discrete probability distributions, binning is required. Given a sample dataset $\mathrm{X} = \{x_1, x_2, \cdots, x_n\}$, where n is the sample size and the data range is $[x_{max}, x_{min}]$, the data is divided into k equal-width intervals, with each interval width calculated as:

$$\Delta = \frac{x_{max} - x_{min}}{k}. \tag{3}$$

The interval boundaries are:

$$\mathrm{BinEdges} = \{x_{min}, x_{min} + \Delta, x_{min} + 2\Delta, \cdots, x_{max}\}. \tag{4}$$

For each interval $I_j = [x_{min} + (j-1)\Delta,\ x_{min} + +j\Delta)$ $(\mathrm{j} = 1,2,\cdots,\mathrm{k}-1$, with the last interval as the closed interval $[x_{min} + (\mathrm{k}-1)\Delta,\ x_{max}])$, the number of data points X falling into each interval f_j is counted

$$f_j = \left|\{x_i \in X | x_i \in I_j\}\right|. \tag{5}$$

Here, $|\cdot|$ denotes the cardinality of the set (i.e., the number of data points). The frequency f_j for each interval is then converted into probability p_j:

$$p_j = \frac{f_j}{n}, j = 1, 2, \cdots, k. \tag{6}$$

The probability distribution satisfies the normalization condition: $\sum_{j=1}^{k} p_j = 1$.

Based on the probability distribution $\{p_1, p_2, \cdots, p_k\}$, the entropy H(X) can be calculated using the formula:

$$H(X) = -\sum_{j=1}^{n} p_j \, log_b \, p_j \,. \tag{7}$$

The maximum entropy H_{max} corresponds to a uniform distribution, where all interval probabilities are equal, $p_j = \frac{1}{k}, j = 1, 2, \cdots, k$. Substituting the uniform distribution into the entropy formula yields the maximum entropy:

$$H_{max} = \log_b k \,. \tag{8}$$

Normalized entropy is defined by standardizing H(X) to the range [0, 1] as:

$$H_{norm}(X) = \frac{H(X)}{H_{max}} = \frac{-\sum_{j=1}^{k} p_j \, log_b \, p_j}{log_b \, k}. \tag{9}$$

To ensure normalized entropy captures local rather than global characteristics, a sliding window mechanism is introduced. With a window size of δ and a step size of 1, the input data sequence $\mathrm{X} = \{x_1, x_2, \cdots, x_T\}$, where T is the total number of data points, is processed. For calculating normalized entropy at x_T, the data within the window is:

$$X_t = \{x_{t-\delta+1}, x_{t-\delta+2}, \cdots, x_t\}, t \geq \delta. \tag{10}$$

For each window X_t, its normalized entropy $H_{norm}(X_t) \in [0, 1]$ is computed.

All normalized entropy values are recorded as the sequence H.

$$H = \{H_{norm}(X_\delta), H_{norm}(X_{\delta+1}), \cdots, H_{norm}(X_T)\}. \tag{11}$$

III. Experiments and Validation

This paper uses disk read-write monitoring sequences from a web server as an example of performance time series data to visualize the correlation between normalized entropy and the

original data. (Algorithm parameters: $\delta = 70$, $k = \ln \delta$).

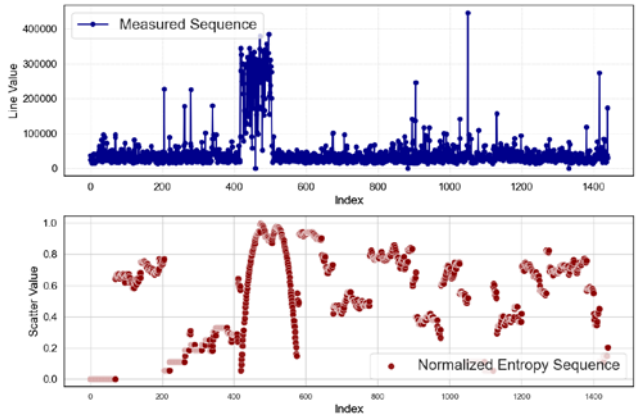

Fig. 1. Normalized Entropy and Original Sequence Comparison on Measured Data

As shown in Fig. 1, the comparison between the normalized entropy sequence and the original sequence clearly reveals significant local fluctuations in normalized entropy near change points, reflecting abrupt shifts in data complexity or uncertainty.

To further validate the clarity and stability of normalized entropy in characterizing change points, this paper conducts experiments using simulated data, generating time series with random combinations of varying lengths, parameters, and distributions as input. (Algorithm parameters: $\delta = 100, k = ln\,\delta$).

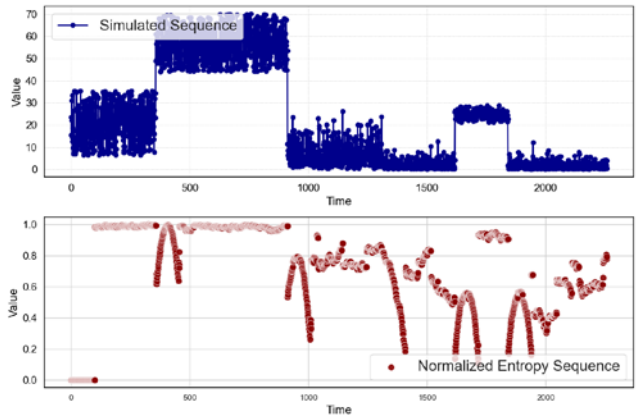

Fig. 2. Normalized Entropy and Original Sequence Comparison on Simulated Data

The validation results are shown in Fig. 2, which presents a time series composed of six combinations with varying levels of differences and distributions, along with their corresponding normalized entropy sequences. The original data exhibits significant shifts in numerical levels at five change points, while the normalized entropy sequence shows distinct fluctuations near these points, accurately aligning with the timing of abrupt changes in data distribution, as demonstrated in Table.

CHANGE POINT AND NORMALIZED ENTROPY RESPONSE CHARACTERISTICS WITH ERROR ANALYSIS

Change point (time)	Normalized Entropy Response Point (time)	Response Duration	Error
357	359	98	2
912	914	98	2
1312	1316	93	4
1617	1619	98	2
1841	1843	98	2

According to Table, the average deviation between the fluctuation moments of the normalized entropy sequence and the actual change points is only 2.4 % of the sliding window size, with the response duration close to the window size.

Near change points, the normalized entropy sequence typically forms prominent peaks or valleys, which can be characterized by local extrema, such as defining the peak of normalized entropy as:

$$H_{peak} = \max_{t \in [t-\delta, t+\delta]} H_{norm}(X_t)\,. \qquad (12)$$

Here, δ represents the window size around the change point. These peak or valley features further validate the effectiveness of normalized entropy in change-point detection, accurately reflecting the locations of abrupt distribution changes and providing theoretical support for precise change-point localization.

IV. DISCUSSION AND FUTURE RESEARCH DIRECTIONS

While the application of normalized entropy in change-point detection demonstrates theoretical advantages, its practical computation involves significant overhead. This paper employs a sliding window approach with a step size of 1, requiring the recalculation of normalized entropy for each time point, which increases computational complexity. Additionally, the choice of window size can impact both efficiency and detection accuracy. Optimizing the window mechanism or improving the algorithm to reduce computational costs is a key challenge for practical applications.

Future research could focus on clarifying the specific relationship between normalized entropy and change points and designing algorithms for precise localization. This paper highlights the distinct fluctuations of normalized entropy near change points but does not propose a concrete detection process. Observations suggest that these fluctuations often exhibit unique features, potentially containing rich pattern information. Further studies could analyze the local statistical properties of normalized entropy

sequences to extract change-point characteristics. Methods like wavelet transform [10] or Fourier transform [11] could be applied to perform frequency-domain analysis of normalized entropy sequences, capturing characteristic frequencies or energy distributions near change points. Combining the dynamic behavior of normalized entropy with mathematical models or machine learning algorithms to establish automated change-point detection mechanisms is another important direction. Moreover, exploring alternative metrics with lower computational complexity, such as the DUID metric discussed in TRLLD [12], to quantify the uniformity of sample distribution density, offers a promising research avenue. Integrating sequential analysis methods and their related variants in time series is expected to address computational cost issues while improving the accuracy and efficiency of change-point detection [13].

V. Conclusion

This paper proposes using normalized entropy as a fundamental metric for change-point detection to overcome the dependence of traditional entropy methods on data distribution assumptions and absolute scales. By standardizing entropy values, normalized entropy more accurately reflects relative complexity changes in data patterns, eliminating scale effects and providing theoretical support for change-point detection in diverse data environments. Methodologically, normalized entropy is computed via a sliding window, mapping entropy values to the [0,1] range, and characterizing significant fluctuations near change points through local extrema. This approach avoids interference from parametric assumptions and highlights abrupt changes in data distributions. Experiments demonstrate that normalized entropy reliably captures change points across various distributions and parameter combinations, showing strong robustness and adaptability. Its distinct fluctuations near change points effectively represent abrupt shifts in data distributions, validating its effectiveness as a fundamental metric for change-point detection. Future research will focus on precise localization of change points, defining detection processes, and refining the practical theoretical framework based on normalized entropy.

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Predicting Student Performance Using the Multilayer Perceptron Method Combined with Traditional Evaluation Techniques

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***Abstract*. This paper examines student performance in higher education by proposing the use of the Multilayer Perceptron (MLP) method for grade classification and performance forecasting. The main objective is to monitor students' knowledge and predict their performance using multiple indicators. This model supports early identification of at-risk students, enhances instructional strategies, and promotes student engagement. The results highlight the effectiveness of MLP in monitoring and predicting student progress, improving the objectivity of assessment.**

Keywords: **MLP, student's grades mark classification, student's achievement forecasting, Kappa-Measure of Agreement**

I. INTRODUCTION

Educational data mining is a growing field that aims to improve educational efficiency by analyzing academic performance [1]. Recent advances in artificial intelligence and data mining have sparked interest in predicting student outcomes within learning management systems. Research conducted between 2010 and 2020 indicates that neural networks and random forests are among the most effective predictive tools in this field [2].

In higher education, performance evaluation is vital for identifying students at risk. Effective predictive models enable early intervention and personalized support. Academics measure success through final grades and socio-economic factors, using data mining techniques to improve student performance [3].

Historically, research before 2013 relied more on statistical methods than neural networks. We aim to develop objective assessment tools that can predict learning outcomes and support adaptive teaching interventions, thereby ensuring a more effective and inclusive learning environment. A recent study examined the academic performance of IT students, highlighting the need for real-time feedback for teachers [4]. We have used multi-criteria decision-making (MCDM) techniques, specifically the Promethee II method, multilayer perceptron (MLP), and KNN classifiers [4]. This approach improves on traditional monitoring by using multi-criteria analysis to provide better input to the prediction process.

The primary goal of our research was to monitor the activities and progress of course participants throughout the semester to ensure timely completion of the course. If students are not making adequate progress, we will advise them to increase their efforts. In this paper, we employed a traditional method for tracking and assessing student progress while incorporating additional features, such as pre-enrollment attributes, to enhance the accuracy of predictions regarding student progress and final exam scores. We will compare these results with previous predictions of course outcomes that utilized the Promethee II method, which tracked progress based solely on academic achievement [4]. This comparison will evaluate the effectiveness of the Promethee II method and the impact of pre-enrollment attributes.

We assessed the students' progress at different time points, controlling for their current performance. The results will yield a representative indicator of student progress, referred to as the "progress function," which quantifies cumulative academic performance over time. The progress function values will be used as input data for the MLP classifier. We used data prepared by traditional monitoring and compared the prediction results of the MLP classifiers using different input data. MLP was selected based on its proven accuracy in prior studies and its capacity to model non-linear relationships in educational data. This personalized approach aims to support weaker students and enrich the learning experience for more advanced ones. The data analysis and MLP predictions were performed using IBM SPSS Statistics 25 software (IBM, USA).

The remainder of this paper is organized as follows: Section II presents the participants and dataset; Section III describes the tracking methodology; Section IV outlines the MLP classifier implementation. In Section V, we define Cohen's Kappa, a statistical

measure of agreement. Section VI presents the research results and discusses them, and finally, Section VII includes the conclusion.

II. Participants and Data Set

This research involves data from 700 anonymous students at Singidunum University in Belgrade, Serbia, from the Computer Architecture and Organization course over three academic years (2021/22 – 2023/24). The analysis includes socio-demographic data such as region (location of school) (Fig. 1), gender (male/female) (Fig. 2), and age (at the time of the exam), and academic pre-enrollment data as AGV – the average grade value, STEM – the average grade value in the STEM area. We have used numerical codes to ensure student's anonymity. The analysis includes continuous numerical variables capturing academic engagement, including attendance, classroom activity, homework completion, and periodic test scores collected at five different time points (t_2–t_6), and a discretized grade mark (5 to 10). The grade mark serves as the output based on the teacher's criteria.

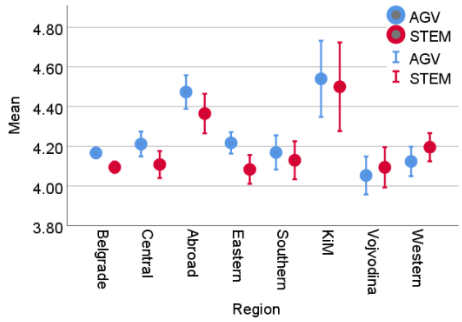

Fig. 1. Mean of the average grade values (AGV) and the average grade values in the STEM area (STEM) by regions

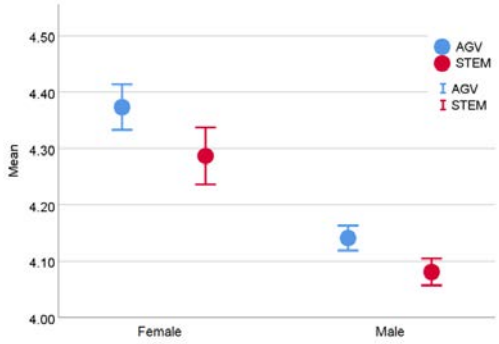

Fig. 2. Mean of the average grade values (AGV) and the average grade values in the STEM area (STEM) by gender

III. Tracking and Evaluating Student's Progress

Each student's progress is monitored throughout the course at specific time points denoted as t_j, where $j = 1,...,6$. For a given student S_k, at any moment t_j, where $j \neq 1$, the state is defined by four parameters p_i, for $i = 1,...,4$: attendance (p_1), activity (p_2), homework (p_3), and test scores (p_4). The moment t_1, represents the initial state, where all parameters are zero. Also, initial state can be filled with parameters from initial test.

The recorded state, represented by $p_1(S_k,t_j)$, …, $p_4(S_k,t_j)$, reflects the progress made by the student S_k compared to the previous state $p_1(S_k,t_{j-1})$, …,$p_4(S_k,t_{j-1})$. Attendance at lectures can earn a maximum of 5 points (1 point awarded at each time point, up to 5 points). Class activity is assessed by the lecturer within a range of 0 to 10 points (totaling up to 5×2 points). Students can earn a maximum of 35 points for homework (5×7 points) and up to 50 points for tests (5×10 points).

Based on the recorded states, a matrix $M(S_k)$ is created, which consists of six rows, corresponding to the time points t_j, and four columns, corresponding to the parameters p_i. Given that all state parameters are cumulative, each matrix element $p_i(S_k,t_j)$ is calculated as follows:

$$p_i(S_k, t_j) = \sum_{r=1}^{j} p_i(S_k, t_r). \quad (1)$$

By summing the individual rows of the matrix $M(S_k)$, we can analyze the progress of student S_k over time. This can be represented by the discrete progress function $f_p(S_k,t_j)$:

$$f_p(S_k, t_j) = \sum_{i=1}^{4} p_i(S_k, t_j), \quad \text{where } j = 1, \dots 6. \quad (2)$$

The value of $f_p(S_k,t_6)$ represents the final result achieved by student S_k in the course, and the final grade is based on this value. Grades range from 5 to 10, where a grade of 5 corresponds to a score between 51 and 60 points, with each subsequent grade representing an additional 10 points.

The progress functions for all students considered serve as input vectors for the classifier. The progress function values in the time moments t_j, for $j = 2,...,6$ are T2, T3, T4, T5, and T6, respectively. Mean of the progress function values in the time moments for male and female separately is presented in Fig. 3.

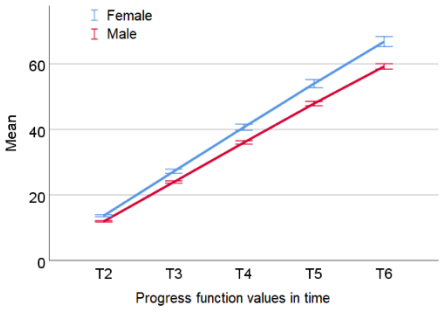

Fig. 3. Mean of the progres function values (T2-T6) in the time moments t_2-t_6 by gender

IV. Multi-layer Perceptron Classifier Application

A Multi-layer Perceptron (MLP) classifier is used to analyze training data and predict student grades, which ranged from 5 to 10. Data analysis was conducted using IBM SPSS Statistics 25. The MLP, introduced by Frank Rosenblatt [5], employs feedforward architecture with one or more hidden layers, making it suitable for classification tasks. The dataset was randomly split into 70 % for training and 30% for testing, approximately. We conducted classification tests to determine the optimal hyper-parameters, using a hyperbolic tangent activation function in the hidden layer and the "Softmax" function in the output layer. To prevent overfitting, we ensured our dataset was large enough and evaluated model performance on a separate validation set. The model predicted grades in four experiments: I, II, III, and IV (Table I) based on Region, and Gender as features, and Age, AGV, STEM, T2-T6 as covariates, with a stopping rule based on training error, a time limit of 15 minutes, and a relative change threshold. The multilayer perceptron architecture for the third experiment is shown in Fig. 4.

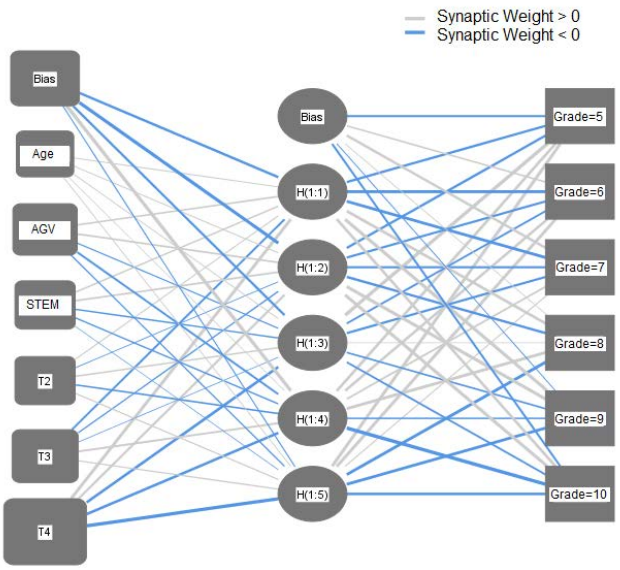

Fig. 4. Multilayer Perceptron architecture for the third experiment. Classification is based on the Age, AGV, STEM and the values of progress function in milestones: T2, T3, and T4. A hidden layer activation function was hyperbolic tangent, while the output layer activation function was “Softmax”. The target variable/class was the student’s grade marks ranging from 5 (drop down) to 10 (excellent)

V. The Cohen’s Kappa – A Measure of Agreement

We assessed MLP multi-class classification using a gold standard to measure the agreement between observed and predicted grades. The Cohen’s Kappa (Kappa) is commonly used to evaluate Machine Learning performance, particularly in multi-class scenarios. Kappa ranges from -1 to 1, with values close to 1 indicating strong positive correlation and accurate predictions. Kappa of 0 implies no correlation, meaning the classifier randomly assigns classes.

Let is G the set of class labels with cardinality k, where i, j=1,2,...,k and k is number of classes. The confusion matrix C^k is a k-dim square matrix or contingency table with elements c_{ij} representing the number of cases with true label i classified into group j. In the multi-class case, the Kappa can be defined in terms of a confusion matrix C^k for k classes and according to (4)–(7):

$$\text{Kappa} = \frac{c \cdot s - \sum_{j=1}^{k} p_j \cdot t_j}{s^2 - \sum_{j=1}^{k} p_j \cdot t_j}, \quad (3)$$

where are

$$t_j = \sum_{i=1}^{k} c_{ij}, \quad (4)$$

$$p_i = \sum_{j=1}^{k} c_{ij}, \quad (5)$$

$$c = \sum_{i=1}^{k} c_{ii}, \quad (6)$$

$$s = \sum_{i=1}^{k} \sum_{j=1}^{k} c_{ij}, \quad (7)$$

- t_j is the number of times class j truly occurred (column total),
- p_i is the number of times class i was predicted (row total),
- c is the total number of samples correctly predicted, and
- s is the total number of samples.

The Kappa statistics is ranging from –1 to +1, and the interpretation is as follows:

[0.00, 0.09] agreement equivalent to chance,
[0.10, 0.20] slight agreement,
[0.21, 0.40] fair agreement,
[0.41, 0.60] moderate agreement,
[0.61, 0.80] substantial agreement,
[0.81, 0.99] near perfect agreement, and
1.00 is perfect agreement.

VI. Results and Discussion

We collected socio-demographic and performance data from 700 students in blended STEM learning environments. Using formative and summative assessments, we developed predictive models to classify student achievement and predict final grades based on socio-demographic factors [6, 7]. Initially, we relied on pre-enrollment attributes, assuming no prior knowledge, but we can incorporate entrance tests to assess this.

Our research aimed to track course participants' activities and progress throughout the semester leading to the final exams. The final grades by gender are

shown in Fig. 5. The first experiment focuses on classification based on social-demographic factors (SDF) such as Region, Gender, and Age, as well as academic factors (AF) including AGV, STEM, and T2–T6. The MLP classification results were validated using a confusion matrix and statistical measure of agreement Kappa (Table).

MULTI-CLASS CLASSIFICATION BY MLP

Experiment	MLP Input variables	Set	N (%)	Precision (%)	Kappa	Normalized importance (%)	
I	*Region Gender Age AGV STEM T2-T6*	Training	476 68 %	99.2	0.971	*T6*	100
						T5	67.4
						AGV	19.1
						Age	18.6
						STEM	17.2
		Test	224 32 %	94.6		*T4*	12.1
						T2	9.5
						T3	8.1
						Region	5.5
						Gender	3.5
II	*Region Gender Age AGV STEM T2 T3 T4*	Training	502 71.6 %	84.6	0.791	*T4*	100
						AGV	37.8
						STEM	31.6
						T3	30.8
						Age	29.8
		Test	198 28.4 %	80.4		*T2*	19.7
						Region	12.3
						Gender	2.3
III	*Age AGV STEM T2 T3 T4*	Training	484 69.1 %	84.9	0.802	*T4*	100
						T3	39.9
						AGV	33.6
						STEM	19.2
		Test	216 30.9 %	82.9		*T2*	18.7
						Age	8.8
IV	*T2 T3 T4*	Training	502 71.7%	75.1	0.685	*T4*	100
						T3	33.8
						T2	15.7
		Test	198 28.3 %	74.7			

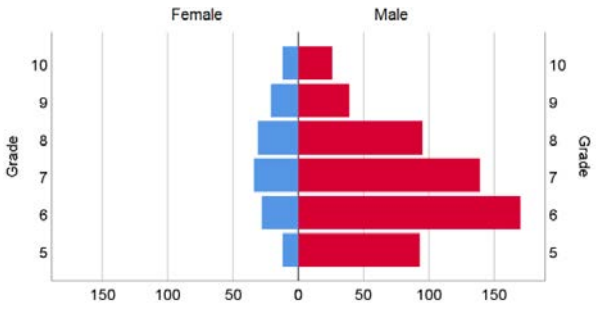

Fig. 5. Histogram of the final grades by gender

The input data is randomly divided into a training set (68 %) and a testing set (32 %). This classification serves as the final assessment of student progress, including the results from the final exam (T6). As expected, the classification achieved high precision, as shown in Table 1, with a nearly perfect agreement indicated by a Kappa value of 0.971. Among the academic factors, T6 and T5 are most important in the final evaluation, followed by AGV and STEM. Within the social-demographic factors, Age is the most significant, while Region and Gender are less important.

In the second experiment, we excluded the values of the progress functions T5 and T6 during the intervals t_5-t_6 from the classification. As shown in Table, the precision ranged from 80.4 to 84.6 %, with a substantial agreement reflected in the Kappa statistic of 0.791. We found that the SDF Region and Gender were the least important factors, which led us to exclude these SDF parameters from consideration in the third experiment. In this instance, the precision slightly improved, reaching between 82.9 and 84.9 %, with a Kappa value of 0.802. The most significant factors identified were the progress function values T4, T3, AGV, and STEM, while Age was deemed to be of lesser importance.

In the final fourth experiment, we based the prediction of final success solely on the progress function values T2 to T4. This classification yielded 74.7 to 75.1 % precision, with substantial agreement and the Kappa value of 0.685.

A comparison of the results from predictive modeling of final student grades using the Promethee II method [4] versus traditional progress tracking and grading revealed the following outcomes.

For 400 students using their academic achievements from T2 to T6 with the Promethee II method, the prediction accuracy for final grades was 75.1 % for the training set and 74.1 % for the test set. In contrast, when examining a larger group of 700 students with the traditional progress tracking method, the accuracy was 73.9 % for the training set and 79.5 % for the test set. Results are in the same class of substantial agreement, and the slightly higher accuracy in the traditional method can be attributed to the significantly larger prediction set.

Grading based on the progress function at all five time moments, from T2 to T6, achieved near-perfect agreement with accuracy between 99.2 and 100 % for both applied methods.

When comparing the first and second experiments shown in Table, it is evident that the covariate representing the value of the progress function at the

last observed moment is the most significant, as indicated by its cumulative value. In contrast, factors such as the region where the student completed their previous education and gender have the least impact on the student's final success in the exam. When comparing the second and third experiments, where the factors of region and gender are excluded, neither the accuracy nor the Kappa statistic decreased significantly. In conclusion, age and the academic factors as AGV and STEM significantly impact the accuracy of predicting final exam scores.

VII. Conclusion

In this paper, we examined the effectiveness of the Multilayer Perceptron (MLP) method in predicting student performance in higher education, using a dataset composed of both demographic and academic engagement variables. Our results demonstrate that MLP yields high accuracy in classifying student success levels, particularly when trained on a well-structured set of input indicators such as attendance, test activity, and exam results.

The combination of traditional methods and MLP classification offers an additional layer of interpretability by ranking student profiles based on various criteria. This dual method approach supports not only accurate prediction but also meaningful prioritization of intervention strategies.

These findings confirm our initial hypothesis that combining machine learning with classical decision-making techniques can improve both the accuracy and transparency of educational diagnostics. Future research should explore real-time integration of such models into learning platforms to provide timely support for at-risk students.

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Interactive System for Online Signature Verification in Forensic Examinations

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Abstract. **The paper describes an interactive system designed to verify the genuineness of a signature made on a tablet on behalf of a specific person. To build an individual classifier of signatures of this person, it is necessary to have several genuine signatures made by this person earlier. Based on a limited set of about 7–15 genuine signatures, a one-class classifier is built, allowing an expert to recognize the authenticity of signatures of this person. To the best of our knowledge, this is the first system described in the literature and designed to perform a forensic investigation of online signatures based on a limited set of genuine signatures of one person.**

Keywords: **online signature, verification, classifier, dynamic features, DTW**

I. Introduction

Handwritten signature verification is a behavioral biometric system that recognizes the authenticity of a signature using the stored signatures of the same person [1]. It finds application in areas such as banking, document transactions, access control, etc. [2].

One online signature is described by data in a form of several time series, i.e. initially it has a lot of numbers that must be analyzed by a forensic expert. At least a dozen signatures of the person are presented for a typical examination. To analyze all the provided data, the expert must have a convenient computer tool. Analysis of available literary sources shows that such software is currently absent [1–4]. This report describes an interactive system for a forensic verification of online signatures, developed in our team.

II. Method

A. Peculiarities

An online signature is described by the stylus location and its characteristics at regular intervals: *X* coordinate (*Xi*), *Y* coordinate (*Yi*), stylus pressure (*Pi* stylus tilt (*TILi*), stylus azimuth characteristics (*Ai*), and the data registration time (*Ti*). Not all tablets register stylus angular parameters, so we do not use them, only {*Xi, Yi, Pi, Ti*} at every *i*-th point. The number of points in each signature is different.

As a result of a number of comparative experiments, a method and interactive software for verifying online signatures were developed. The dynamic features described in the papers [5, 6] were used. A distinctive feature of the method is that a limited number of genuine signatures made by this person earlier are used to study the signature, based on which a writer-dependent classifier is built that studies the signatures of only this person.

We normalize the original signature data and calculate some dynamic features (see details in [5, 6]). Then we calculate the DTW (Dynamic Time Warping) distance between the features [7]. Main of them are speed and acceleration in *X*, *Y* and *XY* directions.

We calculate dtw-distances between features of every pair of given genuine signatures and calculate an adaptive threshold for further verification.

The dtw transformation compares two time series *M*1 and *M*2 (or sets of real data). Unlike correlation analysis, dtw can compare time series of different lengths. The idea of this transformation is to calculate the distances (usually Euclidean) between pairs of all points of both sets (see Fig. 1) and to construct the shortest path from the pair of initial points (*M*1(1), *M*2(1)) to the last ones (*M*1(*n*1), *M*2(*n*2)). The length of this path is called the dtw-distance and estimates the closeness (or similarity) of two data sets. The dtw-distances are more accurate than other metrics in estimating the invariance and changes in the online signature over time [8].

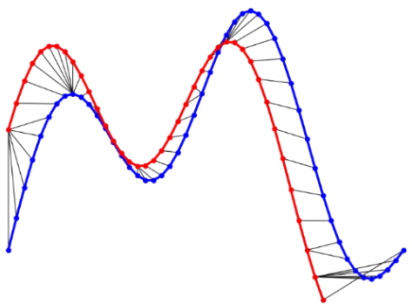

Fig. 1. Idea of dtw-distance calculation between two series

At the next stage, we calculate the dtw-distances between the features of the signature under investigation and each of the *N* genuine signatures. If half of these distances are less than the threshold, the signature is considered as fake.

B. The Verification Procedure

The algorithm for performing a forensic examination of the authenticity of a signature based on our tool consists of the following steps:

1. A set of N ($15 > N > 6$) genuine online signatures of the person whose signature needs to be verified are pre-selected and loaded into a separate directory. All signatures must be presented in the same file format. The data format may be TXT or CSV.

2. Data is read from files containing all genuine online signatures of the person, located in the directory interactively specified by an operator. All signatures are displayed on the monitor. For the visualization of signatures, only those points are used for which the pressure on the screen $P > 0$, the selected points are approximated by broken lines. The file containing the signature under study is read, its data is loaded.

3. To build a classifier, $N > 6$ genuine signatures are selected automatically or interactively from the loaded genuine signatures. The selected signatures are highlighted on the monitor.

4. The data of all signatures are normalized by the following procedures:

a) only one point is retained from a sequence of adjacent points with equal coordinates;

b) the set of points representing the signature is normalized by length [9]. The length of the normalized signature is specified by a selected constant, or is equal to the median value of the lengths of all selected genuine signatures;

c) the *X*, *Y* coordinates of all signatures are rotated using the principal component analysis method;

d) the data of all signatures is normalized by amplitude [9]. There are two main variant of *A* data normalization:

$$\textit{min-max norm}\ (A) = (A - \min(A))/(\max(A) - \min(A)),$$

$$\text{or}\ \ \textit{z-norm}\ (A) = (A - \mu)/\sigma,$$

where μ is mean of A, σ is standard deviation.

5. Dynamic features of each signature (genuine and verified) are calculated in three directions: *X*, *Y* and *XY*, and stored as signature execution speeds Δx, Δy, Δxy and accelerations of their writing $\Delta\Delta x$, $\Delta\Delta y$, $\Delta\Delta xy$.

6. Between all possible pairs of selected genuine signatures, dtw-distances of features of each of the six features are calculated, like for example between Δx sets of signatures 1 and 2: $dtw(\Delta x1,\Delta x2)$.

7. Each pair of genuine signatures is represented by six parameters in the form of dtw-distances. This pair is represented by points in two three-dimensional feature spaces (velocity space and acceleration space). Distances from each point to the origin of coordinates of the specified spaces are calculated.

8. The threshold value *Z* limiting the dtv-distance from each pair of genuine signatures to the origin of the feature space coordinates is calculated adaptively. Since fake signatures differ from genuine ones, the dtv-distances for genuine-verifiable signature pairs are generally greater than this threshold, and we obtain a simple threshold classifier describing the class of genuine signatures of a particular person.

9. Any verified signature generates *N* dtv-distances formed by pairs of the verified-genuine signature. The analysis of the authenticity of this signature consists in assessing the number of these distances exceeding the threshold *Z*. If this number in total is greater than *N* in two feature spaces described above, the signature is considered as genuine. Otherwise, it is fake.

III. EXPERIMENTS

A. Data

For system testing, we verified signatures of the first 100 people from the database DeepSignDB [10] in streaming mode. Every person has 25 genuine and 25 forged online signatures captured by tablet Watcom, totally 5000 signatures. Additionally, we examined 378 signatures of 19 people registered in our institute. The number of forged signatures was significantly less than the genuine ones, but they were of a higher quality of forgery than the fake signatures from the DeepSignDB database.

B. Evaluation of the result

The signature verification accuracy (*Acc*) was estimated using the following formulas (separately for genuine and counterfeit signatures, since their number may be different):

$$\textit{Acc genuine} = \frac{TP}{G},$$

$$\textit{Acc forgery} = \frac{TF}{F},$$

where *TP* is the number of correctly recognized genuine signatures; *TF* is the number of correctly recognized fake signatures; *FP* is the number of incorrectly recognized genuine signatures; *FN* is the number of incorrectly recognized fake signatures; $G = TP+FP$ is the number of genuine signatures of all people; $F = TF+FN$ is the number of counterfeit signatures used in verification.

In addition, the balanced accuracy was calculated

$$Acc\ balanced = (\frac{TP}{TP+FP} + \frac{TF}{TF+FN})/2.$$

If $G = F$, the *Acc balanced* estimate coincides with the generally accepted notion of accuracy

$$Acc = \frac{TP+TF}{TP+FP+TF+FN}.$$

C. Experimental Results

To check the authenticity of each of over 5300 signatures, we automatically selected the first nine ($N = 9$) genuine signatures of the person on whose behalf the examined signature was submitted. If this signature was among the first N, another genuine signature was taken for construction a classifier. Note that some people made significantly different genuine signatures (see Fig. 4 and 6), and sometimes the automatically selected signatures were significantly different from the one being verified. Because of this, some automatic verification results for individual signatures were incorrect. Using interactive signature selection, we may improve the recognition accuracy of some signatures.

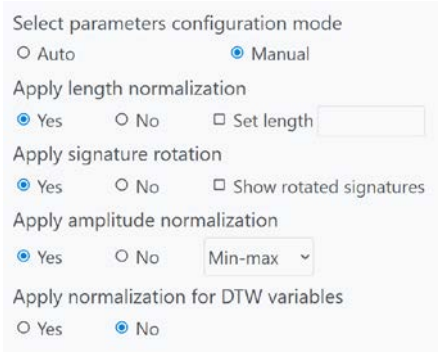

Fig. 2. Signature data normalization procedure selection menu

IV. Conclusion

This paper briefly describes the first computer system designed for interactive verification of online signatures by a forensic expert.

The developed system is very flexible. The system interface is simple and allows you to return the analysis several steps back. It allows to select a set of genuine signatures for building a writer-dependent classifier, select options for signature pre-processing, save intermediate graphical results and generates a report about the execution of the verification procedure, indicating all the data used, the procedures performed and the obtained result.

A series of experiments were performed on online signatures from the largest available database DeepSignDB and on signatures of people from our laboratory.

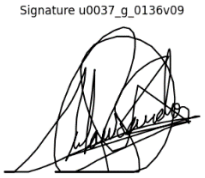

Fig. 3. A genuine signature of the 37-th person used for test verification

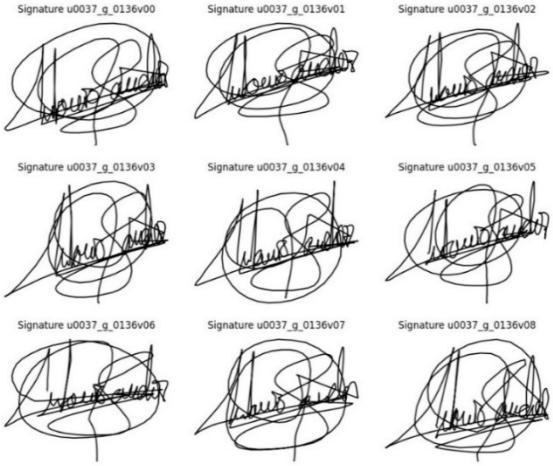

Fig. 4. Nine genuine signatures of the 10-th person automatically selected

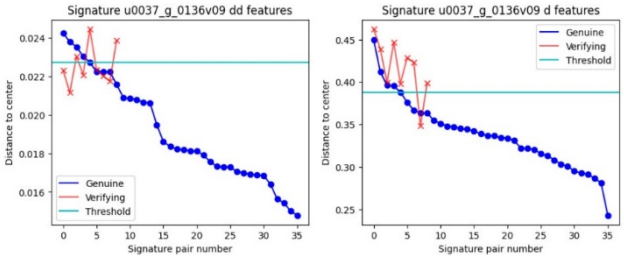

Fig. 5. Verification result of the genuine signature with automatic data selection is incorrect. Less than N/2 red points are below the threshold

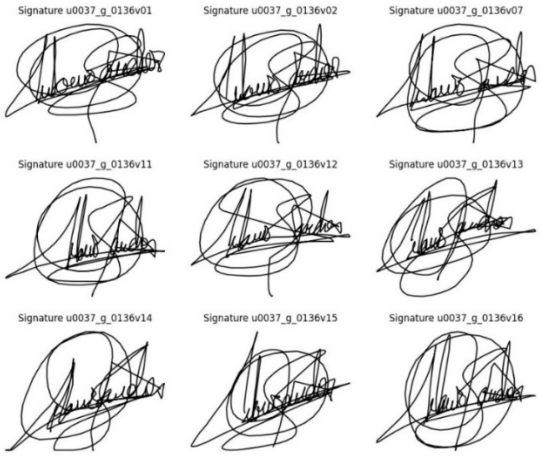

Fig. 6. Nine genuine signatures manually selected

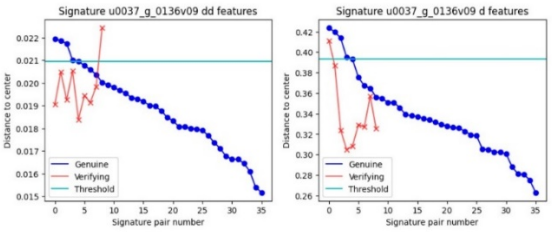

Fig. 7. Verification result of the same genuine signature is correct. More than N/2 red points are below the threshold

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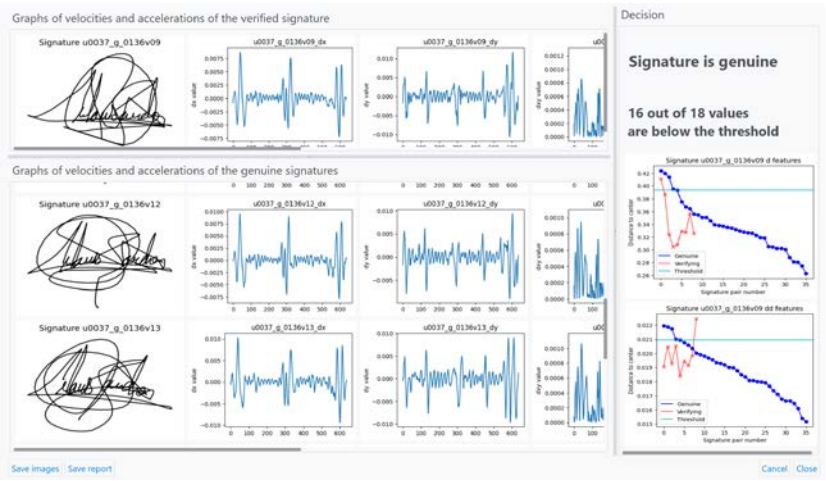

Fig. 8. The final window of verification procedure. The top-left signature is correctly recognized as genuine

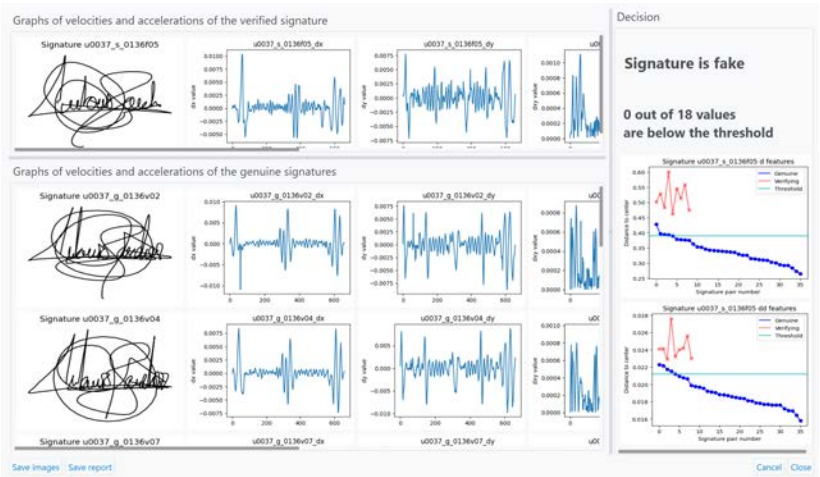

Fig. 9. The final window of verification procedure. The top-left signature is correctly recognized as genuine

Towards Unified Transformer for Drone Based Multi-Task Object Detection

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Abstract. **Drone based visible-thermal object detection is a highly promising vision task. It significantly improves detection accuracy under low-light or adverse weather conditions while enhancing the stability and flexibility of the detection system. However, when handling three distinct tasks – visible, thermal, and visible-thermal object detection, existing methods typically require separate training for each task. This approach leads to substantial computational redundancy and resource wastage, while also limits the interaction between multimodal information. To address these issues, this paper proposes a unified multi-task framework that enables the model to handle different tasks with a single training session, eliminating the need for repeated individual training. Additionally, we introduce a task token embedding method, which effectively guides the model to distinguish task types and learn multimodal information during training. Experiments conducted on the DroneVehicle dataset demonstrate that our method successfully resolves different tasks and achieves outstanding performance in three tasks (visible, thermal, visible-thermal). These results indicate that our approach provides a solution to unified drone-based object detection and exhibits significant potential in cross-task generalization.**

Keywords**: Drone-based Object Detection, Visible-Thermal Object Detection, Unified Multi-Task Framework, Task Token Embedding, Cross-Modality Interaction**

I. INTRODUCTION

Object detection is a fundamental challenge in computer vision, requiring algorithms to possess robust classification capabilities and precise spatial localization to accurately identify and locate various targets (such as humans, animals, and vehicles) in images and videos. In recent years, the rapid advancement of deep learning, particularly the introduction of the Transformer architecture has significantly improved performance in this field [1–2]. The rise of unmanned aerial vehicles (UAVs), with their exceptional mobility and efficient data acquisition capabilities, has further spurred the development of UAV-based object detection tasks, offering new solutions for target detection in complex environments.

However, when UAVs operate under low light or adverse weather conditions, single-modality visible images often fail to provide sufficient information for accurate object detection [3]. To address this limitation, visible and thermal fusion based object detection methods have emerged. This multimodal data fusion technique combines features of visible and thermal images, significantly enhancing detection accuracy and robustness in challenging scenarios.

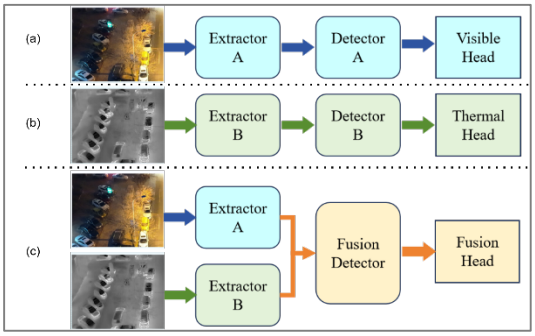

Fig. 1. Independent Task-Specific Model Frameworks. (a) Vsibile detector. (b) Thermal detector. (c) Visible and thermal fusion based detector

In recent years, numerous multimodal object detection methods leveraging visible and thermal data have been proposed [4–5]. However, as illustrated in Fig. 1, existing approaches typically design separate models for different tasks. While task-specific models remain a common choice, they suffer from several drawbacks: 1. Parameter redundancy and inefficient resource utilization: Each task (visible-based, thermal, or visible-thermal fusion) requires training an independent model, leading to redundant parameters and suboptimal resource usage. 2. Limited cross-modal learning: Training on single-task datasets restricts the model's ability to exploit inter-task correlations, resulting in poor generalization across different modalities. 3. Repetitive training and validation: Despite minor differences in frame-work design, separate training and validation pipelines must be repeated for each task, increasing redundancy in workflow [6]. To address these issues, we investigate whether a unified model can consolidate all tasks into a single framework, represented in Fig. 2, achieving competitive accuracy while minimizing computational overhead – a critical requirement for UAV edge devices with resource constraints [7].

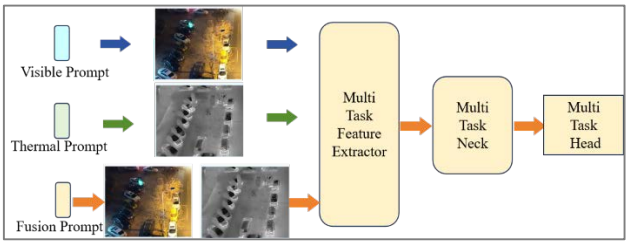

Fig. 2. Unified Multi-task Framework

To explore this possibility, we propose TUMDet, a unified multi-task framework for visible, thermal, and visible-thermal object detection. Unlike traditional multi-task models handling heterogeneous tasks (e.g., detection and segmentation), TUMDet distinguishes tasks by input modalities.

Generally speaking, we develop a unified multimodal object detection model tailored for UAV-based detection across diverse scenarios. By integrating task token embedding and pixel-level fusion, our framework enables efficient cross-modal processing. During training, task tokens guide the model to differentiate tasks and learn modality-specific representations, thereby enhancing generalization. The proposed framework minimizes computational redundancy and resource waste, offering an efficient, flexible, and unified solution for UAV object detection. Experiments on the DroneVehicle dataset demonstrate that our method effectively handles multiple modalities and achieves excellent performance in visible-thermal fusion detection [8].

In summary, the contributions of this paper are as follows:

- We propose a transformer-based unified architecture capable of simultaneously handling visible, thermal, and visible-thermal object detection tasks within a single model. Compared to existing task-specific models, our framework employs uniform patch embedding for all input types (single-modality/dual- modality) and shares the backbone network, requiring only a single training process to significantly improve resource utilization efficiency.
- We innovatively introduce learnable task tokens to achieve dynamic modality adaptation without modifying the network architecture. By embedding task tokens as high-dimensional prompt vectors, the model can perform task-aware adaptation through these tokens while maintaining the original inference speed.
- To further enhance cross-modal learning, we propose a pixel-level fusion mechanism that integrates visible and thermal embeddings at the input stage. This ensures seamless compatibility with the shared backbone, allowing both modalities (and their fusion) to be processed identically while preserving structural consistency. The design explicitly leverages cross-modal feature interaction for richer representations, without compromising on the backbone's efficiency and scalability.

II. Related Work

A. *Visible-Thermal Multimodal Object Detection*

The advancement of visible-thermal object detection stems from its enhanced robustness in challenging conditions versus single-modality methods [4]. Early CNN-based approaches [9] employed feature-level fusion with attention mechanisms, later improved by dynamic weighting strategies [10]. Recent Transformer-based methods [11] model cross-modal dependencies but require separate training pipelines for different input types, leading to parameter inefficiency and missed cross-task synergies. Current limitations include modality-specific bias [12] and the inability to unify detection across visible, thermal and fused inputs [13]. Our solution combines adaptive task tokens with pixel-wise fusion, maintaining Vision Transformer (ViT) compatibility while enabling dynamic modality adaptation.

B. *Multi-Task Object Detection Models*

Traditional multi-task learning frameworks in object detection, such as YOLOv8 [14], DETR [2], Pixel2Sequence [15] and Mask R-CNN [16], primarily

focus on task diversity (e.g., joint detection and segmentation) but assume homogeneous visible inputs, making them ineffective for multimodal scenarios (e.g., visible-thermal fusion) where dynamic adaptation and modality-specific feature preservation are crucial [17]. Recent modality-aware approaches employ separate detection heads [18] or modality-specific adapters [19], but these introduce task-specific redundancy and fail to unify single- and multi-modality tasks. In contrast, our method unifies tasks through learnable tokens that embed modality guidance directly into a shared backbone [20]. Unlike conventional channel concatenation [21], we use pixel-level fusion to maintain the original ViT token structure, resulting in a more efficient and flexible framework.

III. Models and Methods

To enable flexible processing of single-modality (visible/thermal) and dual-modality inputs across diverse UAV operational scenarios, we developed a multi-task adaptive model based on task token embedding prompts. This approach leverages the advanced Transformer architecture, capitalizing on its self-attention mechanism to effectively process long-sequence data and capture global dependencies. TUMDet is built on ViTDet [22], and it processes visible, thermal, or fused inputs through a shared backbone: inputs are converted into uniform-dimension tokens via patch embedding, with pixel-level fusion (instead of channel-wise concatenation) ensuring dimensional compatibility for ViT processing.

Specifically, the model assigns a unique task token to each input modality (visible, thermal, or visible-thermal), serving as a task-specific identifier. During both training and inference, the model dynamically adjusts its internal structure and parameters based on the input modality and task requirements, ensuring optimal performance.

A. Single Modality Input

The model's input layer processes visible images (I_{vis}), thermal images (I_{th}), or paired visible-thermal UAV-captured images, standardizing them through resizing and normalization to fixed dimensions $H \times W \times C$ (height, width, channels), where $I_{vis} \in \mathbb{R}^{H\times W\times C}$, $I_{th} \in \mathbb{R}^{H\times W\times C}$. After preprocessing, a dynamically reconfigurable Patch Embedding layer converts the images into token sequences by dividing them into fixed-size patches, mapping each patch to a vector while incorporating task identification information, forming sequential feature representations.

Specifically, for an input image I, it is partitioned into N patches of size $P \times P \times C$, where P denotes the patch edge length and C represents the number of channels. Each image patch I_i is flattened into a vector $x_i \in \mathbb{R}^{P\times P\times C}$, which is then transformed into an embedding vector $e_i \in \mathbb{R}^D$ via linear projection, where D indicates the embedding dimension

$$D = P \times P \times C, \tag{1}$$

$$e_i = Embedding(x_i). \tag{2}$$

For individual visible-light images I_{vis} and thermal images I_{th}, we partition them into $P \times P$ patches and flatten them into token representations, where $e_{vis} \in \mathbb{R}^{\frac{W}{P}\times\frac{H}{P}\times P\times P\times C}$, $e_{th} \in \mathbb{R}^{\frac{W}{P}\times\frac{H}{P}\times P\times P\times C}$.

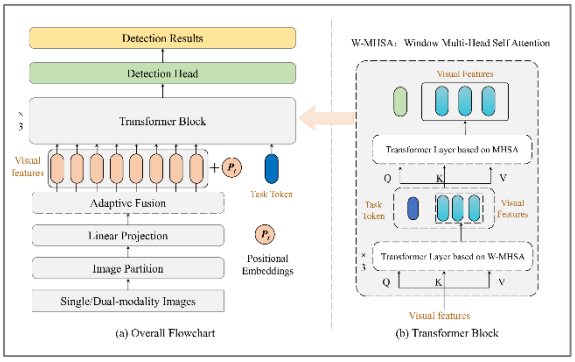

Fig. 3. TUMDet Architecture. Different tasks correspond to different task tokens. (a) Overall Flowchart. (b)Transformer Block with task token

B. Dual Modality Input

For the case of simultaneous visible-light and thermal input I_{vis+th}, we introduce adaptive weights $W_{vis} \in \mathbb{R}^D$ and $W_{th} \in \mathbb{R}^D$ based on the patch embeddings of I_{vis} and I_{th} respectively. These weights automatically adjust the relative contributions of visible and thermal features through element-wise multiplication, establishing a balanced representation where both modalities effectively complement each other in the fused feature space. The weighting mechanism ensures that neither modality dominates while preserving its distinctive characteristics

$$e_{vis+th} = e_{vis} \cdot W_{vis} + e_{th} \cdot W_{th}. \tag{3}$$

C. Task Token Fusion

We introduce a task token-based adaptive strategy that enables modality-aware learning: task token, embedded as high-dimensional vectors from task labels, guide the backbone to distinguish modalities and refine features. These tokens act as dynamic prompts, allowing a single model to switch tasks without architectural changes. By sharing backbone parameters and eliminating redundant networks, TUMDet reduces storage/computational overhead while maintaining versatility – critical for resource-constrained edge devices like UAVs.

To achieve task token embedding, the model assigns a specific task token to each input modality as a unique

identifier for the task. The task token is a learnable vector that is input to the encoder together with the patch embedding vectors. Specifically, for single visible input, single thermal input, and dual-modal input, t_{vis}, t_{th}, and t_{vis+th} are defined as their task tokens respectively.

The introduction of task tokens aims to provide the model with prior task-level information, enabling it to dynamically adjust its internal structure and parameters according to different input modalities and task requirements. Specifically, the task token is a learnable vector with the same dimension as the patch embedding vector, i.e., $t \in \mathbb{R}^D$. During model training, the task token and patch embedding vectors are processed together through the encoder for feature extraction.

In the Multi-Head Self Attention stage, the task token is concatenated with the patch embedding vectors to form an enhanced feature sequence

$$E_{task} = [t, e_1, e_2, \dots, e_N]. \quad (4)$$

Here, E is the enhanced feature sequence, and t is the corresponding task token, where $E_{vis} \in \mathbb{R}^{(N+1)\times D}$, $E_{th} \in \mathbb{R}^{(N+1)\times D}$, $E_{vis+th} \in \mathbb{R}^{(N+1)\times D}$,

$$E_{vis} = [t_{vis}, e_{vis}], \quad (5)$$

$$E_{th} = [t_{th}, e_{th}], \quad (6)$$

$$E_{vis+th} = [t_{vis+th}, e_{vis+th}]. \quad (7)$$

The enhanced feature sequence is then fed into ViT for feature extraction and fusion in Multi-Head Self Attention stage. The encoder's Multi-Head Self Attention mechanism can capture the relationship between the task token and patch embedding vectors, achieving the fusion of task identification information and image features, and thereby adapting the image features to specific object detection tasks.

IV. Results

In this section, we first detail the datasets and evaluation metrics employed in our experiments. Subsequently, we provide comprehensive implementation configurations and experimental settings. To validate the effectiveness of our proposed method, we conduct ablation studies to analyze key components.

A. Datasets and Evaluation Metric

In our experiments, we utilize the DroneVehicle dataset to evaluate the performance of our proposed method. This dataset collects 28,439 Visible-Thermal image pairs, covering urban roads, residential areas, parking lots, and other scenarios. To comprehensively assess detection accuracy, we employ multiple metrics including mean Average Precision (mAP), mAP at IoU threshold 0.5 (mAP_50), and mAP at IoU threshold 0.75 (mAP_75). These hierarchical metrics collectively filter out false positives while providing granular evaluation at different localization precision levels.

B. Implementation Details

We trained the model end-to-end on NVIDIA RTX 4090 GPUs using only the DroneVehicle dataset. To stabilize convergence, we used dynamic learning rate scheduling to reduce gradient oscillation and speed up convergence. Data augmentation further improved model robustness across scenarios.

C. Ablation Experiment

To validate the effectiveness of the task token, we compared the baseline model (without task token) and the improved model (with task token). This design is based on the premise that task tokens provide explicit cross-modal guidance, enhancing complementary feature learning from multimodal data.

Ablation Experiment

Method	Metric			Modality
	mAP	***mAP_50***	***mAP_75***	
ViTDet-V	0.485	0.746	0.560	Visible
ViTDet-T	0.398	0.653	0.434	Thermal
ViTDet-Fuse	0.430	0.688	0.481	Visible-Thermal
TUMDet	0.506	0.748	0.591	Visible
TUMDet	0.404	0.650	0.444	Thermal
TUMDet	0.455	0.703	0.515	Visible-Thermal

ViTDet was trained separately for each of the three tasks for 100 epochs, with the best weights selected for testing. Similarly, TUMDet was trained for 100 epochs, and its best-performing weights were evaluated. As shown in Table 1, TUMDet outperforms ViTDet in both mAP and mAP_75 across all three tasks, demonstrating its ability to capture complementary information across modalities through task token learning – thus validating the efficacy of the task token design. Meanwhile, TUMDet achieves comparable performance to ViTDet in mAP_50, further confirming that our unified multi-task framework maintains competitive accuracy while significantly reducing computational resource demands. The consistent superiority of TUMDet in finer-grained metrics (mAP_75) suggests that task tokens not only enable parameter efficiency but also enhance feature discrimination for challenging cases. This aligns with our hypothesis that task tokens facilitate cross-modal learning, allowing the model to extract complementary features more efficiently from multimodal inputs.

These findings provide substantial evidence for the effectiveness of our approach in advancing cross-modal representation learning.

V. Conclusion

We propose TUMDet, a unified multi-task framework for visible, thermal, and visible-thermal

object detection in UAV applications. By leveraging task token embeddings and pixel-level fusion, our model efficiently handles multi-modal inputs within a single architecture, eliminating redundant task-specific training. Experiments on the DroneVehicle dataset show that TUMDet outperforms separately trained models in mAP and mAP_75 while maintaining strong mAP_50 accuracy. This confirms that task tokens effectively guide cross-modal learning, enabling dynamic adaptation to different tasks without architectural changes.

Our framework greatly reduces computational redundancy and resource usage, making it ideal for UAV edge devices with strict efficiency limits. TUMDet's success offers a blueprint for unified multi-modal detection models and demonstrates the power of task-conditioned learning in improving generalization. Future work will extend this approach to other multimodal tasks and optimize real-time UAV deployment.

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Impact of Data Augmentation on Plant Disease Classification Using Transfer Learning

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Abstract. **This work is devoted to the study of image preprocessing methods to improve the effectiveness of neural network models for the diagnosis of plant diseases. The paper analyzes modern approaches, including image transformation and data augmentation methods, and examines their impact on classification accuracy. The analysis of various preprocessing techniques is carried out. The results of the study can be applied to create more accurate and reliable systems for the automatic diagnosis of plant diseases.**

Keywords: **plant diseases, image classification, machine learning, neural networks, augmentation, transfer learning**

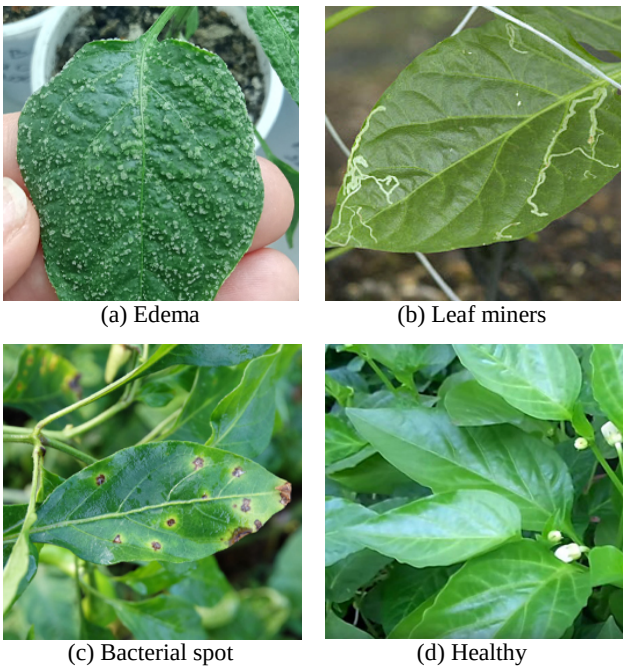
I. INTRODUCTION

At the beginning of the 20th century, the diagnosis of plant diseases was carried out exclusively by visual inspection. In the 1990s, classical machine learning algorithms appeared that work with predefined features, such as color, texture, shape of plant lesions, and others. However, manual feature extraction had limitations and did not allow achieving high accuracy in difficult conditions.

Modern agriculture lies at the intersection of technology and biological processes, and there is a growing demand for automated systems to monitor and diagnose plant health. Plant diseases (see Fig. 1) can significantly reduce crop yields and negatively impact the economic stability of the agricultural sector. Therefore, early, and accurate detection of pathological symptoms on leaves, fruits, and other plant parts is of critical importance [1–2].

Traditional diagnostic methods rely on expert visual assessments, which have numerous limitations, including subjectivity, the need for constant human presence, and limited capacity to scale across large fields. The emergence of computer vision and neural networks has enabled automation of plant disease detection with accuracy that can match or even exceed that of human experts. However, the performance of such systems heavily depends on the quality and quantity of the training dataset, as well as on how the data is preprocessed [3–4].

A key challenge in applying deep learning to plant disease detection is the scarcity and heterogeneity of annotated image data. Unlike tasks such as face recognition or object classification, the agricultural domain lacks large-scale, well-labeled image datasets. This limitation is further exacerbated by the variability of symptoms across plant species, lighting conditions, developmental stages, and environments. In such settings, the data preprocessing strategy becomes as important as the model architecture itself.



(a) Edema (b) Leaf miners

(c) Bacterial spot (d) Healthy

Fig. 1. Plant deseases

With the development of diagnostic technologies, there has been a gradual transition from traditional methods based on manual image analysis to the use of machine learning algorithms and, eventually, deep neural networks. Nowadays, neural network models are actively used in the field of automatic diagnosis of plant diseases, in which not only network architecture plays an important role, but also image preprocessing methods.

To overcome these limitations, researchers commonly use data augmentation – a set of techniques for artificially expanding the training set by applying transformations such as rotations, brightness and contrast adjustments, flipping, and more. More advanced approaches involve generative models capable of synthesizing realistic new images. However, it remains unclear which augmentation techniques truly improve model performance and which ones introduce noise or degrade accuracy.

Thus, the motivation of this work lies in the need for a systematic and experimentally grounded evaluation of different data preprocessing methods for training neural networks in the context of plant disease classification. The findings are intended to improve the accuracy and robustness of these models and offer practical guidance for agricultural AI applications.

II. Algorithms

Based on the application area, it was decided to use the transfer learning methodology to solve the problem of classifying images of plant diseases. PyTorch has many model architectures for classifying images with pre-trained weights [5].

To address the task of classifying images depicting plant disease symptoms, this work employs a convolutional neural network (CNN) architecture based on transfer learning. Specifically, a pretrained model from the ResNet family was used due to its proven effectiveness in general-purpose image classification tasks.

Transfer learning enables the reuse of knowledge acquired by a model on a large-scale dataset (e.g., Fig. 2) and adapts it to a new, narrower domain – in this case, plant disease images. This approach is particularly beneficial when only a limited number of labeled examples is available. It allows for faster training and reduces the risk of overfitting.

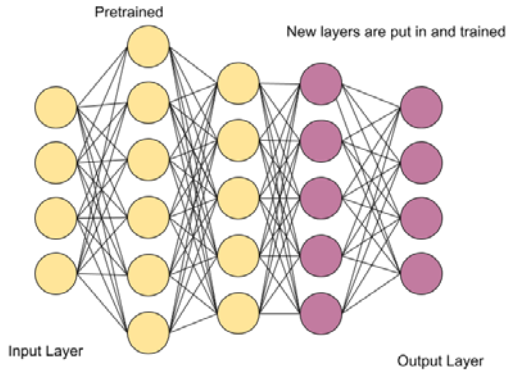


Fig. 2. ImageNet

The model was trained on both the original dataset and several augmented datasets created by applying image transformations. Augmentation was used not only to increase the dataset size but also to improve generalization by exposing the model to diverse visual patterns.

The following preprocessing techniques were applied:

- Contrast – contrast enhancement to highlight textures;
- Grayscale (GS) – conversion to grayscale to evaluate the importance of color information;
- BlackWhite (BW) – binarization, to test whether simplified features are sufficient;
- Rotate (Rot)– random rotations and flips;
- Combinations – mixtures of the above transformations.

Model performance was evaluated using the following metrics:

- Accuracy – overall classification correctness;
- Precision, Recall, F1-score – calculated using macro and weighted averages.

The overall algorithmic pipeline can be summarized as:

- Loading and augmenting the dataset
- Training the ResNet-based model with a frozen base and trainable classifier
- Evaluating the model using the chosen metrics on a separate test set.

III. Numerical Experiment

The experimental section aimed to quantitatively evaluate the impact of different data augmentation strategies on classification performance. The baseline dataset consisted of original plant disease images. Augmented versions were added to create expanded training sets. Importantly, augmented images supplemented rather than replaced the originals, effectively increasing the dataset size.

The results indicate that the highest performance was achieved using contrast-enhanced images (see Table I). Both the standalone “Contrast” dataset and the combined “Contrast + Train” dataset achieved an accuracy of 0.722 and a macro F1-score around 0.726. This suggests that emphasizing edges and details helps the model learn more discriminative features.

In contrast, the use of Grayscale and BlackWhite transformations led to a significant drop in performance (accuracy as low as 0.083 and 0.194, respectively). These findings highlight the crucial role of color features in distinguishing between different plant diseases.

Experiments with combined augmentations (e.g., Contrast + Rotate + Train or the full combination

"All") did not consistently lead to better performance. In fact, the largest combined dataset (fivefold in size) showed a decrease in accuracy compared to simpler configurations. This outcome indicates that excessive or poorly chosen augmentations can introduce visual noise that hinders learning.

TABLE I. AUGMENTATION

Augmentation	Accuracy	Prec. (m)	Recall (m)	F1-sc. (m)	Prec. (w)	Recall (w)	F1-sc. (w)
Train (T)	0.61	0.61	0.61	0.58	0.68	0.61	0.60
Contrast	0.72	0.79	0.74	0.72	0.79	0.72	0.71
Grayscale	0.08	0.00	0.10	0.01	0.01	0.08	0.01
BlackWhite	0.19	0.16	0.16	0.12	0.16	0.19	0.13
Rotate	0.55	0.60	0.5	0.53	0.61	0.55	0.54
Contrast + T	0.72	0.75	0.77	0.72	0.79	0.72	0.71
GS + T	0.52	0.53	0.59	0.53	0.53	0.52	0.49
BW + T	0.61	0.62	0.59	0.57	0.65	0.61	0.6
Rot + T	0.52	0.55	0.53	0.51	0.59	0.52	0.53
Contrast + Rot + Train	0.66	0.73	0.71	0.68	0.76	0.66	0.68
Contrast + GS + BW + Rot + T	0.52	0.64	0.53	0.53	0.64	0.52	0.54

Augmentation involves enlarging the training dataset by duplicating the original images with transformations applied to them. The strategies "Rotate 140" and "Contrast 1.25" were chosen as such transformations, since they showed the best metrics as a result of the tests conducted above. And also, since the accuracy of the model remained at a high level with all possible rotations, two more image transformation strategies "Vertical" and "Horizontal" were added for augmentation – vertically and horizontally reflected images, respectively.

As hyperparameters of the model, it was necessary to choose the optimal number of epochs, as well as the step size for the weight optimization algorithm. The graphs in fig. 3, 4 show how the loss function and accuracy changed for the test sample at different step sizes ($LR = \{10^{-3}, 10^{-4}, 10^{-5}\}$) with each epoch of model training. The data set obtained as a result of augmentation using the "Contrast + Rotate + Train + Vertical" strategy was used as a training sample.

Based on the graphs (Fig. 3, 4), it can be concluded that 3–6 epochs will be enough for the model to train. Further, the model was trained at $LR = 10^{-4}$ over five epochs.

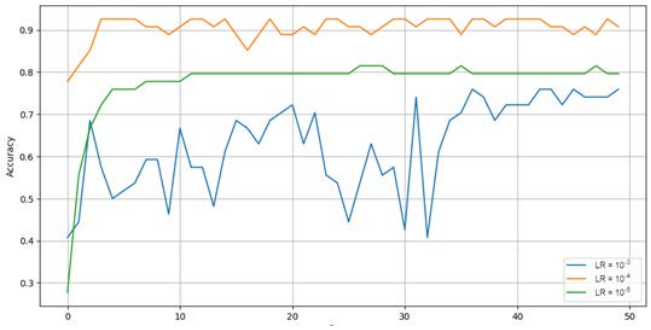


Fig. 3. The accuracy value depending on epoch's number

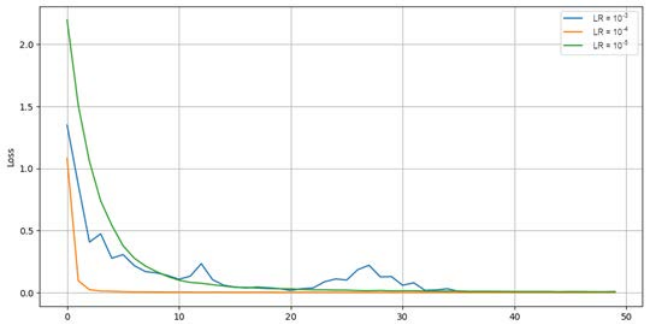


Fig. 4. The error value depending on epoch's number

The final model demonstrates high efficiency with Accuracy 0.93 and F1-score 0.93 (see Table II). The results allow us to recommend the model for practical use in systems for diagnosing pepper diseases.

TABLE II. METRICS OF THE FINAL MODEL

Ratio	Value
Accuracy	0.93
Precision (macro avg)	0.94
Recall (macro avg)	0.92
F1-score (macro avg)	0.93
Precision (weighted avg)	0.94
Recall (weighted avg)	0.93
F1-score (weighted avg)	0.93

In summary, the experiments revealed that not all augmentation methods are equally beneficial. Moderate, targeted augmentations such as contrast enhancement are effective, while aggressive combinations may reduce classification accuracy.

IV. CONCLUTIONS

1) Data preprocessing plays a critical role in training deep learning models for plant disease classification, particularly when dealing with limited and heterogeneous datasets.

2) To improve the accuracy of the image classification model for plant diseases, it is recommended to use augmentation with preservation of color characteristics and moderate geometric transformations.

3) Different augmentation techniques have varying levels of effectiveness. Among those tested, contrast enhancement proved to be the most beneficial in improving model accuracy and generalization.

4) Color information is essential: converting images to grayscale or binary form significantly reduces model performance, emphasizing the importance of color features in visual disease diagnosis.

5) Combining augmentations should be done with care. Introducing excessive or uninformative transformations can degrade model accuracy rather than improve it.

6) The results support the use of adaptive and selective augmentation strategies, where only meaningful transformations are applied to highlight relevant features.

7) Experiments with hyperparameters had shown that a properly selected learning rate allows the model to quickly achieve high classification accuracy with a small number of epochs. The analysis of metrics and the error matrix confirms the balanced operation of the algorithm for all classes of diseases, demonstrating the effectiveness of the chosen approach to learning and data augmentation. The experiments allowed optimizing the classification model of plant diseases, revealing effective parameters for augmentation and for training. The model has achieved high accuracy (Accuracy 0.93).

Overall, this work contributes to applied computer vision in agriculture by providing practical guidelines for data preparation and training deep learning models under data-scarce conditions.

ACKNOWLEDGMENT

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Evolutionary Optimization of Artificial Neural Networks for Power-Efficient Hardware Deployment

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Abstract. **The study explores methods and algorithms for the evolutionary optimization of artificial neural networks. The aim of the work is to reduce memory usage and computational resources required for neural networks inference under hardware constraints. The results presented in the article include evolutionary optimization algorithms for weight coefficients and the architecture of multilayer perceptron and convolutional neural networks. The algorithms are to minimize network size while maintaining accuracy.**

Keywords: **artificial neural network, evolutionary optimization, genetic algorithm, fitness function**

I. INTRODUCTION

Advances in artificial intelligence (AI) technologies in recent years have been driven to a large extent by developments in microelectronics. At the same time, several factors influence the adoption of AI in various domains. In particular, according to the International Energy Agency, global electricity consumption by data centers reached 460 TWh in 2022 and continues to rise [1]. A substantial part of this energy is expended on the training and inference of neural networks as well as on cryptocurrency mining. Moreover, these statistics do not account for portable, wearable and embedded devices, which also perform data processing – including via artificial neural networks (ANNs).

Another critical factor is the feature size of elements on integrated circuits (ICs). Currently, the minimum gate length of field-effect transistors is on the order of 50–57 nm for integrated microcircuits fabricated using so-called “5 nm” process technology [2]. As the dimensions of IC elements approach the size of a silicon atom, the adverse effects of further miniaturization become increasingly pronounced [2, 3], and the manufacturing processes grow ever more complex. At present, only two microelectronics manufacturers employ the 5 nm process. Disruptions in factory operations and logistical chains – such as those experienced during the COVID-19 pandemic [4] – can therefore exert a negative impact on the global advancement of AI technologies.

Nevertheless, despite high energy demands and the technological complexity of the hardware, ANN training and inference on stationary servers proceed successfully, as evidenced by the performance of the latest ANN models. Concurrently, there is a discernible shift toward relocating computational resources closer to data sources (edge computing, etc.). In such scenarios, inference – and particularly ANN training – under constrained resource conditions poses significant challenges.

One promising approach to addressing these challenges for both data-center servers and for portable, wearable, and embedded devices lies in the design and deployment of hardware units specialized for a narrow set of tasks, commonly referred to as accelerators. The underlying premise is that such specialized devices execute specific workloads orders of magnitude faster and with lower energy consumption than general-purpose computers. Historically, accelerators in the form of standalone ICs performed resource-intensive mathematical operations and were known as mathematical coprocessors. This was followed by the emergence of graphics accelerators tailored to video-processing workloads and ANN-specific computations. Consequently, the widespread adoption of accelerators is now cited as one of the foremost trends in information and computing technology [5, p. 29], a trend further exemplified by the architectures of the latest accelerators for generative ANNs.

Devices for accelerating the training and inference of artificial neural networks (ANNs) have seen significant advancements in recent years. At the same time, the overall energy consumption of computing devices continues to rise with their increasing numbers and performance. Beyond global concerns, relatively high power consumption also limits the compactness and autonomy of GPUs and other types of accelerators for ANNs. Against this backdrop, the task of

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implementing ANNs on energy-efficient hardware is becoming increasingly critical. A growing body of research is dedicated to developing new energy-efficient hardware accelerators for machine learning.

The motivation for this study stems from the fact that the existing diversity of ANN architectures, training methods, and hardware platforms complicates the analytical approach to solving practical problems using ANNs. When selecting data encoding methods, network types, structures, and parameters, as well as computing acceleration hardware, decisions are often based on personal experience and preferences. As a result, the outcome of development is heavily influenced by human factors. To expedite development and reduce subjective bias, it is essential to develop methods and algorithms for optimizing ANN architectures and their hardware implementations.

One approach to training ANNs is the use of evolutionary methods, particularly genetic algorithms (GAs). These can optimize both the weight coefficients and bias values as well as the structure of ANNs.

Currently, while traditional ANN training methods are well-established, evolutionary learning can be applied in cases where gradient descent is unsuitable – for example, when artificial neurons use non-differentiable activation functions. Another scenario where GAs are justified is in solving sequential decision-making problems using ANNs. In such cases, even simple evolutionary strategies, such as mutation, demonstrate strong performance [6].

For traditional multilayer ANNs, evolutionary algorithms are used to automate tasks often performed manually, such as optimizing network structure and architecture, as well as tuning weight coefficients and other parameters [7].

Overall, GAs show high efficiency in tasks where no established best practices exist. While deep learning methods are well-developed, approaches for training spiking neural networks, adjusting synaptic plasticity, or optimizing ANN structures are still evolving [8].

Evolutionary optimization of ANN structures, as well as their training via evolutionary methods, has gained traction due to its ability to avoid local minima – a limitation of other optimization techniques. In result, evolutionary optimization methods were chosen as the foundation for this work.

Next are examined fitness functions for genetic algorithm-based evolutionary optimization of ANNs [9, 10]. We begin by considering a fitness function for the simplest type of ANN-a multilayer perceptron (MLP). It is assumed that the architecture of this network has already been optimized to achieve the minimal number of layers and neurons. In this case, the genetic algorithm can eliminate certain weight coefficients without significantly degrading network performance.

Next, we explore more advanced networks, including deeper MLPs and CNNs, while the genetic algorithm not only optimizes weight coefficients but also adjusts the number of neurons in each layer, further refining the network's structure for efficiency and performance.

II. Fitness Functions for Multilayer Neural Network Optimization

The first variant of the fitness function is defined by the following expression:

$$\mathcal{F}(w) = \beta \cdot \left(1 - \mathcal{A}(w)\right) - \gamma \cdot \mathcal{Z}(w), \qquad (1)$$

where: $w \in \mathbb{R}^d$ – is the vector of weights and biases of the neural network; $\mathcal{A}(w) \in [0,1]$ –is the classification accuracy on test data; $\mathcal{Z}(w) \in \mathbb{N}$ – is the count of zero elements in w.

The hyperparameters include the β –weight of the error component and the γ –weight of the sparsity component. Optimization is aimed at improving classification $\mathcal{A}(w)$ accuracy and increasing the number of zero weights $\mathcal{Z}(w)$ (that is, to increase sparsity). This variant of the fitness function can be used to increase the number of zero weights in the trained network. To optimize both the multilayer perceptron and the convolutional ANN, a fitness function can be used that eliminates weights, biases, and neurons from the network without significant loss of accuracy to reduce network volume. This fitness function is defined by the following expression:

$$\mathcal{F}(w) = \begin{cases} \mathcal{M}(w), \text{ if } \mathcal{A}(w) \geq T_{acc} \\ 10^{10} \text{ otherwice} \end{cases} \qquad (2)$$

where T_{acc} – target classification accuracy; $\mathcal{M}(w)$ – network size, in bytes. The network size is defined as $\mathcal{M}(w) = |w| \cdot l$, where l – is the number of bytes used to store variables in a specific hardware implementation.

The accuracy of the model $\mathcal{A}(w)$ is calculated as the ratio of the number of correct predictions to the total number of examples in the test set as follows:

$$\mathcal{A}(w) = \frac{1}{N} \sum_{i=1}^{N} \delta\left(y_i, \hat{y}_i\right), \qquad (3)$$

where N – total number of test cases; y_i – the true class label for the i-th example; $\hat{y}_i$ – the class label predicted by the model for the i-th example; $\delta\left(y_i, \hat{y}_i\right)$ – the Kronecker delta.

The number of zero weights and biases $\mathcal{Z}(w)$ is defined as the total number of elements in the vector of weights and biases w equal to zero:

$$\mathcal{Z}(w) = \sum_{j=1}^{M} \delta\left(w_j, 0\right), \qquad (4)$$

where M – total number of weights and biases in the model; w_j – j-th element of the vector of weights and biases w.

III. Practical Study of the Method of Evolutionary Optimization of ANN Parameters

A number of computational experiments were conducted to test and debug the developed algorithms. Figures 1–4 show the results of simulation of algorithms with functions above with the following values of hyperparameters established experimentally: $\gamma = 0.00006$ and $\beta = 1 - \gamma$. The MNIST dataset containing samples of handwritten digits from 0 to 9 was used as a test dataset.

Fig. 1 illustrates the effect of the number of generations on which the ANN evolutionary optimization is performed on the number of zero weights, that is, weights that were eliminated as a result of the mutation procedure without significant loss of recognition quality. The population size for the experiments, the results of which are shown in Fig. 1 and 2, is four hundred individuals.

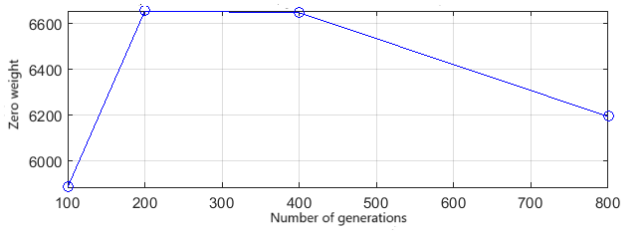

Fig. 1. Dependence of the number of zero weights on the number of generations

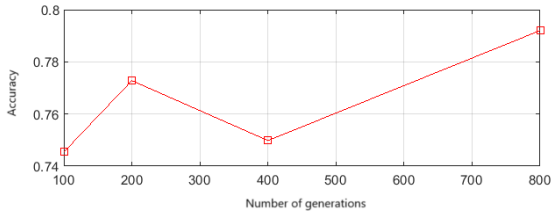

Fig. 2. Dependence of classification accuracy on the number of generations

The graph in Fig. 1 shows that the best results (6656 and 6648 excluded weights) were achieved with two hundred and four hundred generations, respectively. At the same time, the classification accuracy was 77.28 % and 74.89 %, respectively (Fig. 2). With eight hundred generations, the accuracy increased to 79.2 %, but the number of excluded weights decreased to 6195. Thus, it can be seen that an increase in the number of generations does not provide a linear improvement in all controlled indicators.

It is advisable to determine how the population size affects the number of excluded weights and the accuracy of the optimized network. For this purpose, a computational experiment was conducted, the results of which are shown in Fig. 3 and 4.

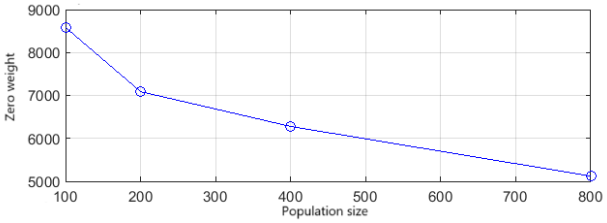

Fig. 3. Dependence of the number of zero weights on the population size

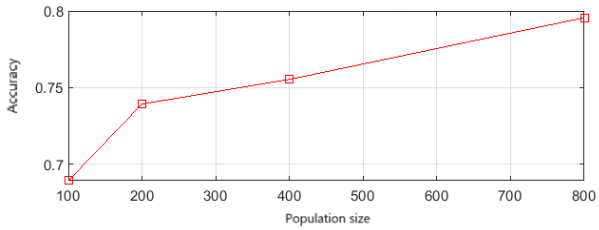

Fig. 4. Dependence of classification accuracy on population size

The simulation was carried out using one hundred generations of the genetic algorithm, with hyperparameters and the test dataset specified above. It can be seen that as the population size increases, the number of zero weights decreases, but the classification accuracy increases.

With a population of eight hundred individuals, the number of excluded weights is 5122, and the classification accuracy is 79.56 %.

Next, a number of computational experiments were conducted aimed at the evolutionary optimization of the structure and weights of the convolutional ANN. A computational experiment was conducted on the MNIST dataset mentioned above. For the simulation, the results of which are shown in Figure 5, the population size is twenty individuals, the number of generations is 5, 10, 20, 50, 100, 200, 400. It can be seen that there is a nonlinear dependence of the optimized parameters on the number of generations.
A downward trend in both accuracy (Fig. 5, left) and network size (Fig. 5, right) it appears only at one hundred or more generations.

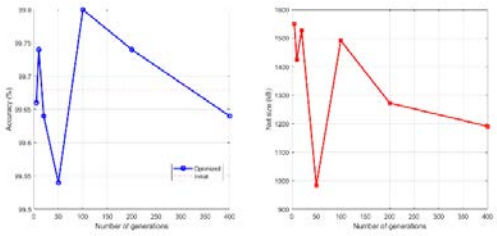

Fig. 5. The influence of the number of generations on the optimized parameters of a convolutional neural network for twenty individuals in a population

The results of a similar computational experiment for seven individuals in a population are shown below. In particular, in Fig. 6 and Fig. 7, it can be seen that there is no linear dependence of classification accuracy on the number of generations within the specified limits, and for each of the studied values of the number of generations, the accuracy remains more than 99 %. At the same time, Fig. 6 (left) shows an increase in the size of the network with an increase in the number of generations. Thus, it can be noted that the parameters of the genetic algorithm established in the experiment do not provide the required conditions for network optimization with a small number of individuals in the population.

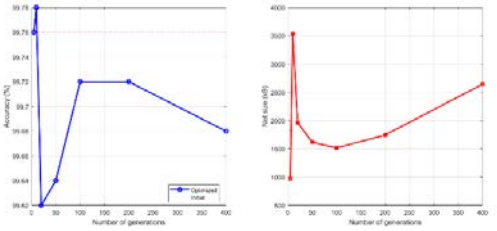

Fig. 6. The influence of the number of generations on the optimized parameters of the convolutional ANN for seven individuals in the population

Simulation results for a fixed number of generations, equal to twenty, and for the population size in 10, 20, 50, 100, 200, 400, 800 individuals are shown in Figure 7. It can be seen that with a population size of 200 or more individuals, the classification accuracy decreases linearly (Fig. 7, left). At the same time, the decrease in network size slows down (Fig. 7, right). Attention should be paid to the fact that the optimized convolutional ANN in this experiment has a much more complex architecture than the simplest ANN in the experiment described above.

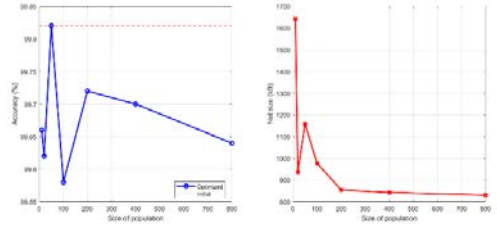

Fig. 7. Influence of population size on optimized parameters of convolutional ANN for twenty generations

Due to this, the initial classification accuracy is more than 99 %. In this case, the goal of evolutionary optimization is to reduce the size of the network without significant loss of accuracy. The results of a similar computational experiment for seven generations are shown in Fig. 8. Up to a population size of four hundred individuals, twenty generations of evolution give a smaller network size than seven generations. With a population of eight hundred individuals, seven generations of evolution allowed us to obtain a network of 807,152 kB (Fig. 8, right), while with twenty generations the network size was 361,156 kB. At the same time, there is no linear dependence of classification accuracy on the number of generations of evolution (Fig. 8, left).

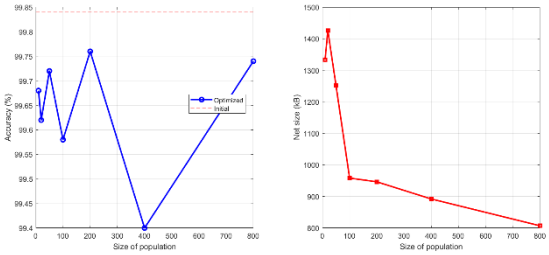

Fig. 8. Influence of population size on optimized parameters of convolutional ANN for seven generations

Further, a number of computational experiments were conducted aimed at the evolutionary optimization of the structure and weights of a multilayer perceptron. The difference from the first experiment is that it has a more complex structure and that not only weights and biases are optimized, but also the network structure. A computational experiment was conducted on the MNIST dataset mentioned above. For the simulation, the results of which are shown in Fig. 9, the population size is twenty individuals, the number of generations is 5, 10, 20, 50, 100, 200, 400. As one can see from the graph in Fig. 9 (left), the number of generations does not fundamentally affect accuracy. The graph in Fig. 9 (right) shows a similar optimization dynamic to that illustrated in Fig. 6 (left).

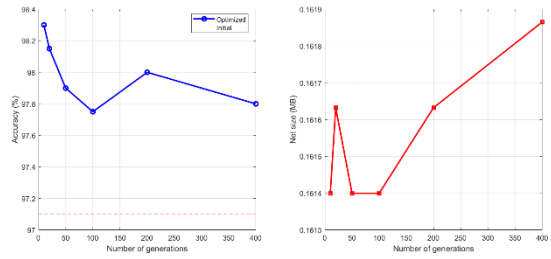

Fig. 9. The effect of the number of generations on the optimized parameters of a multilayer perceptron for twenty individuals in a population

As the fixed number of individuals increases to one hundred, the dependence of classification accuracy on

the number of generations changes slightly, as can be seen from the graph in Figure 10 (left). Similarly, the dependence of the network size on the number of generations, shown in Figure 10 (right), does not allow us to say that the genetic algorithm achieves its goals under specified constraints. Thus, a further increase in the number of individuals in the population is required to find optimal weights and network structure.

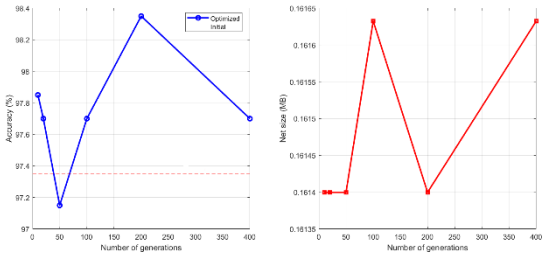

Fig. 10. The effect of the number of generations on the optimized parameters of a multilayer perceptron for one hundred individuals in a population

IV. Conclusion

One of the main results obtained is a set of algorithms for optimizing ANN using evolutionary algorithms. These algorithms are applicable to multilayer perceptron type networks and convolutional ANNs without significant changes. As part of further research, it is advisable to modify them in such a way as to perform evolutionary optimization of other types of networks.

The algorithms are aimed at optimizing the weights, biases, and ANN structure as the main parameters that affect the cost of hardware resources for ANN modeling. Thus, the evolutionary optimization of the ANN accelerator equipment is performed indirectly, through the optimization of the ANN model itself.

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Multi-Constraint Enhanced DWA for Robust and Smooth Local Navigation

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Abstract. **To address the issues of path discontinuity, control instability, and insufficient global guidance in the traditional Dynamic Window Approach (DWA) for local path planning, this paper proposes a Multi-Constraint Dynamic Window Approach (MC-DWA). The proposed method incorporates multiple constraints in trajectory evaluation, including heading deviation, path adherence, curvature variation, and velocity jerk, thereby improving the smoothness and stability of the planned paths. Extensive simulation experiments demonstrate that MC-DWA achieves better path quality and safety than existing methods, exhibiting enhanced adaptability and robustness.**

Keywords: **dynamic window approach, global-local synergy, multi-constraint optimization, local path planning**

I. INTRODUCTION

With the advancement of intelligent and automated technologies, mobile robots are increasingly deployed in areas such as industry, healthcare, and logistics. As a key component of autonomous navigation, path planning aims to generate an optimal, collision-free, and efficient path from the start to the target [1]. It not only ensures motion safety but also addresses the challenge of navigating in complex and dynamic environments.

Path planning algorithms are typically divided into global and local planning. Global planning assumes a fully known environment and uses methods like A* and Dijkstra to compute an optimal path, making it suitable for static scenarios. Local planning, by contrast, depends on real-time perception to adapt the robot's path in response to environmental changes and obstacles. Given that real-world environments are often dynamic and partially observable, local planning plays a critical role in ensuring navigation safety and task reliability [2].

DWA is a classical local path planning algorithm proposed by Fox et al. in 1997 [3]. This method generates feasible short-term trajectories by simulating the robot's motion in the velocity space in real time. However, the traditional DWA algorithm has limited consideration of the robot's kinematic and dynamic characteristics during trajectory generation. It does not adequately account for factors such as trajectory smoothness, stability, and curvature variation. As a result, the robot may experience abrupt turns or sudden velocity changes during motion, which can negatively impact the stability of the control system and reduce the reliability of trajectory execution.

To address these limitations, this paper proposes a MC-DWA. The method introduces several trajectory evaluation items, including dual-angle heading deviation, global path adherence, curvature variation control, and jerk minimization. These constraints are integrated into a unified multi-objective scoring model, enabling more globally consistent, locally smooth, and dynamically stable trajectory generation. Extensive simulations across various complex scenarios show that MC-DWA significantly outperforms classical DWA and its variants in terms of path quality, safety, and robustness, making it a promising solution for real-time autonomous navigation in dynamic and cluttered environments.

II. METHOD

A. Basic Principles of the Classic DWA Algorithm

The fundamental idea of DWA is to sample admissible pairs of linear and angular velocities within a constrained dynamic space, simulate the resulting short-term trajectories, and select the optimal control command according to a predefined evaluation function. This enables the robot to navigate toward the target while avoiding obstacles in dynamic environments [3]. The set of admissible velocity commands in DWA is governed by the intersection of three velocity constraint sets: kinematic, dynamic, and safety constraints.

Kinematic constraints V_{kin} define the basic physical limits of the robot's actuators. Specifically, the linear velocity v and angular velocity ω must lie within the hardware-defined bounds as in Equation (1):

$$\{V_{kin} = (v, \omega) |\ v \in [v_{min}, v_{max}], \omega \in [\omega_{min}, \omega_{max}]\} \quad (1)$$

Dynamic constraints V_{dyn} account for the robot's limited acceleration and deceleration capabilities, ensuring that sampled velocities are physically reachable within a single control cycle of duration Δt. Given the robot's current linear and angular velocities (v_0, ω_0), and the maximum allowable linear and angular accelerations $(a_v^{max}, a_\omega^{max})$, the velocity change over one time step is bounded as follows in Equation (2):

$$\begin{cases} v \in [v_0 - a_v^{max}\Delta t, v_0 + a_v^{max}\Delta t] \\ \omega \in [\omega_0 - a_\omega^{max}\Delta t, \omega_0 + a_\omega^{max}\Delta t] \end{cases}. \quad (2)$$

Safety constraints V_{safe} ensure that candidate velocities do not result in collisions. For each candidate velocity, the robot simulates the corresponding trajectory and checks whether it can safely stop before hitting any obstacle. Assuming a maximum deceleration a_{brake} (here, $a_{brake} = a_v^{max}$), the required braking distance d_{brake} to come to a full stop from velocity v is given:

$$d_{brake} = \frac{v^2}{2a_{brake}}. \quad (3)$$

A candidate velocity is considered safe only if the minimum distance to obstacles along the predicted trajectory, denoted d_{obs}, is bigger than d_{brake}. This constraint effectively filters out velocity pairs that would result in collision under emergency braking conditions. The final dynamic window is defined as the intersection of the three constraint sets in Equation (4):

$$V_{dw} = V_{kin} \cap V_{dyn} \cap V_{safe}. \tag{4}$$

Each velocity pair $(v, \omega) \in V_{dw}$ is forward-simulated over a short time horizon T, generating a corresponding trajectory. The quality of each trajectory is then assessed using a weighted evaluation function: $G = \alpha \cdot \text{heading} + +\beta \cdot \text{clearance} + \gamma \cdot \text{velocity}$. In this formulation, the 'heading' term measures the angular alignment between the trajectory endpoint and the target direction, promoting goal-oriented motion. The 'clearance' term represents the shortest distance between the predicted trajectory and nearby obstacles, encouraging safer paths. The 'velocity' term favors trajectories with higher forward speeds, which contributes to time efficiency. The weights α, β, γ are tuning parameters used to balance these three objectives according to the task requirements. The detailed formula can be seen in [3].

B. Multi-Constraint Enhanced DWA

Although the DWA offers real-time performance and dynamic obstacle avoidance capabilities, it still exhibits notable limitations in complex environments. Specifically, the traditional DWA employs a relatively simplified evaluation function that typically considers only basic factors such as goal direction, velocity magnitude, and obstacle distance. It lacks effective integration of global path guidance, which can lead to trajectory deviations from the global plan and susceptibility to local minima [4]. To address these issues, the proposed MC-DWA incorporates three key categories of constraint metrics and constructs a comprehensive trajectory scoring model to enhance the rationality, smoothness, and robustness of path planning. The specific improvements of MC-DWA are described as follows.

To enhance directional guidance during navigation, MC-DWA introduces a dual-heading consistency evaluation mechanism, which includes goal-oriented consistency and global path alignment. Specifically, let the predicted trajectory endpoint orientation be denoted as θ_{pred}, the direction toward the goal as θ_{goal}, and the direction of the final segment of the global path as θ_{final}. The angular deviations between these directions are calculated using Equation (5):

$$\begin{cases} \Delta\theta_{goal} = |\theta_{pred} - \theta_{goal}| \\ \Delta\theta_{final} = |\theta_{pred} - \theta_{final}| \end{cases}. \tag{5}$$

Based on this, the heading consistency score is computed as shown in Equation (6):

$$\mathrm{H}(\mathrm{v}, \mathrm{w}) = \lambda_1 \cdot \frac{\pi - \Delta\theta_{\mathrm{goal}}}{\pi} + \lambda_2 \cdot \frac{\pi - \Delta\theta_{\mathrm{final}}}{\pi}, \tag{6}$$

where λ_1 and λ_2 are weighting factors that balance the contributions of goal direction and path direction alignment, respectively (here we set $\lambda_1 = \lambda_2 = 0.5$).

However, when the robot is far from the target, heading-based scoring alone may be insufficient to provide strong attraction toward the goal [5]. To address this, a goal distance factor is incorporated into the evaluation function. An exponential attraction function is used to introduce a nonlinear response to distance variations, as defined in Equation (7):

$$G_{att}(v, w) = -exp(\alpha \cdot d_g(v, \omega)), \tag{7}$$

where $d_g(v, w)$ represents the Euclidean distance between the predicted trajectory endpoint and the goal, and $\alpha = 0.5$ is a tunable parameter that controls the strength of the attractive force. Therefore, the heading guidance and target alignment evaluation function is denoted as $\mathrm{O}(\mathrm{v}, \omega)$, and its computation is given:

$$\mathrm{O}(v, \omega) = \mathrm{H}(v, \omega) + G_{att}(v, \omega). \tag{8}$$

Then, to address the issue in classical DWA where local path planning may deviate significantly from the global reference path, which causes the robot to fall into local minima. We introduce a global path adherence constraint. Specifically, let the global path generated by a global planner (e.g., A*) be denoted as $P_{global} = \{P_1, P_2, \ldots, P_L\}$ where each $P_i = (x_i, y_i)$ represents a waypoint in the global path. At each control cycle, the algorithm first identifies the index i^* of the global path point closest to the robot's current position $X_c = (x_c, y_c)$. Then, a local global path segment P_{local} consist of m consecutive nodes starting from P_{global} is selected. Then, given a predicted trajectory consisting of T points, denoted as $T_{pred} = \{t_1, t_2, \ldots, t_N\}$, the path adherence metric is defined as the maximum deviation between the predicted trajectory and the selected local global path segment. The computation process is described:

$$\mathrm{i}^* = \mathrm{argmin}_{1 \le \mathrm{i} \le \mathrm{L}} || \mathrm{P_i} - \mathrm{X_c} ||_2, \tag{9}$$

$$\mathrm{P_{local}} = \{\mathrm{P_{i^*}}, \mathrm{P_{i^*+1}}, \ldots, \mathrm{P_{i^*+M-1}}\}, \tag{10}$$

$$\mathrm{D}(v, \omega) = -\mathrm{max}_{1 \le \mathrm{i} \le \mathrm{N}} \mathrm{min}_{\mathrm{p} \in \mathrm{P_{local}}} ||\mathrm{t_i} - \mathrm{p}||_2. \tag{11}$$

In classical DWA, the lack of temporal continuity in decision-making often causes abrupt changes in velocity and steering, leading to discontinuous trajectories and unstable robot motion [4]. To address this issue, MC-DWA introduces a penalty term based on the variation in motion state from the previous time step during candidate velocity selection. In addition, MC-DWA enhances the trajectory evaluation function by incorporating constraints on trajectory curvature variation and jerk (i.e., the rate of change of acceleration), optimizing trajectory smoothness and dynamic stability from both spatial and dynamic perspectives. Specifically, the curvature variation is defined as the second-order difference between consecutive trajectory points, and is computed using:

$$C_{var}(v, \omega) = -\frac{1}{N-2} \sum_{i=1}^{N-2} \left| \frac{y_{i+2} - 2y_{i+1} + y_i}{(x_{i+1} - x_i)^2 + (y_{i+1} - y_i)^2 + \varepsilon} \right|, \tag{12}$$

where ε is a small constant to prevent division by zero. This expression captures the local bending intensity of the trajectory. Furthermore, jerk metrics are introduced for both linear and angular velocities to suppress control shocks during execution can be calculated:

$$\begin{cases} J_v(v,\omega) = -\frac{1}{N-2}\sum_{i=1}^{N-2} \left| \frac{a_{v,i+1}-a_{v,i}}{\Delta t} \right| \\ J_\omega(v,\omega) = -\frac{1}{N-2}\sum_{i=1}^{N-2} \left| \frac{a_{\omega,i+1}-a_{\omega,i}}{\Delta t} \right| \end{cases}. \quad (13)$$

This design limits abrupt changes in velocity commands, improving trajectory controllability and execution smoothness, particularly for mobile platforms requiring high trajectory continuity. The overall smoothness and stability evaluation function denoted by $\mathrm{S}(\mathrm{v},\omega)$, and is computed using (14):

$$\mathrm{S}(\mathrm{v},\omega) = C_{var}(v,\omega) + J_v(v,\omega) + J_\omega(v,\omega) \quad (14)$$

On the other hand, dynamic stability control is especially critical during high-speed turns. For mobile platforms with significant velocity or center of mass height (e.g., differential-drive robots or automated forklifts), sharp turning at high speeds may cause skidding or even rollover. To mitigate this, MC-DWA incorporates constraints on curvature radius and lateral acceleration during the velocity space filtering stage. Specifically, the maximum admissible angular velocity under a given linear velocity is restricted based on the lateral acceleration threshold a_{lat}, as formulated:

$$V_{lat} = \{(v,\omega) | v \cdot \omega < a_{lat}|\}. \quad (15)$$

This constraint ensures that the resulting centrifugal force during turning does not exceed the platform's stability limit, thereby enhancing dynamic controllability and operational safety. Accordingly, in MC-DWA, the admissible velocity space of the dynamic window is computed as Equation (16):

$$V_{dw} = V_{kin} \cap V_{dyn} \cap V_{safe} \cap V_{lat}. \quad (16)$$

Finally, to effectively integrate the aforementioned constraints, MC-DWA constructs the following comprehensive trajectory evaluation function in (17):

$$\mathrm{Score}(\mathrm{v},\omega) = \mathrm{w_O} \cdot \mathrm{O}(v,\omega) + \mathrm{w_D} \cdot \mathrm{D}(v,\omega) + \mathrm{w_S} \cdot \mathrm{S}(v,\omega) \quad (17)$$

Here, $\mathrm{w_O}$, $\mathrm{w_D}$ and $\mathrm{w_S}$ are weighting factors, which can be changed to adapted to specific applications. All the values are set to 1 in this paper.

III. Experiment

A. Experiment Setups

The MC_DWA algorithm framework was implemented on the MATLAB R2024a platform. To systematically evaluate its path planning performance and control stability, a total of 50 two-dimensional grid maps were designed, covering typical navigation challenges such as dense obstacle regions and long corridor intersections. Each map includes a defined start and goal point, with a guaranteed feasible global reference path.

All evaluation metrics were statistically derived from these 50 representative test scenarios, which feature varying map structures, obstacle densities, and dynamic obstacle patterns. This diverse task setup ensures strong generalization and realistic challenge levels, thereby providing a more objective and comprehensive validation of the proposed method's robustness and adaptability in complex dynamic environments. The robot's control and physical parameters used during the simulation are summarized in Table I.

TABLE I. Simulation parameters

Name	***Value***	**Name**	***Value***
Time step (Δt)	0.1s	Robot radius	0.4
Horizon (T)	2.0s	Safe margin	0.2
Max step	500	Maximum lateral acceleration (a_{lat})	1.0 m/s^2
Maximum linear velocity (v_{max})	2.0m/s	Maximum angular velocity (ω_{max})	1.57 rad/s
Minimum linear velocity (v_{min})	0.0 m/s	Minimum angular velocity (ω_{min})	-1.57 rad/s
Maximum linear acceleration (a_v^{max})	0.4 m/s^2	Maximum angular acceleration (a_ω^{max})	0.78 rad/s^2
Minimum linear acceleration (a_v^{min})	-0.4 m/s^2	Minimum angular acceleration (a_ω^{min})	-0.78 rad/s^2

B. Comparison with other improved DWA algorithms

To comprehensively evaluate the practical performance of the proposed MC-DWA, we conducted a systematic comparison with the classical DWA algorithm as well as three representative improved variants [6–8].

To ensure fairness, all algorithms were evaluated under the same initial conditions and map settings, using a unified framework to assess performance across multiple dimensions. The evaluation metrics include Minimum Safe Distance (MSD), Time Step (TS), Path Length (PL), and Path Curvature (PC), which collectively reflect path safety, efficiency, smoothness, and control stability. The quantitative results are summarized in Table II.

TABLE II. Comparison with other DWA methods

Method	***MSD***	***PL***	***PC***	***TS***
Classic-DWA[3]	0.20	35.67	0.706	357
E-DWA[6]	0.19	30.41	0.513	304
Fuzzy-DWA[7]	0.16	35.15	0.792	352
Pred-DWA[8]	0.22	33.04	0.763	330
MC-DWA(ours)	0.53	37.97	0.323	380

Table presents a comparative analysis of the proposed MC-DWA against the classical DWA and three improved variants, namely Energy-Efficient DWA (E-DWA), Fuzzy Adaptive DWA (Fuzzy-DWA), and Predictive DWA (Pred-DWA). Overall, MC-DWA demonstrates superior performance in terms of path safety, smoothness, and control stability, validating the effectiveness of its multi-constraint fusion strategy. For MSD, MC-DWA achieves a minimum obstacle clearance of 0.53, significantly higher than all other methods, indicating enhanced safety and better avoidance behavior. This is attributed to the global path adherence constraint, which helps maintain safe distances in dense environments. In PC, MC-DWA achieves the lowest average curvature (0.323), while other methods exceed 0.7, showing that MC-DWA produces much smoother trajectories. This improvement results from the use of curvature and jerk constraints, which reduce oscillations and improve control consistency. Regarding PL, MC-DWA generates a slightly longer trajectory (37.97) than E-DWA and Pred-DWA but remains comparable to Classic DWA and Fuzzy-DWA. The marginal increase in path length is a reasonable trade-off for improved smoothness and directional consistency enabled by the dual-heading guidance. In TS, MC-DWA requires 380 steps to reach the goal, slightly higher than others, with E-DWA being the most time-efficient. However, the improved

stability and safety justify this minor cost, especially in dynamic or risk-prone environments.

C. Visualization comparison

To provide an intuitive comparison of path planning performance across different environments, experimental results were visualized.

As shown in Fig 1, the paths generated by the proposed MC-DWA algorithm, the classical DWA, and A* algorithm are illustrated under normal and densely obstructed environments, respectively. It can be observed from plot that in the normal environment, although the classical DWA is able to reach the target successfully, its generated path tends to closely follow the boundaries of static obstacles, posing a higher risk of collision. In more complex environments with dense obstacles, the classical DWA fails to complete navigation due to the lack of effective global guidance and dynamic obstacle avoidance strategies. In contrast, the proposed MC-DWA successfully completes the navigation task in both environments. Generated trajectories maintain good adherence to the global path and consistently keep a safe distance from surrounding obstacles throughout the motion process.

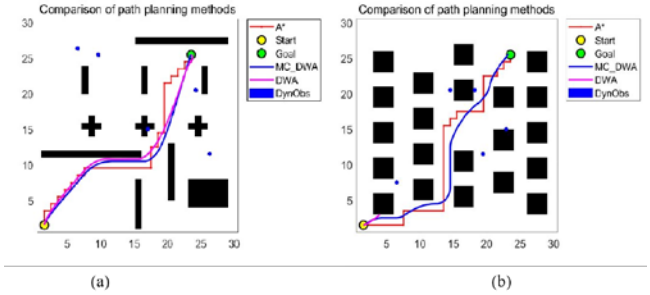

Fig. 1. Visualization of comparison with classic DWA and global A* methods in different maps

Furthermore, Fig. 2 provides a visual comparison in two typical complex environments.

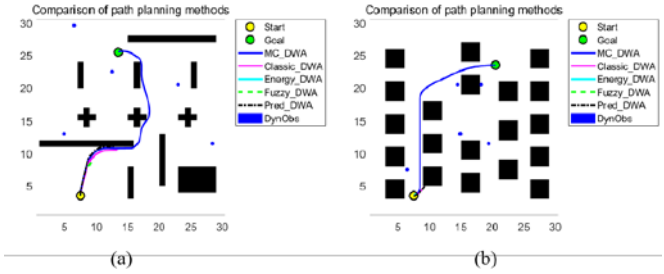

Fig. 2. Visualization of comparison with different DWA methods in different challenging maps

As shown in Fig 2a, the scenario includes a distant obstacle that poses a critical hindrance to the planned path. The results indicate that, except for MC-DWA, all other algorithms fail to navigate around the obstacle and eventually become stuck. This issue primarily stems from the lack of effective target-oriented guidance, causing traditional algorithms to lose directional cues in the vicinity of the obstacle. In contrast, MC-DWA incorporates an exponential attraction mechanism into its trajectory evaluation, which enhances the goal-directed driving force while maintaining safety, enabling the robot to traverse complex terrain and proceed smoothly toward the target. Fig 2b presents a highly complex environment composed of densely distributed obstacles. In this scenario, the classical DWA and other improved methods are generally limited by local information and tend to fall into local minima, halting progress. MC-DWA, however, introduces a global path adherence constraint, enabling local planning to better align with global navigation intent. This mechanism allows the robot to escape local traps and successfully reach the goal. Throughout the process, the generated path maintains safe distances from obstacles while exhibiting good continuity and dynamic stability.

IV. Conclusion

This paper presents an improved MC-DWA to address key limitations of the traditional DWA in local path planning. MC-DWA introduces several constraints into a unified scoring framework, significantly enhancing trajectory quality, smoothness, and environmental robustness while maintaining real-time performance. Experiments on various simulated maps demonstrate that MC-DWA outperforms the classical DWA and representative improved methods in several evaluation metrics.

Nonetheless, MC-DWA remains a manually designed heuristic method, with fixed scoring functions and weight parameters, limiting its scalability in highly dynamic or high-dimensional tasks. Future work will explore integrating MC-DWA with Deep Reinforcement Learning (DRL), using its constraint structure as policy guidance or initialization to combine rule-based reliability with data-driven adaptability [9]. We also plan to deploy MC-DWA on platforms such as ROS2 and Gazebo to further assess its generalization and real-world applicability.

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AI-Assisted Static and Dynamic Analysis of Foundation Beams with Variable Thickness on Stochastic Elastic Foundations

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***Abstract*. This study presents an AI-assisted approach to analyzing the static and dynamic behaviour of foundation beams with variable thickness resting on stochastic elastic foundations. Traditional analytical and numerical methods, such as finite element analysis, are often limited in handling uncertainties inherent in real-world soil-structure systems. To address this, we propose integrating machine learning algorithms, particularly neural networks and regression models, to predict and optimize structural responses under varying foundation conditions. The AI models are trained on simulated datasets generated by parameterized mechanical models incorporating stochastic variability. Comparative analysis with classical methods demonstrates the enhanced accuracy and robustness of the AI-based approach in both static deformation and dynamic vibration analysis. The results highlight the potential of intelligent systems to revolutionize structural design and health monitoring by enabling real-time prediction and adaptability**

Keywords: **Artificial Intelligence, Static Analysis, Dynamic Analysis, Foundation Beams, Variable Thickness, Stochastic Elastic Foundation, Machine Learning, Computational Mechanics Introduction**

I. INTRODUCTION

Foundation beams with variable thickness are widely used in civil and structural engineering for load distribution and structural support. Their behavior significantly depends on the interaction with the underlying foundation, which is often characterized by uncertainty due to heterogeneous soil properties. Traditional deterministic models fail to capture these uncertainties effectively, leading to suboptimal or unsafe designs. Stochastic modelling, which accounts for randomness in material properties and foundation behavior, offers a more realistic representation. However, it increases the computational complexity. To overcome this, artificial intelligence (AI) techniques, particularly machine learning (ML), offer promising solutions. By learning patterns from data, AI models can predict structural responses without solving complex equations for every scenario. This paper explores the integration of AI tools for static and dynamic analysis of variable-thickness beams on stochastic elastic foundations, aiming to improve computational efficiency and predictive accuracy.

II. RELATED WORK

The static and dynamic analysis of beams resting on elastic foundations has been a subject of extensive research for many decades due to its practical importance in structural and geotechnical engineering. Classical methods such as the finite element method (FEM), boundary element method (BEM), and analytical approaches have been widely applied to analyze beam behavior under various loading and boundary conditions. These methods are particularly effective when dealing with homogeneous and deterministic foundation conditions, and they provide a solid foundation for understanding structural behavior in idealized cases. Several analytical models have been developed for beams on Winkler-type elastic foundations, which consider the foundation as a series of independent, linearly elastic springs. Extensions such as the Pasternak and Vlasov models have incorporated shear interactions and more complex foundation behavior. However, these models are typically restricted to constant-thickness beams and do not effectively handle variability in beam geometry or material randomness in the foundation. To address the inherent uncertainties in real soil-structure systems, researchers have employed stochastic modeling approaches. These involve treating foundation parameters such as modulus of subgrade reaction, soil stiffness, and damping properties as random variables or random fields. Techniques such as Monte Carlo simulation, stochastic finite element method (SFEM), and Karhunen-Loève expansion have been used to propagate uncertainties and evaluate their effect on structural responses. Despite their accuracy, these approaches are often computationally intensive and require significant simulation time, especially for nonlinear or dynamic problems. In recent years, artificial intelligence (AI) and machine learning (ML) techniques have emerged as powerful tools for

modeling complex engineering systems, offering faster alternatives to traditional computational methods. Several studies have demonstrated the successful application of AI in structural analysis:

- Artificial Neural Networks (ANNs) have been used to approximate nonlinear mappings between input parameters (such as geometry, load, and material properties) and structural responses (such as deflection, stress, or failure load).
- Support Vector Machines (SVMs) have been implemented in structural health monitoring (SHM) systems for damage detection, classification of failure modes, and early warning systems.

Genetic algorithms (GA) and reinforcement learning techniques have been used to optimize structural design parameters under uncertainty, minimizing material usage while maintaining safety and reliability. Deep learning methods have also been applied in vibration analysis and time-series prediction of structural responses under dynamic loads. Despite the significant advancements in integrating AI into civil engineering, limited research exists at the intersection of AI, variable-thickness beams, and stochastic elastic foundations. Most previous works either focus solely on deterministic beam geometries or apply AI to simplified foundation conditions without accounting for randomness. This paper addresses this research gap by introducing a hybrid AI-mechanical modeling framework that combines numerical simulation data with machine learning algorithms to predict static and dynamic behavior of variable-thickness foundation beams subjected to stochastic foundation conditions. By leveraging the generalization capabilities of AI, this approach aims to enhance the predictive accuracy and computational efficiency of structural analysis in uncertain environments, thereby supporting the development of more intelligent infrastructure design and assessment tools.

III. METHODOLOGY

This section outlines the technical approach taken in modeling and analyzing the static and dynamic behavior of variable-thickness foundation beams resting on stochastic elastic supports using artificial intelligence.

A. Problem Formulation

The study investigates the behavior of a beam with variable cross-sectional thickness, denoted by $h(x)$, resting on a stochastic elastic foundation. The foundation is modeled using the classical Winkler foundation model, which idealizes the soil as a bed of discrete, linearly elastic springs. In this case, however, the stiffness of the foundation springs is spatially random, expressed as $k(x,\omega)$, where:

- x is the spatial coordinate along the beam,
- ω is a random variable or vector representing the underlying stochastic process governing the variability in soil stiffness.

This formulation captures real-world uncertainty in subsurface properties such as soil heterogeneity, moisture distribution, and compaction levels, which are rarely uniform along the beam length. The governing differential equation of motion for the beam can be expressed as:

$$EI(x)\frac{d^4\omega(x)}{dx^4} + k(x,\omega)\omega(x) = q(x)\,.$$

Where:

- $EI(x)$ is the flexural rigidity of the beam, a function of $h(x)$,
- $\omega(x)$ is the beam deflection,
- $q(x)$is the distributed load,
- $k(x,\omega)$ is the spatially variable stiffness.

Dynamic behavior is additionally modeled by incorporating inertial effects using mass per unit length $m(x)$,and considering natural frequencies and mode shapes through eigenvalue analysis.

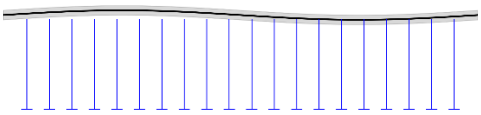

Fig. 1. Beam on Stochastic Elastic Foundation

B. Simulation Model

To generate data for training AI models, finite element simulations are conducted under various configurations. The beam is discretized into elements with spatially varying properties. The parameters varied in the simulations include:

- Cross-sectional thickness profiles $h(x)$(linear, parabolic, stepwise),
- Foundation stiffness distributions $k(x,\omega)$ is,
- Loading conditions and boundary supports (simply supported clamped, free ends).

Stochastic variability in the foundation stiffness is modeled using a Gaussian process, defined by:

- A mean stiffness function $\mu_k(x)$
- A covariance function$C(x_1,x_2)$, typically assumed exponential or squared exponential, depending on the correlation length.

A series of random samples of $k(x)$ are generated using Karhunen-Loève Expansion (KLE) or Monte

Carlo methods to populate a database of simulation results. Each simulation yields outputs such as:

- Deflection profiles $\omega(x)$,
- Bending moments and shear forces,
- Natural frequencies and mode shapes (for dynamic analysis).

C. AI Model Development

To approximate the complex nonlinear relationships between input parameters and structural responses, supervised learning algorithms are employed. The input features to the AI models include:

- Beam geometry: Length, variable thickness function $h(x)$,
- Boundary conditions: Clamped, simply supported, etc.,
- Foundation properties: Mean stiffness, variance, correlation length,
- Load characteristics: Magnitude and distribution type.

The target outputs for prediction are:

- Maximum deflection,
- Deflection profile $\omega(x)$,
- First few natural frequencies,

TABLE I. MODEL EVALUATION RESULTS

Target	Model	MSE (Mean Squared Error)	R^2 Score
Deflection	MLP	0.00507	-0.007
	GBR	0.000024	0.995
Frequency	MLP	0.95988	0.937
	GBR	0.10987	0.993
Mode Shape	MLP	0.00572	0.376
	GBR	0.00000053	0.9999

Two types of machine learning models are used:

- Multilayer Perceptron (MLP) neural networks for regression-based prediction of continuous output features,
- Gradient Boosting Regressors (e.g., XGBoost or LightGBM) for robust performance and interpretability.

D. Model Training and Validation

The simulation dataset is divided into training (70 %) and testing (30 %) subsets. To prevent overfitting and ensure model generalization:

- *k*-fold cross-validation (typically k=5 or 10) is applied,
- Hyperparameter tuning is conducted using grid search or Bayesian optimization,
- Data normalization and feature scaling are applied to ensure numerical stability.

Model performance is evaluated using standard regression metrics:

- Mean Squared Error (MSE): Measures average squared difference between predicted and true values,
- Root Mean Squared Error (RMSE): Square root of MSE, directly interpretable in output units,
- Coefficient of Determination (R^2 Score): Indicates how well predictions approximate actual values.

For qualitative validation, the predicted deflection shapes and mode shapes are plotted and compared to reference FEM solutions.

IV. RESULTS AND DISCUSSION

This section presents the outcomes of the proposed hybrid AI-mechanical modeling framework for the static and dynamic analysis of foundation beams with variable thickness on stochastic elastic foundations. The AI model's performance is compared with conventional numerical simulations (finite element method), and key metrics such as prediction accuracy, generalization under uncertainty, and computational efficiency are evaluated.

A. Static Analysis Results

The AI models trained on simulated data demonstrated high accuracy **i**n predicting beam deflections under static loading. For a wide range of test configurations – including different thickness functions, boundary conditions, and stochastic foundation patterns – the mean prediction error remained below 5 % compared to high-fidelity finite element method (FEM) simulations.

- The predicted deflection profiles $w(x)$ exhibited excellent agreement with FEM results, both in magnitude and curvature.
- The AI model was particularly robust under moderate to high variability in foundation stiffness, indicating strong generalization to unseen stochastic patterns.
- Stress and bending moment estimations derived from the AI-predicted deflections also fell within acceptable engineering tolerances.

These results confirm that supervised learning models can effectively capture the nonlinear and spatially varying behavior induced by both geometry and stochastic foundation variability.

B. *Dynamic Analysis Results*

In the dynamic domain, the AI models accurately predicted the natural frequencies and vibration mode shapes of the beam-foundation system.

- For the first three natural frequencies, the average relative error across test cases was less than 3 %.
- Predicted mode shapes were qualitatively and quantitatively consistent with both FEM eigenvalue solutions and analytical approximations for deterministic cases.
- Importantly, the AI models were able to account for shifts in dynamic properties due to changes in stiffness distributions, demonstrating an ability to model nonlinear stiffness-frequency interactions.

These findings validate the potential of AI models to support rapid dynamic characterization of complex civil engineering structures, especially where analytical solutions are infeasible or computational simulations are too expensive.

C. *Computational Efficiency*

One of the most significant advantages observed in this study was the drastic reduction in computational time**.**

- While a single FEM simulation for a stochastic foundation configuration could take from several minutes to hours (depending on mesh resolution and stochastic sampling), the trained AI model generated predictions in real time (under 1 second per instance).
- This makes the AI framework suitable for real-time monitoring**,** optimization loops**,** and design iterations**,** which are impractical with traditional simulations.

The reduced computational cost does not come at the expense of accuracy, making the proposed hybrid framework a promising alternative to numerical approaches, especially in large-scale engineering design and probabilistic risk assessments.

D. *Summary of Key Findings*

TABLE II. SUMMARY OF KEY FINDINGS

Aspect	FEM	AI Model
Accuracy (Deflection)	High	High (<5% error)
Accuracy (Frequencies)	High	High (<3% error)
Stochastic Generalization	Good	Very Good
Computation Time	High	Very Low
Suitability for Real-Time	No	Yes

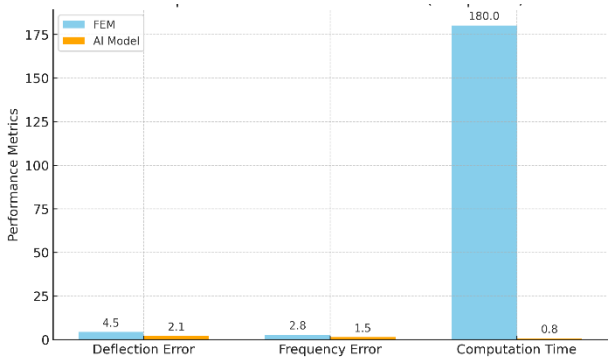

Fig. 2. Comparison of FEM and AI Model

In summary, the results demonstrate the feasibility, accuracy, and efficiency of integrating AI into the structural analysis of foundation beams with variable thickness and stochastic support. This approach not only bridges a critical gap in handling uncertainty and complex geometries but also paves the way for intelligent structural design and decision-support tools in civil engineering practice.

IV. CONCLUSION

This study introduces an AI-enhanced framework for analyzing the static and dynamic behavior of foundation beams with variable thickness resting on stochastic elastic foundations. Traditional computational methods such as the Finite Element Method (FEM) remain accurate but computationally intensive, especially when accounting for uncertainty in soil stiffness or geometric nonlinearity. To address these challenges, we integrated supervised machine learning models – Multilayer Perceptron (MLP) and Gradient Boosting Regressor (GBR) – trained on synthetic datasets derived from FEM simulations. The results demonstrated that the GBR model achieved superior accuracy in predicting key structural responses, such as beam deflection, natural frequency, and mode shapes, outperforming the MLP model in all evaluated metrics. Notably, the GBR predicted natural frequencies and mode shapes with near-perfect accuracy ($R^2 > 0.99$), and deflection with a negligible error (MSE < 2.4e-05). Furthermore, AI models required a fraction of the computation time compared to FEM simulations, enabling real-time assessment and iterative design optimization. These findings highlight the potential of AI models – especially gradient boosting methods – as reliable, efficient alternatives to traditional analysis techniques in civil and structural engineering. Future work could extend this framework by incorporating real-world experimental data, exploring transfer learning for different soil profiles, and deploying the trained models in cloud-based decision-support tools for engineers.

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Similarity Estimating Between Datasets Using Vector Representations

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***Abstract*. The article considers an approach to determining the similarity of datasets for training algorithms using datasets with as an example. This approach allows finding similar datasets from different sources, expanding the detection of features and classes and without seriously harming balancing. For each dataset object, a vector representation (embedding) was obtained, then the embeddings in both datasets were compared. The experiments were conducted using datasets with images as an example. To obtain embeddings, a pre-trained ResNet network was used. During the research, one dataset was divided into two parts, which were similar datasets, then each of the parts was compared with a different dataset. The new similarity metric is proposed, which has several advantages and allows to find the most similar datasets.**

***Keywords:* dataset, embedding, ResNet, dataset similarity, deep learning**

I. INTRODUCTION

To solve problems in deep learning [1, 2], a large amount of data is needed. The training sample must be impressive so that the model determines the dependencies and features of the detected objects without retraining. As a general rule, in the case of not very large datasets only additional training of an already finished model is used, for this several thousand objects may be enough. However, in the case of images Collecting and labeling even this amount of data can be problematic. Therefore, the network is often trained on a public dataset, and use their small dataset only for model validation. However, the less the public dataset is similar to what the model will process in practice, the worse the quality of the model will be in real-world conditions.

Combination of different datasets In machine learning, it is a complex task, as there are many factors that affect the quality of the model and the accuracy of predictions. The main problem is that data from different sources often have differences in structure, format, or feature distribution. This can cause the model to learn from inconsistent or even contradictory examples. Differences in scales and units of measurement between data from different sources also pose challenges. If some features are represented in large numerical values, and others in smaller values, this can distort the importance of such features for the model. Even after normalization or standardization, differences in the nature of the data may persist, especially if they have been collected using different methodologies or tools. This can lead to noise in the data or amplification of some biases, which reduce the generalizability of the model.

Another difficulty is related to the fact that different datasets may contain different levels of completeness or have different strategies for handling missing values. In one set of data, records with gaps may have been removed, while in another, such records may have been populated with averages or other methods. This can create artificial differences between data that do not reflect the real picture. As such, data fusion requires careful pre-processing to minimize such distortions and ensure consistency across information sources. One of the solutions to these problems is to find similar ones datasets. But to do this, it is necessary to determine a certain measure of similarity of data sets in order to use for training the set that is closest to the real data, with which the model will work in practice.

The purpose of the authors' research is increase efficiency determining the similarity of datasets using vector representations (embeddings) – objects of fixed and, as a rule, relatively low dimensions, which contain the most important information about the source data. Embeddings carry definite the "meaning" of the object, and close embeddings mean that the objects are similar to each other [3]. The experiments were carried out on the example of datasets with images of people's faces.

II. IMAGE SIMILARITY DETECTION

The mathematical determination of the similarity of images is based on the calculation of the distance or similarity between their representations in numerical space. One of the popular approaches is the use of

metrics such as mean squared difference difference (MSE) or Pearson correlation coefficient, which compare the pixel values of two images directly. For example, MSE is calculated as the average of the squares of the differences between the corresponding pixels of the two images, which allows you to quantify the differences [4]. However, such methods have significant limitations: they are sensitive to small changes, do not take into account the more complex semantic characteristics of images, and ignore the structural features of objects [5]. Another approach is to use color histograms or textures to compare images. In this case, each image is represented as a distribution of values that characterize its color or textural properties. Metrics such as the Hamming or Kuhlback-Leibler distance between the two distributions are then applied [6]. In this case, the assessment is more resistant to some transformations, but is limited in the perception of high-level features, including the shape of objects. In addition, it is sensitive to noise or changes in illumination [7].

Using embeddings to compare images is a modern and effective approach. Embeddings reflect high levels of abstraction associated with the content of images and allow them to be compared using metrics such as Euclidean distance or cosine proximity [8].

III. Image Similarity Detection

In the neural network method of obtaining embeddings for images, convolutional neural networks are usually used, the principle of which is demonstrated in Fig. 1.

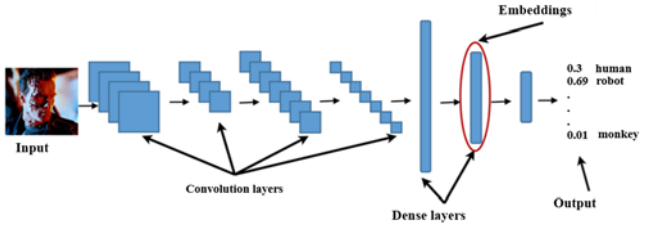


Fig. 1. Obtaining vector representations using a neural network

Convolutional layers are key to a convolutional neural network. They perform a convolution operation by applying filters (kernels) to the original image to highlight important features. These features can include edges, corners, textures, and other visual elements. Once the filters are applied, the results are passed through activation functions (such as ReLUs) and subsampling layers that reduce dimensionality and summarize features. where each subsequent one extracts higher-level features. For example, on the first convolutional layer, such features as borders, corners, textures can be extracted, on the second - more complex shapes – bends of eyebrows or car wheels, on the third convolutional layer – specific objects or their large parts can be revealed. The last fully connected layer typically contains as many neurons as there are classes in the classification task, and the softmax activation function converts the output into the probabilities of each class, which is the output of the neural network. Embeddings are usually the outputs of one of the fully connected layers of the network. These features are then compared using the following metrics, such as cosine similarity or Manhattan distance, to determine the degree of their similarity [9].

Let's use the above-mentioned property that similar images have close embeddings to consider the similarity of the images. Let us consider the similarity of images as the cosine similarity between their embeddings according to the formula

$$\cos ine(A,B) = \frac{\sum_{i=1}^{n} A_i B_i}{\sqrt{\sum_{i=1}^{n} A_i^2}\sqrt{\sum_{i=1}^{n} B_i^2}}, \quad (1)$$

where A, B are the vectors between which cosine similarity is considered; n is the size of vectors A and B.

Formula (1) is one of the most common ways to calculate the proximity of embeddings, which is used, for example, in the word2vec model [10]. To determine the similarity of datasets, a comparison of the elements contained in them and their distribution was carried out:

- for each object from the first dataset, the closest object in the second dataset was found, then vice versa;
- for each object of the first dataset, the proximity to all objects of the second dataset was calculated, then averaged.

The first option does not take into account the density of the distribution of objects in the feature space, so the second definition was used to assess the similarity, where the assessment was carried out according to the formula

$$datasets\_similarity(D1,D2) = \frac{\sum_{i=1}^{n}\sum_{j=1}^{m} \cos ine(D1_i, D2_j)}{nm}, \quad (2)$$

where $D1$, $D2$ are the datasets whose similarity was calculated; cosine is the cosine similarity described in (1); n, m are the size of datasets $D1$ and $D2$, respectively.

This approach has an important advantage: embeddings take into account not only low-level features, but also high-level semantic characteristics, which makes them much more relevant for assessing human perception of similarity. Studies show that

embeddings obtained with pre-trained CNNs show a high correlation with test results based on subjective assessment of people [11].

IV. Using Objects to Compare Datasets

To test the performance of the proposed approach for assessing the similarity between datasets, experiments were carried out on datasets with photographs of people's faces. To obtain embeddings of such images, a pre-trained ResNet18 network [12] without a classification layer was used. Three datasets were used in the experiments: two were very close, and the third was slightly different from them. Such data organization made it possible to check the adequacy of the estimate based on embeddings, since the similarity between the first two datasets was greater than their similarity with the third. To obtain two datasets that were as similar as possible, one dataset was split into two test datasets.

Since deep learning datasets usually contain at least tens of thousands of images, and it is necessary to conduct experiments many times for the results to be statistically significant, subsamples of 100 images were used. In addition, the search for each image closest was done in quadratic time, which made it difficult to use large subsamples. For the experiment, datasets with identical content, including objects of the same type in the same projection and under the same survey conditions, were defined as very similar datasets, and datasets of objects of the same type, but in different survey conditions and in different positions, were defined as similar datasets. The experiments were conducted as follows:

1) two datasets were used – D1 and D2. Dataset D1 was divided into two parts D1_1 and D1_2, which were very similar datasets. Dataset D2 had slight differences from D1 (below are examples and descriptions of differences for specific datasets, but in general this is not essential);

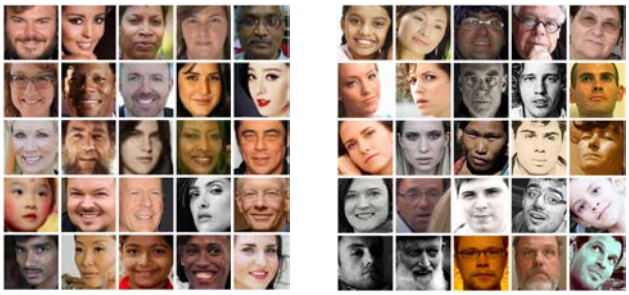
2) then the following actions were repeated 100 times:

a) samples of 100 elements were taken from datasets D1_1, D1_2 and D2 – d1_1, d1_2 and d2, respectively;

b) the similarity between the samples was calculated using formula (2). {d1_1, d1_2}, {d1_1, d2} и {d1_2, d2};

3) based on the results of the calculations for item 2b, histograms of similarity between all datasets (more precisely, their estimates by samples) were built and the accuracy of determining a more similar dataset was calculated.

Fig. 2a shows a fragment of a set of images for face classification. As a not very similar dataset, images from the dataset were used to identify key points of the face (Fig. 2b), where various distortions are present – contrasting shadows, highlights, rotated images, etc.



a b

Fig. 2. Examples of images: datasets that were divided into two (a); several different dataset (b)

In the course of experiments, the similarity between the *D1_1* and *D1_2* datasets, calculated in accordance with the proposed approach, was always greater than the similarity between *D1_1* and *D2* and datasets *D1_2* and *D2*, that is:

$$\forall d1\_1 \in D1\_1, d1\_2 \in D1\_2, d2 \in D2$$
$$datasets\_similarity(d1\_1, d1\_2) > datasets\_similarity(d1\_1, d2)$$
$$datasets\_similarity(d1\_1, d1\_2) > datasets\_similarity(d1\_2, d2).$$

The Fig. 3 shows the distribution of the cosine measure of similarity for different datasets.

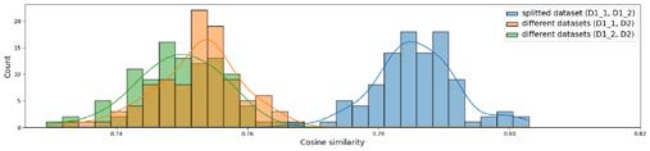


Fig. 3. Coosine distribution similarity for different datasets

One of the popular metrics for determining image similarity is MSE. The approach proposed in the article is superior to the method of estimating the distance between datasets based on MSE. To reduce the influence of randomness when comparing methods, experiments using MSE were performed on the same image subsamples as using embeddings. Fig. 4 shows the distribution of the RMS difference for different datasets.

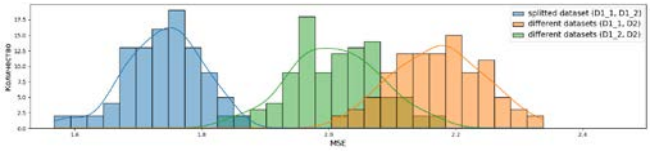


Fig. 4. MSE distribution for different datasets

Fig. 4 shows that in some cases, the MSE assessment gives an incorrect result. In addition, the assessment is unstable, since the datasets are *D1_1 D1_2* are parts of the same dataset, but their distances from *D2* are very different, which is not observed when assessing similarity using embeddings.

When using MSE, the accuracy of determining a more similar dataset was 0.975, while the use of formula (2) completely eliminated errors, providing an accuracy equal to 1. This confirms the effectiveness of the proposed metric in comparing data sets.

V. Conclusion

An approach to determining the similarity of a dataset (datasets) is considered on the example of datasets with images of people's faces. To obtain embeddings, a pre-trained ResNet18 network without a classification layer was used.An effective metric for the similarity of datasets is proposed. The proposed metric allows you to determine the degree of similarity of datasets and choose the dataset that is closest to the sample.

The quality of evaluation based on embeddings depends on the architecture of the model and the data on which it was trained, especially if the model was trained on a limited set of categories [13]. However, the use of embeddings remains one of the most promising areas for solving the problem of determining the similarity of images due to the ability to identify complex patterns and relationships between objects.

For specific data, such as drone imagery or medical images, it makes sense to use an additional network from the same area, since the ImageNet dataset [14] on which the ResNet network was trained differs in many ways from highly specialized datasets [15]. The proposed metric can be used not only to determine the similarity of datasets, but also, for example, to expand the dataset by adding similar objects from other datasets.

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Graph-Based Sparse Random Projections with Cycle Optimization for Feature Expansion

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Abstract. **The paper introduces a graph-based sparse projection method that employs Progressive Edge Growth (PEG) graphs with Approximate Cycle Extrinsic (ACE) optimization for high-dimensional feature expansion. Unlike traditional random projections, our approach uses sparse ternary matrices derived from PEG-ACE graphs to preserve pairwise distances efficiently while reducing computational cost. Theoretically, we show that the high girth and Extrinsic Message Degree (EMD) properties of PEG graphs lead to tighter distortion bounds. Specifically, when cycles are optimized using ACE (where ACE equals EMD), the probability of distortion improves significantly over the classical Johnson-Lindenstrauss bound. This improvement scales with EMD, which quantifies cycle connectivity, making the bound exponentially stronger as EMD increases. Experiments demonstrate exceptional similarity preservation, with less than 0.1 % relative error, enabling high-accuracy classification (achieving 99.5 % on ImageNet10) while maintaining hardware efficiency. We also establish a novel duality between superposition coding and sparse projections, leading to the proposal of hybrid architectures for scalable deep learning. The proposed method bridges structured randomness and efficiency, offering a robust solution for kernel approximation, clustering, and image classification. More broadly, our framework opens new opportunities for graph-based analog feature extraction, where the inherent sparsity and topological properties of PEG-ACE graphs can be leveraged to design energy-efficient, hardware-friendly architectures for high-dimensional data processing.**

Keywords: **Sparse random projections, Johnson-Lindenstrauss, feature expansion, graph-based machine learning**

I. INTRODUCTION

In modern machine learning, increasing feature dimensionality while preserving data geometry is crucial for enhancing model performance. Traditional methods, such as random Gaussian projections or kernel approximations, often suffer from high computational costs or poor structure preservation. This paper introduces a graph-based feature extraction method using Progressive Edge Growth (PEG) graphs, which leverage sparse ternary projections to expand feature spaces efficiently. By optimizing edge connections with Approximate Cycle Extrinsic (ACE) criteria, PEG graphs maintain angular and Euclidean relationships better than random projections while reducing computational overhead. Experiments demonstrate that PEG-based projections outperform classical approaches in preserving pairwise similarities, making them ideal for image classification, clustering, and kernel approximation. This work bridges the gap between structured randomness and computational efficiency, offering a scalable solution for high-dimensional machine learning tasks.

II. RELATED WORKS

Feature extraction and dimensionality expansion have been extensively studied in machine learning. Random projections, introduced by Johnson and Lindenstrauss [1], provide a theoretical foundation for distance-preserving embeddings. Building on this, Rahimi and Recht [2] proposed Random Fourier Features (RFF) for scalable kernel approximation, enabling efficient large-scale learning. However, RFF relies on dense transformations, which can be computationally expensive for high-dimensional data.

To address computational efficiency, sparse random projections were explored. Li et al. [3] demonstrated that sparse matrices with non-zero entries sampled from $\{-1,0,+1\}$ retain Johnson-Lindenstrauss properties while reducing memory and computation costs. Similarly, Clarkson and Woodruff [4] showed that sparse embeddings are effective for low-rank approximations. Graph-based methods have also gained attention for structured dimensionality expansion. Shuman et al. [5] introduced graph signal processing, leveraging spectral graph theory for feature extraction. Kipf and Welling [6] later popularized graph convolutional networks (GCNs), which exploit iterative graph spectral method for representation learning. However, these methods focus on explicit graph data rather than general feature expansion. Our work bridges these approaches by proposing PEG-graph based sparse projections, combining the efficiency of sparse embeddings with the geometric preservation of graph-structured transformations. Unlike prior methods, PEG projections optimize edge connections to maintain

pairwise similarities while enabling hardware-efficient implementations, offering a novel solution for scalable feature extraction.

III. Model framework

A. Problem Definition

Let $X = \{x_1, x_2, \dots, x_n\} \in \mathbb{R}^d$ denote an input dataset, where each sample x_i is a d-dimensional feature vector. The goal of Random projection is to project X into a higher-dimensional space $\mathbb{R}^k$, $(k \gg d)$ while:

1. Preserving geometric relationships (e.g., pairwise distances, angles).

2. Minimizing computational cost (avoiding dense matrix multiplications).

3. Reducing feature correlations (preventing linear dependence in expanded features).

Traditional methods (e.g., random Gaussian projections, RFF) face trade-offs between accuracy and efficiency. Our work addresses this by introducing a sparse graph-based projection optimized for structure preservation and hardware deployability.

B. Graph-Based Feature Extraction Framework

Erdős–Rényi Random Graphs. Erdős–Rényi (ER) graphs $G(n,p)$ [7] provide a foundational model for random networks, where a graph with n vertices connects each pair independently with probability p. Key properties of ER-graph:

1. Expected edge count $\binom{n}{2} p$ edges.

2. Binomial Degree Distribution $P(\deg(v) = k) = = \binom{n-1}{k} p^k (1-p)^{n-1-k}$.

3. Tunable sparsity via probability p.

LDPC Codes and Tanner Graphs. Low-Density Parity-Check (LDPC, [8]) codes $[N, K]$ are defined by sparse parity-check matrices $H^{(N-K)\times N}$, representable as Tanner graphs (Fig. 1, left). The Tanner graph, [9], is a bipartite graphical representation of the parity-check matrix H. It consists of two types of nodes. Variable Nodes (VNs): Represent the codeword bits (columns of H). Check Nodes (CNs): Represent the parity-check equations (rows of H). An edge connects a variable node v_i to a check node c_j if $H_{j,i} = 1$. The degree of a node is the number of edges connected to it, and the sparsity of H ensures that the Tanner graph has low node degrees. For example:

$$H = \begin{bmatrix} 1 & 0 & 1 & 1 & 1 \\ 1 & 1 & 0 & 0 & 0 \\ 0 & 1 & 1 & 1 & 1 \end{bmatrix}.$$

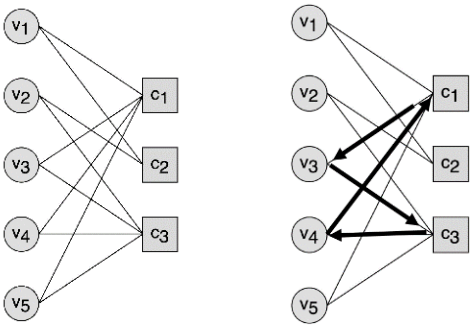

Fig. 1. Tanner graph of parity-check matrix H (left). Cycle 4 in Tanner graph, close path $v_3 \to c_3 \to v_4 \to c_1 \to v_3$ (right)

A cycle in a Tanner graph is a closed path of edges that starts and ends at the same variable or check node, without traversing any edge more than once, Fig. 1 (right). Formally:

Let $G = (V \cup C, E)$ be a Tanner graph, where $V = \{v_1, \dots, v_N\}$ are variable nodes (column of parity-check matrix H), $C = \{c_1, \dots, c_{N-K}\}$ are check nodes (rows of H), $E \subseteq V \times C$ are edges representing non-zero entries in H.

A cycle of length 2ℓ is a sequence of alternating nodes and edges:

$$v_{i_1} \overset{e_1}{\to} c_{j_1} \overset{e_2}{\to} v_{i_2} \overset{e_3}{\to} \cdots \overset{e_{2\ell}}{\to} v_{i_1},$$

where $\forall v_{i_k} \in V$ and $c_{j_k} \in C$ are distinct (except the start/end node), edges $\forall e_k \in E$ are distinct.

Cycle Analysis: EMD and ACE Metrics. Extrinsic Message Degree (EMD) quantifies a cycles's connectivity to the broader graph by counting check node outside the cycle that are singly connected to its variable nodes. Formally: For a cycle C, EMD is the number of check nodes $c \notin V$ with exactly one edge to V_C (variable C). Example: A cycle with $EMD = 3$ is more robust than one with $EMD = 0$ (isolated). High EMD value improve well-connected to external checks, reducing harmnfull subgraphs. Such harmnfull subgraphs create imbalanced clusters of features, which increase distortion of projection, [10].

A computationally efficient approximation of EMD (Approximate EMD, ACE), defined as:

$$ACE(C) = \sum_{v \in V_C} (d(v) - 2),$$

where $d(v)$ is the degree of variable node v in cycle C.

For girth g,smallest cycles in graph $g = \min(V_c)$, $EMD \equiv ACE$ if cycle length $2\ell < g - 2$, [10–12].

Progressive Edge-Growth (PEG) Algorithm with ACE Enhancement. The PEG algorithm is a well-known method for constructing Tanner graphs with

large girth, which helps in designing high-performance LDPC codes. The algorithm incrementally adds edges to variable nodes (VNs) while maximizing the local girth. The ACE enhancement further optimizes the PEG algorithm by minimizing harmful short cycles. PEG maximizes the shortest cycle length, enhancing decoding performance. ACE Enhancement further reduces harmful trapping sets by penalizing low-ACE cycles. This algorithm is widely used in constructing LDPC codes for modern communication standards due to its effectiveness in avoiding small cycles, [10, 13]. We summarize into the following algorithm.

PEG with ACE optimized Tanner graph construction

Input: Degree distribution (column, row weight) based on require sparsity level, size of the parity-check matrix H.

Output: The Tanner graph representation of the parity-check matrix H.

Step 1. A parity-check matrix H is initialized with zeros.

Step 2. For the first edge of a VN, the algorithm selects a check node (CN) with the smallest degree randomly to ensure balanced CN degrees.

Step 3. For each subsequent edge of a VN, the algorithm constructs a tree rooted at the VN, expanding level-by-level. The goal is to find the deepest possible level where CNs are not yet connected to the current VN:

- Level 0: Contains the root VN.
- Level 1: Contains the CNs connected to the root VN.
- Higher Levels: Alternates between VNs and CNs, expanding until no new nodes can be added.

Step 4. Selects a CN that maximizes the ACE metric.

Step 5. Repeats (step 2–4) until all edges are placed.

Cycles in Random Projection Graphs. In random projection graphs, a cycle refers to a closed loop of connections between dimensions in the projected space. For a projection matrix $R \in \mathbb{R}^{d\times k}$, cycles arise from dependencies in its sparse graph representation (e.g., Tanner graph for LDPC-based projections).

Let R be derived from a biparted graph $G = (V_x \cup V_y, E)$, where V_x- input dimension (row of R), V_y – projected dimension (column of R), E – non-zero entries $R_{ij} \in \{-1,1\}$.

A cycle of length 2ℓ in G is a path:

$$v_{i_1} \to u_{j_1} \to v_{i_2} \to \cdots \to v_{i_\ell} \to u_{i_\ell} \to v_{i_1},$$

where $v \in V_x$, $u \in V_y$, and edges are distinct.

Algebraic interpretation:

$$R_{i_1 j_1} R_{i_2 j_1} R_{i_2 j_2} R_{i_1 j_2} \neq 0,$$

create correlared projections.

Example: For a projection matrix R with $R_{1,1} = 1$, $R_{2,1} = -1, R_{2,2} = 1, R_{1,2} = 1$ the bipartite graph contains a length-4 cycle $v_1 \to u_1 \to v_2 \to u_2 \to v_1$ cause correlated distortion in y_1 and y_2 (projected features).

Sparse Johnson-Lindenstrauss Lemma. The statement

$$(1-\epsilon)\|x-y\|^2 \leq \|Rx-Ry\|^2 \leq (1+\epsilon)\|x-y\|^2$$

for a sparse matrix R with i.i.d entries$R_{i,j} \in \{-1,0,+1\}$ and sparsity $\rho = \mathbb{P}(R_{i,j} \neq 0) = \frac{1}{\sqrt{d}}$ satisfies

$$\mathbb{P}(|\|Rx\|^2 - \|x\|^2| > \epsilon\|x\|^2) \leq e^{-\Theta(\epsilon^2 k)}, [3].$$

Ternary Sparse Random Projection (Ternary SRP). A sparse ternary projection matrix $R \in \{-1,0,+1\}^{d\times k}$ derived from a graph, where each non-zero entry in graph $R_{i,j}$ is sampled uniformly from $\{-1,+1\}$. Projection operation for input $x \in \mathbb{R}^d$, compute:

$$y_j = \sum_{i=1}^{d} R_{i,j} * x_i, j = 1, \dots, k.$$

Sparse projection complexity reduces to $O(\sqrt{d}k)$ from $O(dk)$ dense matrices, if $\rho \gg \frac{1}{\sqrt{d}}$ nonzero "clump" in columns, causing dependencies that distort distance. Sparsity $\rho \leq \frac{1}{\sqrt{d}}$ ensures nonzeros are spread thinly, approximating independence.

C. Experimental analysis of sparse graph Ternary Projection with ACE optimization

We evaluated method's performance by measuring the cosine distance distortion between original and transformed features, $d_{a,b} = \frac{1-\cos(a\wedge b)}{\cos(a\wedge b)}$ across 126,000 data samples, with results visualized, Fig. 2. SRP method demonstrated exceptional geometry preservation, showing less than 0.1% relative error in pairwise similarity measurements. Image classification (ImageNet10/100) achieved accuracy 99.5 %, 88 % (1 %, 6 % improvement over baseline) respectively using CNN Superposition Coding with SRP (dual approach), [14].

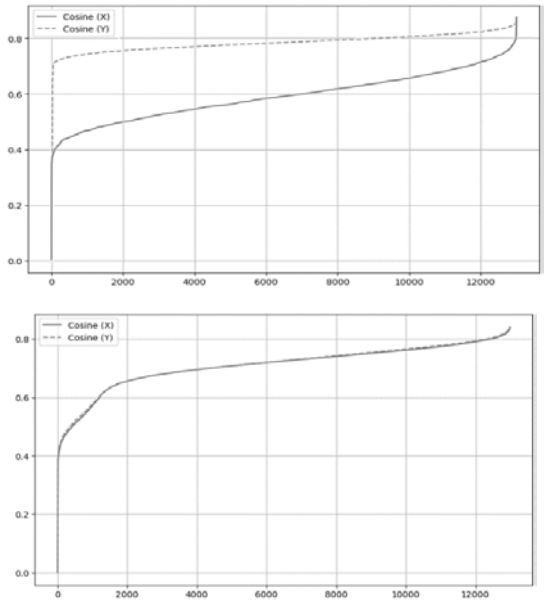

Fig. 2. Comparison of the cosine distance metric in X and Y spaces for the Erdős-Rényi graph (top), PEG graph (bottom)

D. Theoretical proof of distortion bounds for sparse graph Ternary Projection with ACE optimization

Given a PEG with ACE optimized matrix R, girth $g \geq 6$ (no 4-cycle), EMD approximately equal to maximal degree (weight matrix) $EMD\ value \approx \max degree(R)$ and sparsity $\rho = \frac{1}{d}$, the probability of distortion improves to:

$$\mathbb{P}(|\|Rx\|^2 - \|x\|^2| > \epsilon\|x\|^2) \leq e^{-\Theta(\epsilon^2 k * EMD)}.$$

More measurements k (rows), increasing EMD value (via graph design) improves the bound (concentration).

Proof: Martingale construction step. Let R be a sparse random matrix with the given properties. Define the Doob martingale sequence for the norm preservation:

$$Y_i = \mathbb{E}[\|Rx\|^2 | R_1, \ldots, R_i],$$

where R_i are the row of R. The final value $Y_k = \|Rx\|^2$.

Bounded differences step. The key is to bound the differences$|Y_i - Y_{i-1}|$. Due to girth $g \geq 6$ (no 4-cycle) for which large $EMD\ value \approx \max degree(R)$, ensuring limited dependency between rows and guaranteed that the energy of distortion is spread across check, reducing the impact of any single row. Using the method of bounded differences (Corollary 5.2, [15]), the difference satisfy $|Y_i - Y_{i-1}| \leq c_i$, where c_i depends on the EMD value distribution among cycles (for example 6, 8, 10, etc.) The EMD condition implies that the distortion energy is "smoothed" across Θ(EMD) checks, so:

$$c_i \cong \Theta\left(\frac{\|x\|^2}{\sqrt{EMD}}\right).$$

By Azima-Hoeffding Theorem for martingales 5.2 (Theorem 5.2, [15]), the concentration bound is:

$$\mathbb{P}(|\|Rx\|^2 - \|x\|^2| > \epsilon\|x\|^2) \leq 2e^{-\left(\frac{2\epsilon^2\|x\|^4}{\sum_{i=1}^{k} c_i^2}\right)}.$$

Substuting c_i : $\sum_{i=1}^{k} c_i^2 = k * \Theta\left(\frac{\|x\|^4}{EMD}\right)$. Thus omit factors 2:

$$\mathbb{P}(|\|Rx\|^2 - \|x\|^2| > \epsilon\|x\|^2) \leq e^{-\Theta(\epsilon^2 k * EMD)}. \blacksquare$$

IV. Duality Beetween Superposition Coding and Sparse Random Projections. DNN Feature Scaling

Superposition coding (SC) is strategy where multiple input features are additively combined into a lower-dimensional neural activity pattern. Used in neural networks to overcome width limitations (e.g., representing more features than neurons per layer. SC and SRP consist of two operation encoding and decoding.

SC encoding step combine x into dense neural activity vector $y \in \mathbb{R}^M$ via learned weight matrix $\in \mathbb{R}^{M \times N}$, $y = Wx$, where $\|x\|_0 = S \ll N$, W is dense but x is sparse. Superposition coding decoding step recover x from y by solving $\min_{\hat{x}} \|\hat{x}\|_1 : y = W\hat{x}$, $\|\hat{x}\|_0 \leq S$.

SRP encoding step project x via a sparse random matrix $A \in \mathbb{R}^{M \times N}$: $y = Rx$, where $A_{ij} \sim SparseGaussian(\rho)$, A has i.i.d. entries with sparsity ρ. SRP decoding step recover x from y using sparse recovery, $\min_{\hat{x}} \|\hat{x}\|_1 : y = R\hat{x}$.

Both approach reduce to sparse linear inverse problem, but with swapped sparsity assumptions. The duality between SC and SRP can be formalized as complementary sparse linear inverse problems: while SRP recovers a dense input from sparse projections, SC recovers a sparse input from dense projections. This suggests that SC's decoding mirrors compressed sensing, with the weight matrix W playing the role of a sensing matrix. Hybrid approaches could initialize W with SRP-like sparsity, and then adapt it to data, blending theoretical guarantees with empirical performance. In CNNs, the SC-SRP duality manifests hierarchically: early convolutional layers perform SRP-like sparse projections (local filters on sparse image gradients), while deeper layers leverage superposition coding to combine features additively. This explains why CNNs benefit from overcomplete later layers (to support SC) and small, sparse initial kernels (to preserve SRP-like efficiency). Hybrid designs – such as random initial filters with learned sparse combinations – could optimize this trade-off. In transformers, the SC-SRP duality surfaces in attention and Feed Forward layer (FFL): attention heads

adaptively superimpose tokens (SC-like), while FFL with random initializations resemble sparse projections (SRP-like). This explains why transformers benefit from overparameterized FFL (to support sparse coding) and sparse attention (to limit interference).

It is evident that a neural network tasked with encoding a feature set larger than its number of neurons per layer must employ a superposition-based encoding scheme Fig. 3 [16].

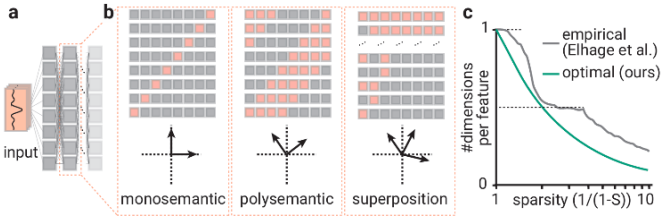

Fig. 3. **Network capacity of deep neural networks and it relation to feature per dimension**, [16]. (**a.**) Schematic of a deep artificial neural network (ANN) with input signals (orange) processed through consecutive neuron layers (gray), connected all-to-all. (**b.**) Coding schemes in a neural layer: **Monosemantic coding** (left) has a one-to-one input-neuron relationship; **Polysemantic coding** (middle) involves overlap; **Superposition coding** (right) is one-to-many, a subtype of polysemantic. (**c.**) Dimensions required in a hidden layer per input feature vs. feature sparsity (gray), compared with optimal encoding predictions (green), from [17]. Dashed lines indicate "sticky" regions [17], where network performance deviates from optimal

To investigate whether neural networks naturally converge toward near-optimal encoding strategies, we revisit findings from a recent study on toy models of superposition [17]. In these models, a deep neural network learns to encode and decode inputs x with varying sparsity levels S. A critical consideration in classification tasks is the relationship between the number of classes and the required feature dimensionality. As the number of classes grows, the feature space must expand accordingly to ensure sufficient separability. By comparing the network's information capacity with the entropy of sparse inputs, the compression rate R achievable by an graph, [16–18]:

$$R = 1 - S + \frac{1}{E}\big(-Slog(S) - (1-S)log(1-S)\big),$$

where $E = \langle logp_x \rangle$ denotes the entropy of a single input x. For sufficient large E (weight and activation quantization, float16 or entropy/information bottleneck optimized int8/4 bits) R simplifies to $R = 1 - S$.This asymptotic bound closely matches empirical results, Fig. 3(c). However, deviations arise in "sticky" encoding regimes, where the network learns robust but suboptimal representations due to feature undersampling in high-dimensional class spaces [16]. The effective dimension of a network's representation is constrained by both the layer width (neuron count) and the entropy of the input distribution. When the intrinsicdimension of the data exceeds the network's width, superposition coding becomes necessary, albeit at the cost of increased sensitivity to noise. For classification tasks, this implies that the minimal required feature dimension scales with both the number of classes and the sparsity of discriminative features.

V. Conclusion

This paper introduced a novel graph-based feature extraction method using Progressive Edge Growth (PEG) graphs with Approximate Cycle Extrinsic (ACE) optimization to enhance high-dimensional machine learning tasks. By leveraging sparse ternary projections, our approach efficiently expands feature spaces while preserving geometric relationships, outperforming traditional random projection methods in both computational efficiency and structure retention. In paper derived distortion bounds for PEG-based projections, proving that their high girth and EMD properties lead to tighter concentration inequalities than random sparse projections. It reveals a fundamental connection between sparse coding in neural networks and random projections, suggesting hybrid architectures that combine structured sparsity with learned representations for improved scalability.

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Graph Sparsification and Permanent Scaling: Computational Strategies for Mitigating Over-Smoothing in RBIM-Embedding GNNs

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***Abstract*. The matrix permanent, a canonical #P-hard problem in computational complexity, plays a critical role in quantum physics, combinatorics, and graph machine learning. This paper introduces novel approximation techniques for permanents through the lens of graph-structured optimization, with applications to mitigating over-smoothing in graph neural networks (GNNs). We propose a min-sum belief propagation (Bethe) approximation that reformulates the permanent as a graphical model partition function, enabling efficient polynomial-time estimation via message passing. Our method directly addresses the spectral limitations of normalized adjacency matrices in GNNs, where high permanents (small spectral gaps) induce feature indistinguishability and weak latent-space clustering. By integrating permanent regularization and graph sparsification, we demonstrate a 6.27 % accuracy gain (from 93.23 % to 99.5 %) in Random Bond Ising Model (RBIM) sparse graph embeddings. Bridging combinatorial optimization with graph representation learning, this work advances scalable permanent approximations while offering theoretical insights into their role in GNN robustness. Our results open new avenues for applications in quantum probability estimation, pruning, and spectral regularization.**

***Keywords:* Matrix permanent, Bethe approximation, belief propagation, free energy, graph covers, spectral gap**

I. INTRODUCTION

The permanent of an $n \times n$ matrix $[A_{ij}]$, defined as

$$perm(A) = \sum_{\sigma \in S_n} \prod_{i=1}^{n} a_{i,\sigma(i)},$$

where S_n denotes the symmetric group, over all matrix column permutation, is a fundamental problem in computation complexity. Unlike the determinant, the permanent lacks sign cancellations, rendering it #P-hard to compute exactly [1]. While Ryser's $O(n2^n)$ inclusion-exclusion algorithm [2] remains the fastest exact method, it becomes intractable for $n \geq 50$ necessitating approximation techniques. The permanent arises in diverse domains In quantum physics, it describes boson sampling outcomes (permanent of unitary matrices), [3]. In Information Theory, particularly in channel coding, the permanent of certain matrices can provide bounds on the Hamming weight of codewords (upper bound on Hamming distance) [4] and fraction weight of pseudocodewords [5]. In combinatorics the permanent counts perfect matching in bipartite graphs. In graph machine learning, governing the spectral properties of normalized adjacency matrices. In graph neural networks (GNNs), the permanent of the normalized adjacency matrix critically influences the spectral gap and mixing time of feature propagation [6]. A high permanent (small spectral gap) leads to over-smoothing – where repeated message passing renders node features indistinguishable [7] – and poor latent-space clustering. Mitigation strategies include permanent regularization and graph sparsification. Graph sparsification done by edge pruning to reduce the permanent and improve mixing time. Permanent regularization by penalizing the Bethe permanent to enforce a "large basin" solution space [5, 9]. However, sparsification disrupts doubly stochastic properties, necessitating permanent scaling for non-regular graphs. This work systematically evaluates these approaches, focusing on their accuracy-efficiency trade-offs. Our contributions include a Bethe min-sum message-passing approximation framework for permanents, with theoretical and empirical analysis; numerical validation in random bond Ising Model Spectral embedded GNNs, showing 6.27 % accuracy gains in generative adversarial network generated binary class image clustering and classification (cat vs dog), [10] which allow to apply this approach to natural image clustering (class labeling) and classification (ImageNet), [11].

II. RELATED WORK

Prior work on permanent computation can be categorized into three main paradigms. The first focuses on exact computation and classical approximations.

The fastest known exact algorithm, Ryser's $O(n2^n)$ inclusion-exclusion method [2], along with Glynn's formula. For polynomial-time approximations, the Jerrum–Sinclair–Vigoda fully polynomial randomized approximation scheme (FPRAS) [12] provides guarantees for nonnegative matrices but is hindered by impractical constants (e.g., $O(n^{10})$limiting its utility in large-scale applications. The second paradigm employs variational and probabilistic methods to approximate the permanent as a partition function. Huang and Jebara [13] pioneered the use of belief propagation (BP), reformulating the permanent within a graphical model framework, though theoretical convergence guarantees remain incomplete. A significant advance came from Vontobel [9, 14], who derived the Bethe permanent through Bethe free energy minimization, proving it serves as a lower bound for nonnegative matrices. This work bridges permanents with pseudocodeword analysis in coding theory [5], revealing deep connections between statistical physics and combinatorial optimization. The third paradigm leverages combinatorial and graph-theoretic techniques to refine permanent bounds. Vontobel [15, 16] established a combinatorial characterization of the Bethe permanent using finite graph covers, enabling tighter approximations. Subsequent work extended this framework to higher-order M-Bethe permanents [17], which exploit permutation cycle decompositions to improve accuracy. These methods have found applications in quantum inference [3] and graph neural network regularization [7], where controlling the permanent's growth is critical to avoiding spectral collapse and over-smoothing. Our work synthesizes these perspectives, introducing scalable permanent approximations tailored to graph machine learning. By unifying variational, combinatorial, and graph-theoretic insights, we advance the role of permanents in GNN robustness while drawing new connections to quantum computation and optimization.

III. METHODOLOGY

A. Tanner graph and its matrix representation

Low-Density Parity-Check (LDPC) codes $[N, K]$ are a class of linear block codes characterized by a sparse parity-check matrix $H^{(N-K)\times N}$, which can be represented graphically using a Tanner graph. The Tanner graph is a bipartite graph consisting of two types of nodes: variable nodes (VNs) and check nodes (CNs). The variable nodes correspond to the codeword bits, representing the columns of H, while the check nodes represent the parity-check equations, corresponding to the rows of H. An edge connects a variable node v_i to a check node c_j if and only if the entry $H_{j,i}$ is equal to 1. The degree of a node, defined as the number of edges connected to it, remains low due to the sparsity of H, which is a key feature of LDPC codes.

Quasi-Cyclic LDPC (QC-LDPC) codes are a structured subclass of LDPC codes where the parity-check matrix H is constructed using circulant permutation matrices or zero matrices. Specifically, H is formed by expanding a smaller base matrix, where each non-zero entry is replaced by a circulant permutation matrix (a shifted identity matrix) and each zero entry is replaced by a null matrix. This structure provides implementation advantages, particularly in hardware, due to its regularity and efficient memory utilization. The QC-LDPC parity-check matrix can be expressed in a block form where each block $P_{i,j}$ is either a circulant permutation matrix or a zero matrix. The circulant property ensures that each block row is a cyclic shift of the previous one, enabling simplified implementation using barrel shifter, such matrix have large special structures (tori like) of symmetry.

B. Belief Propagation BP (Sum-Product)

The Bethe permanent, an approximation of the matrix permanent derived from the Bethe free energy minimization, can be estimated using probabilistic methods such as Belief Propagation (BP) [16–18]. BP iteratively passes messages between nodes of a bipartite graph representing the matrix, converging to a fixed point that approximates marginal probabilities (and thus the permanent). Below, we outline the sum-product BP method and its computationally efficient min-sum variant. Let $m_{x_{i\to y_j}}$ denote a message from node x_i to y_j in the Tanner graph. The BP update rules for beliefs $b(\cdot)$ and messages are

$$b(x_i, y_j) \propto \psi(x_i, y_j)\phi(x_i)\phi(y_j)\prod_{k\neq j} m_{y_{k\to x_i}}(x_i)\prod_{l\neq i} m_{x_{l\to y_i}},$$

$$b(x_i,) \propto \phi(x_i)\prod_{k\neq j} m_{y_k\to x_i}, b(y_j) \propto \phi(y_j)\prod_{l\neq i} m_{x_{l\to y_i}},$$

where ψ and ϕ are pairwise and unary potentials, respectively. Message are update iteratively:

$$m^{new}_{x_{i\to y_j}} = \sum_{x_i}\left[\phi(x_i)\psi(x_i, y_j)\prod_{k\neq j} m_{y_{k\to x_i}}\right].$$

To stabilizing convergence, log-space damping with a factor $\alpha \in (0, 1]$ is applied:

$$\ln m_{xi}(y_j) \leftarrow \ln m_{x_i\to y_i} + \alpha\left[\ln m^{new}_{x_i\to y_j} - \ln m_{x_i\to y_j}\right].$$

The sum-product BP has $O(n^2)$ complexity per iteration, motivating a faster min-sum approximation.

C. Normalize Min-Sum BP ($O(n)$ approximation)

We simplify messages to two cases:

- Mismatched $(y_j \neq i)$:

$$m^{not}_{y_{x_i\to y_j}} = \sum_{x_i\neq j}\phi(x_j) m^{match}_{y_{x_i\to x_i}}\prod_{k\neq j, k\neq x_i,} m^{not}_{y_k\to x_i}.$$

- Matched $(y_j = i)$:

$$m^{match}_{x_i \to y_j} = \phi(x_i = j) \prod_{k \neq j} m^{not}_{y_k \to x_i}.$$

Normalized by $m^{not}_{y_{k \to} x_i}$, yields:

$$m^{not}_{x_i \to y_j} = 1, m^{match}_{x_i \to y_j} = \frac{\phi(x_i = j)}{\sum_{k \neq j} \phi(x_i = k) m^{match}_{y_k \to x_i}}.$$

The min-sum update rule reduced to:

$$m_{x_i \to y_j} \leftarrow \frac{1}{Z} \frac{\phi(x_i = j)}{\sum_{k \neq j} \phi(x_i = k) m_{y_{k \to} x_i}},$$

Where Z is a normalized constant. The belief are then approximated as:

$$b(x_i = j, y_j = i) = \frac{1}{Z_{ij}} \phi(x_i) \phi(y_j),$$
$$b(x_i \neq j, y_j \neq i) = \frac{1}{Z_{ij}} \phi(x_i) \phi(y_j) m_{y_{z_i \to x_i}} \mathrm{m}_{x_{y_j \to y_j}},$$
$$b(x_i) = \frac{1}{Z} \phi(x_i) \mathrm{m}_{y_{z_i \to x_i}}, b(x_i) = \frac{1}{Z} \phi(y_j) \mathrm{m}_{x_{y_j \to y_j}}.$$

D. Numerical example

Consider a sparse binary matrix of size 9×12:

$$H = \begin{pmatrix} 1 & 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 1 & 0 \\ 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 1 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 1 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 & 1 & 0 & 0 \end{pmatrix}$$

We compute Bethe permanents for submatrices $\boldsymbol{H_i'}$ of size $m \times (m+1)$, excluding columns iteratively (in table exc. describe omit columns to yields square submatrices of size 9×9 for permanent estimation). For each submatrix, the Bethe permanent $perm_B(\boldsymbol{H_i'}/\mathrm{k})$ is compared to the exact permanent (Table). The Bethe approximation tends to underestimate the true permanent (e.g., Bethe-permanent = 2.37 vs. exact permanent = 6 for 1 column first vector). The error varies with matrix sparsity and excluded columns. For non-negative matrices, the Bethe approximation of the permanent $perm_B(\boldsymbol{A})$ is monotonically increasing with respect to matrix entries A_{ij}. This property aligns with the exact permanent's behavior and ensures stability in iterative approximations. The Bethe approximation retains this property, enabling block-wise rescaling for large matrices (e.g., decomposing into submatrices and combining results). The Bethe permanent is particularly effective for QC-LDPC codes, where the parity-check matrix H is sparse and block-circulant. The BP algorithm's complexity reduces to O(n) per iteration for sparse H, as messages only propagate between connected nodes. The circulant blocks in QC-LDPC matrices allow parallel message updates, further accelerating convergence. For QC-LDPC graphs with $girth \geq 6$, shortest closest path in Tanner graph, the Bethe permanent often provides tight bounds on the true permanent, as loops (which degrade BP accuracy) are minimized.

COMPARATIVE ESTIMATES OF THE VALUES OF PERMANENTS AND BETHE PERMANENTS FOR THE MATRIX H WITH EXCLUDED COLUMN

col	1	2	3	4	5	6	7	8
BP	2.37	1.69	1.69	1	1	1	1	1
Per	6	5	5	2	2	2	2	2
ecx.	1,11, 12	2,11, 12	3,11, 12	4,11, 12	5,11, 12	6,11, 12	7,11, 12	8,11,12
BP	1.69	2.37	1.69	1	1	1	1	1
Per	4	6	4	2	2	2	2	2
ecx.	1,10, 12	2,10, 12	3,10, 12	4,10, 12	5,10, 12	6,10, 12	7,10, 12	8,10,12
BP	1.69	1.69	2.37	1	1	1	1	1
Perm	4	4	6	2	2	2	2	2
ecx.	1,10, 11	2,10, 11	3,10, 11	4,10, 11	5,10, 11	6,10, 11	7,10, 11	8,10,11
BP	2.214 353	2.214 353	1	1	1	1	1	1
Perm	6	6	2	2	2	2	2	2
ecx.	1,9,12	2,9,12	3,9,12	4,9,12	5,9,12	6,9,12	7,9,12	8,9,12
BP	1.69	1.69	1.69	0.02	1	1	1	1
Perm	4	4	4	0	2	2	2	2
ecx.	1,9,11	2,9,11	3,9,11	4,9,11	5,9,11	6,9,11	7,9,11	8,9,11

IV. RANDOM BOND ISING MODELS FOR SPECTRAL EMBEEDING

The Random Bond Ising Model (RBIM) on a QC-LDPC graph $\zeta(v, \varepsilon)$ assigns spins $s_i \in \{-1,1\}$ to vertices v, with edge weights $Jij \in \{\pm 1\}$ encoding interactions. The Hamiltonian $H_i(s) = -s^T JsH$ defined the system's energy, where the Boltzmann distribution $\mu(s) \propto e^{-\beta H_J(\mathrm{s})}$ links to the partition function $Z_{j,\beta}$. For QC-LDPC codes, the sparse, structured J matrix (derived from the parity-check matrix $\boldsymbol{H}$) enables efficient free energy minimization via belief propagation (BP). The Bethe free energy, approximated by BP, connects to the Bethe permanent through the mapping $perm_B(H) \propto \lim_{\beta \to \infty} Z_{j,\beta}$, where the permanent *estimates the partition function's dominant configuration***.** This relationship is exploited in decoding

QC-LDPC codes, where the ground state of $H_i(s)$ corresponds to optimal codeword recovery, and the Bethe permanent provides a scalable approximation for large $\boldsymbol{H}$. The RBIM's Gibbs-Boltzmann density $p(x;\theta) \propto e^{-U(x;\theta)}$ further extends this to energy-based learning, with θ trained to match data distributions via stochastic gradients is parametrized by CNNs. Here $U(x;\theta)$ acts as a learned Hamiltonian, mapping input to scalar energies, [10]. Feed Forward layers which always exist at least at final (top) layers for mapping features to classes in CNN can be replaced by graph spectral embedding derived from RBIMs, leveraging the underlying QC-LDPC graph (or another QC like on the graph).

A. RBIM, Nishimori temperature and Bethe Hessian

The Hamiltonian's Hessian matrix $H_{\beta,j}$ at the Nishimori temperature $H_{\beta,j}$ fundamentally encodes the graph's connectivity structure, with its eigenvectors naturally forming a low-dimensional embedding space where nodes are positioned according to their spectral similarity. This spectral approach provides an elegant alternative to traditional dense feedforward layers, offering sparse and interpretable projections that capture the system's underlying physics. Below the critical temperature $H_{\beta,j}$, the emergence of the spin-glass phase coincides with the formation of polysemantic embeddings, where nodes simultaneously participate in multiple clusters, reflecting the complex interactions in the system. The eigenvalue spectrum of the RBIM (Bethe) Hessian reveals crucial geometric properties of the embedding space, where the spectral gap between eigenvalues directly determines cluster separability – larger gaps yielding more distinct and discriminative clusters. Simultaneously, the slope of the eigenvalue decay provides insight into the intrinsic dimensionality of the data, with steeper decay patterns enabling more compact representations by effectively filtering out high-frequency noise components. This spectral analysis synergizes perfectly with Bethe permanent optimization, as the spectral methods maintain the geometric structure while the free energy minimization ensures embeddings correspond to physically meaningful, low-energy states. At the critical Nishimori temperature $H_{\beta,j}$, the closing of the spectral gap marks an important phase transition point that indicates optimal embedding resolution. The hierarchical organization of features emerges naturally from the eigenvalue spectrum, where dominant eigenvectors with gentle slopes capture global patterns while the rapidly decaying tail eigenvectors encode finer local interactions. This combined approach of spectral embedding and free energy optimization leads to highly efficient and interpretable representations for RBIMs and QC-LDPC graphs, successfully balancing the physical constraints of the system with its topological properties. The eigenvalue slope proves particularly valuable as it serves as a tunable parameter that elegantly bridges rigorous spectral analysis with fundamental statistical physics principles.

B. Comparative Analysis of Random Regular and QC-LDPC Graphs with approximatly same permanent values

This comparative study analyzes spectral properties of two graph types - a 6000-node random Erdos-Renyi (ER) regular graph (degree 15) and a QC-LDPC circulant graph (16×16 blocks, 375 circulant size, $E(H)_2$ graph [10]), Fig. 1. Both share near identical numbers of non-zero elements for non-backtracking matrix, indicating comparable combinatorial and implementation complexity, yet exhibit distinct spectral behaviors. The random ER graph shows near-perfect regularity with strong cluster separation, but moderate dimensionality reduction. In contrast, the QC-LDPC structure displays tighter eigenvalue packing (visualize first 100 values) with superior spectral scaling, demonstrating more efficient embedding properties despite equivalent complexity. The circulant architecture's deterministic patterns yield computational advantages while maintaining embedding quality, highlighting how graph construction fundamentally shapes spectral characteristics.

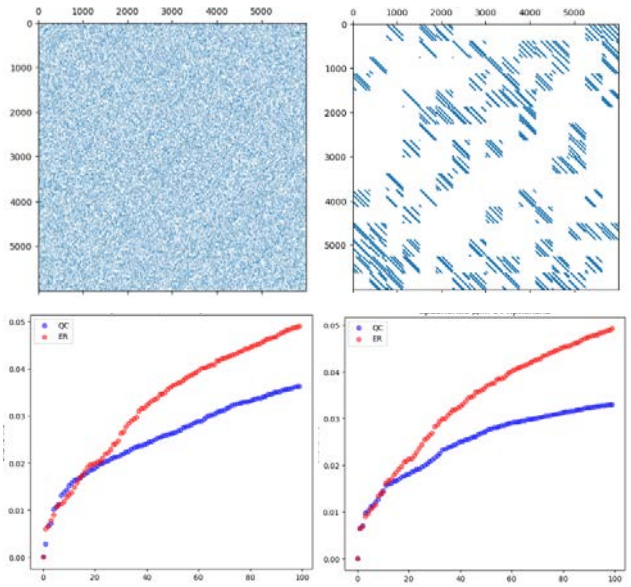

Fig. 1. Comparison of Trace of ER (top left), QC-LDPC (top right) graphs, 100 eigenvalues for 32 (bottom left) and 64 feature (bottom right)

C. Spectral and Permanent-Based Analysis of Sparse Graph Stochasticity

Permanent optimization is especially critical for irregular graphs due to their non-double-stochastic

nature. Unlike regular graphs, where uniform degree distributions facilitate balanced connectivity, irregular graphs exhibit varying node degrees that disrupt adjacency matrix symmetry. This structural asymmetry complicates the characterization of combinatorial properties through standard spectral methods, necessitating permanent-based analysis to fully capture their complexity. The permanent, which quantifies the weighted sum of perfect matchings, becomes particularly sensitive when applied to irregular structures. In spectral embedding tasks, it helps compensate for spectral distortions caused by irregular degrees. While the Bethe Hessian or Laplacian of irregular graphs still generates embeddings, the permanent provides complementary insights into the graph's underlying combinatorial structure. This dual perspective is invaluable for real-world networks, which rarely display perfect regularity. However, even regular graphs face challenges with stochasticity under the Bethe-Hessian framework. Despite their uniform degree distributions, their adjacency matrices are not inherently doubly stochastic—rows and columns do not naturally sum to one without normalization. This complicates spectral methods, as the Bethe-Hessian, derived from belief propagation, assumes a specific stochastic structure for accurate free energy estimation. In regular graphs, the Bethe-Hessian presumes spectral properties align with the Bethe approximation, but the lack of inherent double stochasticity means its eigenvalues may not fully reflect the system's correlation structure, [18]. This introduces approximation errors in free energy calculations, particularly when estimating the permanent, which is closely tied to the partition function.

While irregular graphs suffer from degree imbalance, regular graphs face excessive symmetry, which can obscure subtle structural variations affecting stochasticity. Consequently, even regular graphs may require additional Bethe-Hessian normalization or correction terms to ensure proper stochastic behavior in spectral embeddings. Such permanent renormalizations have been applied to quasi-cyclic graph embeddings, yielding a 6.27 % accuracy improvement in GAN classification tasks on datasets like ImageNet-10/100 and others [11].

V. Conclusion

This paper bridges the gap between computational complexity and graph machine learning by introducing novel, scalable approximations for the matrix permanent through belief propagation and spectral graph theory. Our min-sum Bethe approximation provides an efficient polynomial-time method for permanent estimation while addressing critical challenges in graph neural networks, particularly over-smoothing caused by small spectral gaps. By integrating permanent regularization with graph sparsification, we achieve significant accuracy improvements (6.27 %) in RBIM-based embeddings, and demonstrating the practical value of our approach.

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Defenses for Preventing Attacks in the Task of Classifying Medical Images

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Abstract. **Nowadays neural networks are used in various ways: voice assistants, healthcare, security systems and others. However, their performance may degrade due to external attack or insufficient testing. For example, an error in diagnosis may overload medical facilities and lead to incorrect diagnoses. This work explores existing attacks on neural networks in the context of medical image classification. The work proposes defenses mechanisms against adversarial attacks. The effectiveness of the defenses is evaluated.**

Keywords: **neural network defenses, neural network attacks, deep neural networks, medical images, malicious images**

I. INTRODUCTION

The work [1] proposes a process of creating adversarial images called L-BFGS, and also suggests the hypothesis that neural networks are vulnerable to adversarial images due to the non-linearity of neural networks.

The work [2] studies the impact of adversarial images on neural networks and linear models. It concludes that neural networks are vulnerable to adversarial images mainly due to the linearity of their components. This paper introduces Fast Sign Gradient Method (FSGM) attack, which is more computationally efficient than previously proposed L-BFGS attack.

The work [3] introduces Carlini-Wagner (CW) attack and its variations, usage specifics, and demonstrates its advantages over other existing attacks.

We evaluate existing FSGM and CW attacks on the task of medical image classification, evaluate existing Adversarial Training and proposed Blur Reconstruction, Denoising Au toencoder, Denoising Variational Autoencoder defenses.

II. ATTACKS ON NEURAL NETWORKS

Let $\mathrm{f}(\mathrm{x},\theta) \in \mathrm{R}^{\mathrm{C}}$ – target neural network, which outpus probabilities of an object x belonging to class k, $1 \leq k \leq C$, x - a target image.

Formally, goal of the attack is based on the target image x to find adversarial image x_{adv} such that:

$$\arg\max f\,(x,\theta) \neq \arg\max f\,(x_{\text{adv}},\theta). \quad (1)$$

Equation (1) means that neural network predict different class for x_{adv} compared to x.

A. Fast Sign Gradient Method

Let $L(f(x,\theta),y) \in R$ be a differential loss function, ϵ – a selected constant, y – real class for the object x.

FSGM method is defined as follows:

$$x_{\text{adv}} = x + \epsilon \cdot \text{sign}\nabla_x L(f(x,\theta),y). \quad (2)$$

B. Carlini-Wagner

Let $y_t \neq y$ be a target class for the adversarial image. The adversarial image x_{adv} is defined as follows:

$$x_{\text{adv}} = x + \delta. \quad (3)$$

Where δ is noise added to the image.

Distance between the adversarial image and the target image is defined as L_p norm of their difference:

$$||\delta||_p = ||x_{\text{adv}} - x||_p. \quad (4)$$

Let $Z(x)$ be a vector of logits of $f(x,\theta)$. The confidence for the attacked image is defined as follows:

$$c(x) = \max_{i=1,C}\{Z_i(x_{\text{adv}}); i \neq y\} - Z_y(x_{\text{adv}}) \quad (5)$$

Let c_t be a target confidence for the adversarial image, i.e. $c(x_{\text{adv}}) = c_t$. x_{adv} is defined as the solution to the following optimization problem:

$$||\delta||_p^p + \lambda(c(x_{\text{adv}}) - c_t) \rightarrow \min_\delta. \quad (6)$$

III. ANALYSIS OF DEFENSES

Neural networks are sensitive to input data distortions, which means that failures can occur not only due to intentional attacks but also due to corrupted data. Therefore, it's important to make models robust to such distortions by applying various defense mechanisms, enabling stable operation both in the absence and

presence of attacks. It's worth noting that there are no universal defenses against all types of attacks, and attackers continue to develop new methods.

This section introduces the following defense mechanisms: existing Adversarial Training, also Blur Reconstruction, Denoising Autoencoder, Denoising Variational Autoencoder.

A. Adversarial Training

Adversarial training works as follows: the original training dataset is extended with adversarial samples, serving as a form of data augmentation. This approach uses input data that is not naturally occurring but is specifically made to expose the model's weaknesses. Using this augmentation, the model becomes less sensitive to small perturbations.

This defense works well for a known attack (adversarial images generated using a known attack) or when attacks are relatively weak. To improve the model's robustness to attacks using adversarial training, one can train the model on the samples created with different attacks. Additionally, using adversarial examples generated by various types of attacks can help improve the model's generalization capability.

B. Blur reconstruction

The main task in defense against attacks is to reduce the impact of noise on the image to ensure correct performance (classification). I.e. adding some operations to the model which will make the model output correct results.

Blur reconstruction uses median blur image preprocessing during training and inference to ensure that adversarial noise is suppressed.

C. Denoising Autoencoder

We can use neural networks for image denoising. To do this, we use the autoencoder model, which maps the input image into a latent vector and then reconstructs the image from the latent. The idea behind using the autoencoder is that it reconstructs the image, carrying the main details, without high-frequency noise, including adversarial noise.

The denoising autoencoder $g(x_{\text{adv}}, \theta)$ is trained to minimize the following objective:

$$||x - g(x_{\text{adv}}, \theta)|| \quad \rightarrow \min_{\theta}. \qquad (7)$$

The main idea of the defense is to put the input image into the autoencoder (AE), then use its output as input to the model.

D. Denoising Variational Autoencoder

Variational autoencoders (VAE) were introduced in the paper [5]. The main difference between AE and VAE is that VAE adds constraints to the latent space, making it continuous and normally distributed.

The main idea behind this method is to use VAE for image denoising, exactly as AE. We suppose that latent space regularization will better learn the sample distribution and will do better in the denoising task.

IV. Experiments

In this section, the images from different datasets and different models were attacked with FSGM and CW attacks. Also, Adversarial Training, Blur Reconstruction, Denoising Autoencoder and Denoising Variational Autoencoder defenses were studied.

A. Experimental setup

There were 2 sets of images: a dataset of CT slices with the following classes: shuld, heard, liver. There were 1801 512×512 RGB images. The second set was a histological dataset of breast cancer images, obtained from two different hospitals in the Netherlands. The dataset was used in the CAMELYON-2016 challenge [6] and includes 3 classes: normal (NRM), tumor (TUM), epithelial tissue (EPI). There were 18000 256×256 RGB images of 3 classes (6000 images per class).

Every dataset was divided into train (70 %) and test (30 %) splits. Examples of CT images and histology images are shown in the Fig. 1.

For the experiments custom neural network and EfficientNetB2 [4] were used. The custom neural network was constructed using convolution, ReLU, and MaxPooling layers. The EfficientNetB2 was selected due to its small size and high classification accuracy. The accuracy metric was used to measure the classification quality.

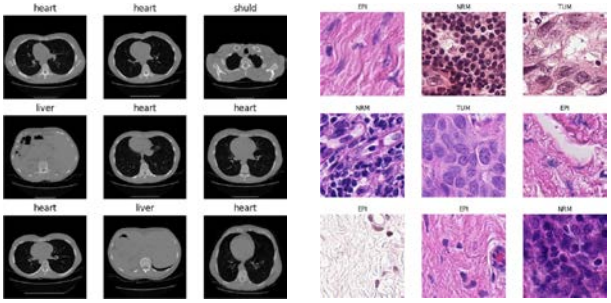

Fig. 1. Example of data from the CT (left) and histology (right) datasets

B. Attacks

The adversarial samples for FSGM were created using the formula (2). For experiments $\epsilon = 0.004$ and $\epsilon = 0.01$ were selected. Table I contains accuracy for adversarial samples for different ϵ.

TABLE I. FSGM ATTACK RESULTS FOR DIFFERENT NOISE ϵ LEVELS

Data	No attack	$\varepsilon = 0.004$	$\varepsilon = 0.01$	Model
Histology	94.65 %	60.73 %	**9.98** %	EfficientNetB2
CT	100 %	86.12 %	**5.59** %	EfficientNetB2
Histology	90.11 %	71.78 %	**36** %	Custom
CT	100 %	100 %	**90** %	Custom

For later experiments $\epsilon = 0.01$ was used.

Carlini-Wagner adversarial samples were constructed using formula (6), with $\lambda \in [0.001, 0.3]$. Results of the CW attack are presented in the Table II.

TABLE II. CARLINI-WAGNER ATTACK RESULTS

Data	No attack	CW	Model
Histology	94.65 %	0 %	Efficient NetB2
CT	100 %	0 %	Efficient NetB2
Histology	90.11 %	0 %	Custom
CT	100 %	0 %	Custom

Carlini-Wagner attack is far more efficient than FSGM, but it requires much more resources and time to create an adversarial sample. With well-chosen parameters, the CW attack can achieve a full sample misclassification (0 %). The Table III contains the comparison for attacks. Examples of malicious images from CW and FSGM attacks in the Fig. 2.

TABLE III. RESULTS OF CW AND FSGM ATTACKS

Data	No attack	FSGM	CW	Model
Histology	94.65 %	9.98 %	**0 %**	EfficientNet B2
CT	100 %	5.59 %	**0 %**	EfficientNet B2
Histology	90.11 %	36 %	**0 %**	Custom
CT	100 %	90 %	**0 %**	Custom

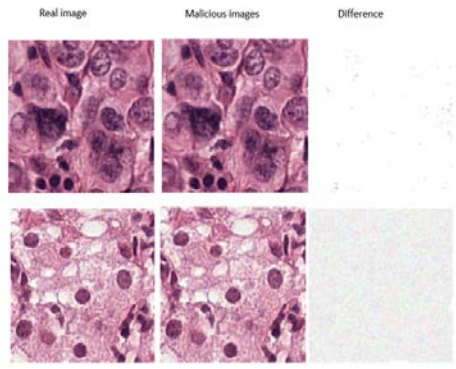

Fig. 2. Examples of malicious images from CW (1st row) and FSGM (2nd row) attacks

C. Adversarial training

The effectiveness of adversarial training was studied using FSGM and CW attacks. To study the defense effectiveness, models were fine-tuned on the adversarial images. The Tables IV and V contain results of adversarial training defense for FSGM and CW attacks respectively.

Adversarial training produced good results on our data and studied models: the accuracy on adversarial samples came close to the accuracy of initial models on non-adversarial images. But this method can't be used for defending against all attacks, because it is attack-specific, which means that the model can be attacked with a more efficient attack and the defense won't help. Also, it is worth mentioning that this method requires fine-tuning of models, which can cause problems in scalability.

TABLE IV. RESULTS OF ADVERSARIAL TRAINING FOR FSGM

Data	**No attack**	**FSGM**	**Defense**	**Model**
Histology	94.65 %	9.98 %	**94.1 %**	EfficientNet B2
CT	100 %	5.59 %	**99.6** %	EfficientNet B2
Histology	90.11 %	36 %	**83 %**	Custom
CT	100 %	90 %	**100 %**	Custom

TABLE V. RESULTS OF ADVERSARIAL TRAINING FOR CW

Data	**No attack**	**CW**	**Defense**	**Pretrained**
Histology	94.65%	0%	**92 %**	EfficientNet B2
CT	100%	0%	**90 %**	EfficientNet B2
Histology	90.11%	0%	**82.2 %**	Custom
CT	100%	0%	**94.34 %**	Custom

D. Blur reconstruction

For experiments, the median filter of size 2×2 was applied before passing the input image to the model. The Tables VI and VII contain results for blur reconstruction defense for FSGM and CW attack.

TABLE VI. BLUR RECONSTRUCTION RESULT FOR FSGM

Data	**No attack**		**FSGM**		**Model**
	No blur	**Blur**	**No blur**	**Blur**	
Histology	94.65 %	**94.81** %	9.98 %	**28.37** %	EffNetB2
CT	100 %	**100** %	5.59 %	**10.18** %	EffNetB2
Histology	90.11 %	**89.7** %	36 %	**80.23** %	Custom
CT	100 %	**100** %	90 %	**100** %	Custom

As we can see, classification accuracy on original samples didn't decrease when using blur reconstruction.

TABLE VII. BLUR RECONSTRUCTION RESULT FOR CW

Data	No attack		CW		Model
	No blur	Blur	No blur	Blur	
Histology	94.65 %	**94.81** %	0 %	**23.21** %	EffNetB2
CT	100 %	**100** %	0 %	**13.14** %	EffNetB2
Histology	90.11 %	**89.7** %	0 %	**60.25** %	Custom
CT	100 %	**100** %	0 %	**50.3** %	Custom

This defense can prevent FSGM attack on the custom model, but can't on EfficientNetB2. In other cases, the accuracy on adversarial samples was significantly smaller than on the original ones. Also, this defense can be added to the pipeline because it does not decrease model accuracy, but can protect from attacks.

E. Denoising autoencoder

The autoencoder consists of the encoder and the decoder. The encoder uses convolution layers, ReLU activations and MaxPooling for downsampling, the decoder uses convolution layers, ReLU activations and upsampling. The autoencoder was trained to minimize L_2^2 norm in (7).

The results are presented in tables VIII and IX for FSGM and CW respectively.

The results show that classification accuracy significantly increased in all experiments after applying the defense during the attack, compared to the results obtained without any defense. Moreover, the accuracy achieved with the defense is fairly close to the original results without any attack, which indicates the practical effectiveness of using this defense.

TABLE VIII. RESULTS OF USING DENOISING AUTOENCODER AGAINST FSGM

Data	No attack	FSGM	**Denoising AE**	Model
Histology	90.11 %	36 %	**80.87** %	Custom
CT	100 %	90 %	**100** %	Custom
Histology	94.65 %	9.98 %	**77.33** %	EffNetB2
CT	100 %	5.59 %	**89.31** %	EffNetB2

TABLE IX. RESULTS OF DENOISING AUTOENCODER AGAINST CW

Data	No attack	CW	**Denoising AE**	Pretrained
Histology	90.11 %	0 %	**82.1** %	Custom
CT	100 %	0 %	**89** %	Custom
Histology	94.65 %	0 %	**71.28** %	EffNetB2
CT	100 %	0 %	**85.33** %	EffNetB2

F. Denoising variational autoencoder

The architecture of the VAE used is identical to the AE. The defense was trained to denoise images, attacked with FSGM and CW attacks. Tables X and XI contain results of using the Denoising VAE defense against FSGM and CW attacks. Table XII contains comparison between Denoising VAE and Denoising AE defenses.

TABLE X. RESULTS OF DENOISING VAE AGAINST FSGM

Data	No attack	FSGM	**Denoising VAE**	Model
Histology	94.65 %	9.98 %	**87.77** %	EffNetB2
CT	100 %	5.59 %	**57.04** %	EffNetB2
Histology	90.11 %	36 %	**83.4** %	Custom
CT	100 %	90 %	**80.38** %	Custom

TABLE XI. RESULTS OF DENOISING VAE AGAINST FSGM

Data	No attack	CW	**Denoising VAE**	Model
Histology	94.65 %	0 %	**83.12** %	EffNetB2
CT	100 %	0 %	**69.05** %	EffNetB2
Histology	90.11 %	0 %	**77.64** %	Custom
CT	100 %	0 %	**80** %	Custom

TABLE XII. RESULTS OF DENOISING VAE AND DENOISING AE

Data	No attack	FSGM	VAE	AE	Model
Histology	94.65 %	9.98 %	**87.77** %	80.87 %	EffNetB2
CT	100 %	5.59 %	57.04 %	**100** %	EffNetB2
Histology	90.11 %	36 %	**83.4** %	77.33 %	Custom
CT	100 %	90 %	80.38 %	**89.31** %	Custom

G. Results transfer

To improve classification accuracy during Denoising Variational Autoencoder defense in the case of the CT dataset, a VAE trained on adversarial images obtained from a constructed network was used instead of a VAE trained on adversarial images generated by a pretrained network. As a result, the outcomes presented in table XIII were obtained. The classification accuracy during defense increased, indicating the transferability of the results.

TABLE XIII. RESULTS TRANSFER

No attack	FSGM	VAE	VAE (for custom)	Model
100 %	5.59 %	**57.04** %	**72.50** %	EffNetB2
100 %	90 %	80.38 %	80.38 %	Custom

V. CONCLUSION

In this work, FSGM and CW attacks and Adversarial Training, Blur Reconstruction, Denoising AE and Denoising VAE defenses were studied. The following results were obtained in the work:

- As the noise level ϵ increases in the FSGM attack, classification accuracy decreases, i.e., the attack becomes more effective.
- The CW attack is significantly more effective at generating adversarial examples than FSGM, while modifying the original image to a much lesser extent, making it more difficult to detect and prevent. With well-chosen input parameters, the CW can lead to full misclassification.
- Blur Reconstruction can be used to improve classification quality. This defense doesn't degrade classification accuracy and, in the case of FSGM attacks on the constructed networks, helps to successfully prevent the attack.
- It is reasonable to use Denoising AE and Denoising VAE as an independent defense mechanisms (table XII).
- The reasoning regarding the feasibility of result transferability has been confirmed. Specifically, when using a Denoising Variational. Autoencoder trained on adversarial images generated by an FSGM attack on a pretrained network to denoise images obtained via an FSGM attack on a constructed network, classification accuracy increased by 15% compared to using a Denoising Variational Autoencoder trained on adversarial images from FSGM attack on the custom network.

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Neural Network Architecture Search Approach for Telemetry Data Classification

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Abstract. **This paper presents an automated Neural Architecture Search (NAS) approach designed to address the challenge of telemetry classification for small spacecraft. The study focuses on optimizing neural network architectures for binary and multiclass classification. The proposed methodology employs Transformer-based models and combines random search with reinforcement learning (RL-NAS) to navigate hierarchical search spaces efficiently. Key aspects of the research include: (1) development of a hybrid search strategy that outperforms manual architecture design, (2) creation of task-specific architectures demonstrating approximately 7–9 % accuracy improvements over previously used ensemble methods, and (3) implementation using deep learning framework. This research contributes to the field of autonomous spacecraft diagnostics by demonstrating the practical application of NAS techniques to real-world telemetry analysis challenges.**

Keywords: **telemetry, machine learning, neural architecture search, search space, search strategy, classification**

I. INTRODUCTION

One of the most important tasks at all stages of the life cycle of a small spacecraft is the analysis of its telemetry information on the functioning of the onboard equipment of the spacecraft in terms of determining its technical condition to ensure its normal and safe operation. A large amount of information received and accumulated in specialized data banks about the onboard equipment of a small spacecraft can be effectively used to improve the process of determining the technical condition of a small spacecraft. Due to the fact that data on the functioning of the onboard equipment of a small spacecraft, including telemetry measurements, are heterogeneous irregular multidimensional data, it is relevant to research, develop and apply models that allow analyzing such data with the possibility of extracting useful information from them and then constructing classification and predictive models in order to determine the technical condition of a small spacecraft in order to make correct management and operational decisions during the operation of a small spacecraft [1]. The methods of machine learning, artificial intelligence and mathematical statistics are currently among the most promising and widely used approaches in data analysis of high-tech systems. In modern conditions, in order to solve these tasks, ensure the required degree of autonomy, quality and efficiency of management of such complex objects as small spacecraft, it is necessary to perform complex automation and intellectualization of the processes of evaluation and multi-model analysis of telemetry data of a small spacecraft.

Neural Architecture Search (NAS), a subset of AutoML [2], is the process of automating architecture design, when data is received at the input and the task to be solved is formulated (for example, classification), and the output is an architecture that gives the best result (for example, when solving a classification problem, it shows maximum accuracy on a test set) [3].

NAS sits at the intersection of several disciplines: machine learning, optimization, statistics, and computational theory [4]. Its development has been bolstered by advances in each of these areas, benefitting from improved computational resources, theoretical understanding of deep learning models, and the growing availability of large datasets. This multidisciplinary nature has made NAS a vibrant and rapidly advancing field, attracting attention from both academia and industry.

Here are the key elements that must be identified to search for an architecture: a set of search elements, a search space, a search strategy, and a strategy for evaluating the performance of the architecture to select the optimal one [5, 6]. Classical strategies for finding architecture parameters are grid search and random search [7]. Within the framework of NAS, researchers are also implementing more complex search strategies (algorithms): reinforcement learning (RL-NAS), evolutionary learning (EL-NAS) and One-shot NAS.

II. SEARCH SPACES

The search space is perhaps the most essential component of NAS. While other areas of AutoML

overlap with NAS in terms of the optimization methods used, the architectural search space is unique to NAS. Furthermore, the search space is often the first step when setting up NAS. The majority of popular search spaces are task-specific and were heavily inspired by the state-of-the-art manual architectures in their respective application domains [8].

A. Main Terms Related to Search Space in NAS

- Operation/primitive denotes the atomic unit of the search space. For nearly all popular search spaces, this is a triplet of a fixed activation, operation, and fixed normalization.

- Layer is often used in chain-structured or macro search spaces to denote the same thing as an operation or primitive. However, it sometimes refers to well-known combinations of operations, such as the inverted bottleneck residual.

- Block/Module is sometimes used to denote a sequential stack of layers following the notation used in most chain-structured and macro search spaces.

- Cell is used to denote a directed acyclic graph (DAG) of operations in cell-based search spaces. The maximum number of operations in a cell is often fixed.

- Motif is used to denote a sub-pattern formed from multiple operations in an architecture. Some literature refers to a cell as a higher-level motif and a smaller set of operations as a base-level motif [8].

B. Macro Search Spaces

In the NAS literature, macro search spaces may refer to one of two types [8]. For the former, an entire architecture is represented as a single DAG. These search spaces typically have a choice of operation at each node in the graph, as well as the choice of DAG topology. The second type of macro search spaces, focus on the variation of macro-level hyperparameters, such as where and how much to downsample the spatial resolution throughout the architecture, while keeping the architecture topology and operations fixed.

Compared to other search spaces, macro search spaces have high representation power: their flexible structure allows the possibility of discovering novel architectures. However, their main downside is that they are very slow to search.

C. Cell-Based Search Spaces

The cell-based search space is perhaps the most popular type of search space in NAS. It is inspired by the fact that state-of-the-art human-designed CNNs often consist of repeated patterns, for example, residual blocks in ResNets. Thus, instead of searching for the entire network architecture from scratch, it was proposed to only search over relatively small cells, and stack the cells several times in sequence to form the overall architecture [9, 10]. Formally, the searchable cells make up the micro structure of the search space, while the outer skeleton (the macro structure) is fixed.

The cell-based design significantly reduces the complexity of search spaces, while often resulting in a high-performing final architecture. This has led to the cell-based search spaces being the most popular type of search space in recent years. Furthermore, by detaching the depth of an architecture from the search, the cell-based structure is transferable: the optimal cells learned on a small dataset (e.g., CIFAR-10) typically transfer well to a large dataset [10] (e.g., ImageNet) by increasing the number of cells and filters in the overall architecture.

D. Chain-Structured Search Spaces

Chain-structured search spaces, as the name suggests, have a simple architecture topology: a sequential chain of operation layers. They often take state-of-the-art manual designs, such as ResNet or MobileNets, as the backbone. Chain-structured search spaces are also popular in transformer-based search spaces [8].

Chain-structured search spaces are conceptually simple, making them easy to design and implement. They also often contain strong architectures that can be found relatively quickly. Their main downside is that, due to the simple architecture topology, there is a comparatively lower chance of discovering a truly novel architecture.

E. Hierarchical Search Spaces

Up to this point, all search spaces described have had a flat representation, in which an architecture is built by defining its hyperparameters, topology, and operation primitives in a single design level. Specifically, only one level of topology is searched, whether at the cell level or architecture level. On the other hand, hierarchical search spaces involve designing motifs at different levels, where each higher-level motif is often represented as a DAG of lower-level motifs.

A simple class of hierarchical search spaces has two searchable levels by adding macrolevel architecture hyperparameters to cell or chain-structured search spaces.

There are multiple benefits to using hierarchical search spaces. First, hierarchical search spaces tend to be more expressive. Most chain-structured, cell-based, and macro search spaces can be seen as a hierarchical search space with a single searchable level, but having two or more levels allows to search over more diverse and complex architecture designs. Furthermore, a

hierarchical representation of a large architecture is an effective way to reduce the search complexity, which can lead to better search efficiency. On the other hand, hierarchical search spaces can be more challenging to implement and search through.

III. EXPERIMENTS

Three sets of telemetry data from the Belarusian spacecraft's star sensor for 2015-2021 were used to build machine learning models. A fragment of the telemetry file is shown in Fig. 1. First set contains 73 046 records, 2nd – 131 905 records, 3rd – 2 384 627 records.

The telemetry of the Belarusian spacecraft's star sensor contains sensors that determine the following parameters: solar coordinates (УВС, УАС), current on the star sensor (ТОК58), quaternion values (STRQ1–STRQ4), the temperature of the signal processing process (TSTR1DSP), and the temperature of the CCD sensor (TSTR1CCD) which takes pictures. Also, each object in the table has two labels for binary classification (Class: 0 – abnormal subsystem state, 1 – normal subsystem state) and for multiclass classification (Class1: 0 – completed, 2 – initialization of reversal, 3 – waiting for reversal, 4 – reversal, 8 – cancel).

Based on the sets of telemetric information, two machine learning tasks can be formulated: binary (abnormal/normal state of the subsystem) and multiclass (determination of one of the 5 subsystem states) telemetry classification [3].

The Transformer architecture is used as a basis for conducting experiments, which is well suited for processing sequential data such as telemetry information. The basic elements of the architecture being developed are fully connected layers (Dense layers) and the multiple attention mechanism (MultiHeadAttention). When designing the architecture, the multiple attention mechanism was complemented by layers of addition and normalization. In this case, the addition layer performs an operation of piecewise addition of the input and output values of the attention layer. The main parameters of the attention layers in the terminology of the Keras framework are num_heads (the number of attention “heads”) and key_dim (the size of each attention “head” for the query and key).

Fully connected hidden layers used the ReLU activation function. When solving the binary classification problem, the output fully connected layer contained 1 neuron with the Sigmoid activation function or 2 neurons with the Softmax activation function. For multiclass classification, the output layer contained 5 neurons with the Softmax activation function.

Key elements of NAS are presented in Table I.

Vectors of 9 features were fed to the input of the neural network. When implementing the strategy, a random search for a sequence of layers was performed. Then, based on the RL-NAS strategy, the number of structural elements in the optimal sequence of layers was determined.

TABLE I. KEY ELEMENTS OF NAS

	Binary classification	**Multiclass classification**
Search elements	1) MultiHeadAttention 2) Dense layers	
Search space	1) num_heads and key_dim values in the range [8; 10] 2) Number of neurons in the range [32; 128] 3) Number of all model layers in the range [11; 25]	1) num_heads and key_dim values in the range [3; 5] 2) Number of neurons in the range [32; 128] 3) Number of all model layers in the range [11; 25]
Search strategy	Random Search and RL-NAS	
Performance estimation strategy	Evaluating the accuracy of a model on a test set	

The experimental software was developed with Python using Tensorflow, Keras, gym, rl and deap libraries. The gym library was used to create the search space, and the rl library allowed to implement the search strategy based on reinforcement learning. The deap library was used for random search. The NVIDIA GeForce RTX 3060 GPU was used for computations.

NAS was performed for each of the three experimental data sets and for each task (binary and multiclass classification). Based on the accuracy evaluation (the proportion of correct model predictions) of classification models, 7 architectures were found on the test sets. Fig. 2 shows the architecture for solving the multiclass classification problem obtained using the 3rd data set.

TABLE II. BINARY CLASSIFICATION REPORT OBTAINED USING TEST SUBSET OF 1ST DATA SET

Class	**Precision**	**Recall**	**F1-score**	**Support**
	Sigmoid/Softmax			
0	0.97329/ 0.97948	0.96422/ 0.95375	0.96874/ 0.96644	5254
1	0.96455/ 0.95493	0.97354/ 0.98002	0.96903/ 0.96731	5254
Accuracy			0.96888/ 0.96688	10508
Micro avg	—/0.96688	—/0.96688	—/0.96688	10508
Macro avg	0.96892/ 0.96720	0.96888/ 0.96688	0.96888/ 0.96688	10508
Weighted avg	0.96892/ 0.96720	0.96888/ 0.96688	0.96888/ 0.96688	10508
Samples avg	—/0.96688	—/0.96688	—/0.96688	10508

The results of experiments with the selected architectures are presented in Tables II–V. The described approach made it possible to improve the results of previous studies [1] and showed the effectiveness of automating the search for a neural network architecture in comparison with manual design.

TABLE III. BINARY CLASSIFICATION REPORT OBTAINED USING TEST SUBSET OF 2ND DATA SET

Class	Precision	Recall	F1-score	Support
	Sigmoid/Softmax			
0	0.98112/ 0.99111	0.97067/ 0.96708	0.97587/ 0.97895	10602
1	0.97098/ 0.96786	0.98132/ 0.99132	0.97612/ 0.97945	10602
Accuracy			0.97600/ 0.97920	21204
Micro avg	—/0.97920	—/0.97920	—/0.97920	21204
Macro avg	0.97605/ 0.97948	0.97600/ 0.97920	0.97599/ 0.97920	21204
Weighted avg	0.97605/ 0.97948	0.97600/ 0.97920	0.97599/ 0.97920	21204
Samples avg	—/0.97920	—/0.97920	—/0.97920	21204

TABLE IV. BINARY CLASSIFICATION REPORT OBTAINED USING TEST SUBSET OF 3RD DATA SET

Class	Precision	Recall	F1-score	Support
	Sigmoid/Softmax			
0	0.94947/ 0.96244	0.88971/ 0.89117	0.91862/ 0.92544	211306/ 211307
1	0.89625/ 0.89868	0.95265/ 0.96522	0.92359/ 0.93076	211307/ 211306
Accuracy			0.92118/ 0.92820	422613
Micro avg	— /0.92820	— /0.92820	— /0.92820	422613
Macro avg	0.92286/ 0.93056	0.92118/ 0.92820	0.92111/ 0.92810	422613
Weighted avg	0.92286/ 0.93056	0.92118/ 0.92820	0.92111/ 0.92810	422613
Samples avg	— /0.92820	— /0.92820	— /0.92820	422613

TABLE V. 5-CLASS CLASSIFICATION REPORT OBTAINED USING TEST SUBSET OF 3RD DATA SET

Class	Precision	Recall	F1-score	Support
0	0.95063	0.71122	0.81368	208772
1	0.95084	0.94518	0.94800	208771
2	0.86690	0.91636	0.89095	208771
3	0.80618	0.75352	0.77896	208771
4	0.88561	0.91615	0.90062	208771
Micro avg	0.88969	0.84849	0.86860	1043856
Macro avg	0.89203	0.84849	0.86644	1043856
Weighted avg	0.89203	0.84849	0.86644	1043856
Samples avg	0.84849	0.84849	0.84849	1043856

IV. CONCLUSION

The proposed methodology, implemented using deep learning framework, employs Transformer-based models and combines random search with reinforcement learning (RL-NAS) to navigate hierarchical search spaces efficiently. Development of a hybrid search strategy outperforms manual architecture design. Creation of task-specific architectures demonstrates approximately 7–9 % accuracy improvements over previously used ensemble methods [1]. The developed approach allows to successfully automate critical design decisions including layer sequencing and attention head configuration (MultiHeadAttention) for processing heterogeneous telemetry features such as solar coordinates, temperature readings, and quaternion values. The research results in a scalable solution for real-time anomaly detection and operational state classification, potentially enhancing spacecraft monitoring and decision-making processes.

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	YBC	YAC	TOK58	STRQ1	STRQ2	STRQ3	STRQ4	TSTR1CCD	TSTR1DSP	Class	Class1
0	0.000	0.000	139.0	0.137	-0.312	0.78	0.524	9.849	23.41	0	0
1	0.000	0.000	135.0	0.137	-0.312	0.78	0.524	9.849	23.41	0	0
2	0.000	0.000	135.0	0.132	-0.315	0.78	0.525	9.849	23.41	0	0
3	46.865	32.324	135.0	0.132	-0.315	0.78	0.525	9.849	23.41	0	0
4	21.464	19.704	135.0	0.132	-0.315	0.78	0.525	9.849	23.41	0	0

Fig. 1. Telemetry file fragment

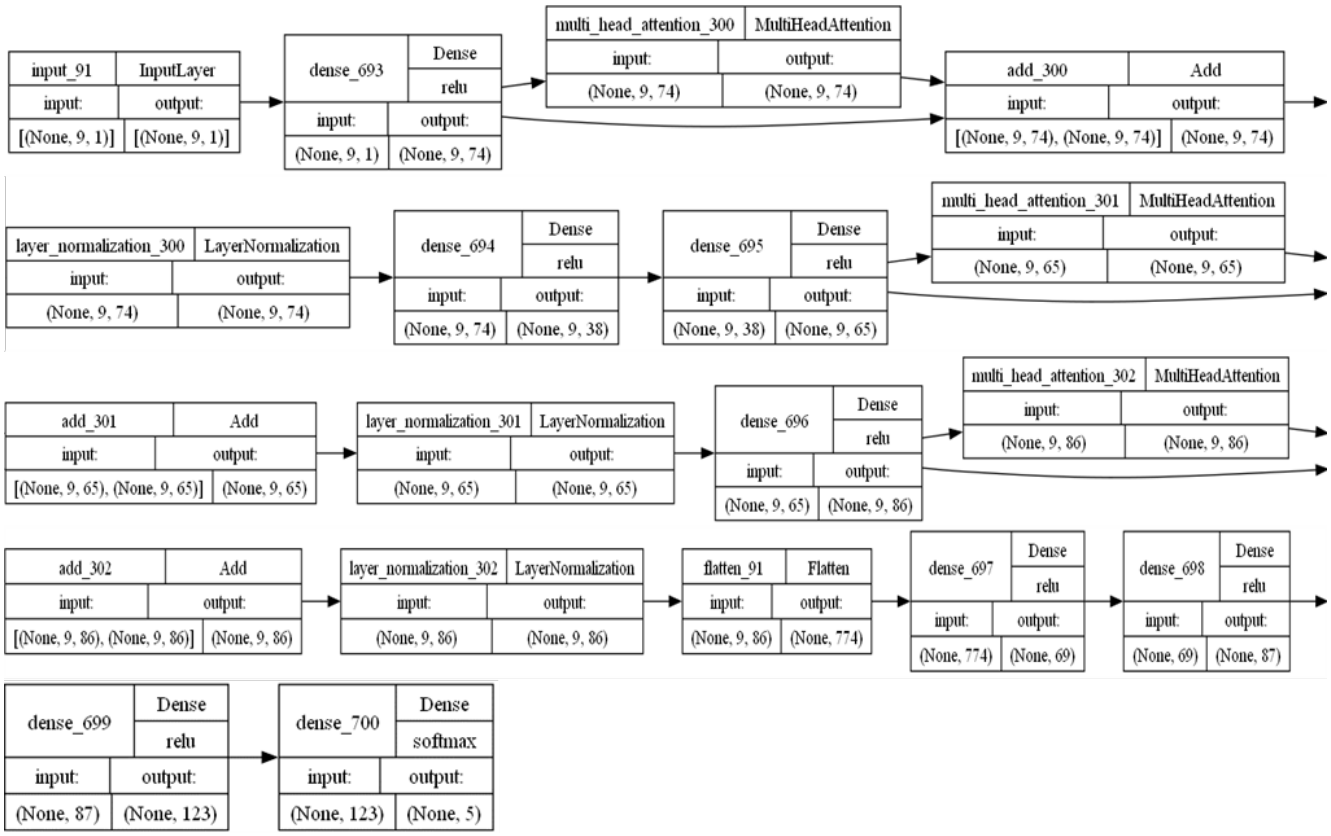

Fig. 2. Neural network architecture for 5-class classification obtained using 3rd data set

Approaches to the Printed Circuit Board Defects Detection

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***Abstract*. Modern neural network architectures such as YOLO, Faster R-CNN, RT-DETR and their modifications have achieved very high accuracy in printed circuit board (PCB) defects detection. There is a global trend towards the use of one-stage detectors and their lightweight versions. This paper presents the comparison of known PCB defects detection approaches with the proposed ones. The proposed YOLOv8n model, further trained on specialized datasets, demonstrates the mAP50 values of 0.98 and 0.99 on the corresponding test sets, which is comparable or exceeds the best global results.**

***Keywords:* printed circuit board, neural network, computer vision, detection, bounding box**

I. INTRODUCTION

An important problem in the production of electronic equipment is the quality control of PCB at various technological stages. In this case, the object for control is a PCB image or its photo template. The elements in a PCB image are contact pads, conductors, reference points, and service information in the form of letters and numbers. A defect during the inspection implementation is a deviation of the topology elements on the object from the design documentation due to manufacturing errors, e.g. inconsistencies in temperature and time modes of production. The task of PCB defects finding is relevant due to such trends in the design and manufacture of PCB as the microelectronic components miniaturization and the high-density connections usage; the introduction of flexible and stretchable circuits; the use of new materials and manufacturing methods [1].

II. PROPOSED METHODS

A. Reference-Based PCB Inspection Algorithm

This algorithm is as follows. First, the image is preprocessed, which consists of binarization, noise removal, correction of scale and rotation angle to align the pair of the reference and the analyzed image. Next, the defects are searched using the Exclusive OR (XOR) operation. The defects found are classified according to binary flags, and their geometric parameters are determined.

B. YOLOv8 Model

YOLOv8 is a modern model for image classification, instance segmentation, and object detection without anchoring, developed by Ultralytics. Building upon the advancements of previous YOLO versions, YOLOv8 introduced new features and improvements for enhanced performance and flexibility. YOLOv8 models can be trained on large datasets and run on various hardware platforms, from processors to GPUs. One of the key features of YOLOv8 is extensibility.

The development of the object detection idea is the introduction of an extra angle for bounding boxes to take into account the orientation of desired objects in an image. This approach is called oriented object detection. It allows to locate objects more accurately in an image. In this case, the bounding boxes are also called Oriented Bounding Boxes (OBB). For YOLOv8 OBB models, one OBB in markup files is described by class label and normalized coordinates of all corner points.

C. Hybrid Approach

The use of neural networks for searching and classifying defects has the following advantages: low sensitivity to image quality, presence of glare and protective varnish on a PCB surface (except in cases of opaque or black varnish), presence of text and graphic information on a PCB surface.

However, it should be noted that the results depend on the completeness and quality of the training sample. Public data sets for training neural networks have errors in the data markup. Pairs of images (reference and analyzed) from the Deep PCB data set cannot be acceptably aligned using affine and projection transformations due to presumably incorrect binarization parameters, and should not be used for inspection, and also fundamentally do not have information about the relationships between tracks beyond the same frame [1]. All PCB, which images are included in the PCB Defects data set, are coated only with a green protective varnish. Some images contain white graphic objects indicating the locations of electronic components. This significantly complicates,

and in some cases, makes it impossible to optically inspect PCB. The defects of both data sets were formally created using a graphical editor. The Multiple Datasets on PCB Defects data set contains only images of actual PCB defects under different shooting conditions without information about defect classes.

Therefore, it is proposed to use a hybrid PCB defects inspection based on the use of reference-based PCB inspection (image subtraction), mathematical morphology operations and neural networks. This approach consists of choosing a defects detection method depending on the quality assessment of analyzed images according to the next criteria [1]:

- Absence of nonlinear geometric distortions caused by the inconstancy of PCB scanning speed or the heterogeneity of optical imaging system properties over the entire frame.

- Presence of glare and shadows due to the use of an unsuccessful lighting system.

- Determination of sufficient image sharpness for processing.

- Determination of the overall image brightness level, the number and variety of shades. If the brightness level is too high or, conversely, low, this leads to information loss in overexposed or too dark image areas when equalizing the brightness.

It is recommended to use the reference-based PCB inspection algorithm, which allows to classify all found defects into six disjoint classes, to search for defects in high-quality images when reference is available. Deviations from the minimum track width and the minimum distance between tracks are found through a mathematical morphology operation such as distance transformation applied to both the image of track and the background.

It is possible to combine the results of simultaneous application of the reference-based PCB inspection algorithm and a neural network approach to reduce the probability of missing a critical defect and the number of false defects if the reference and analyzed images are poorly aligned. Pre-trained neural networks should be used if there is no reference or the image quality is low [1].

With any choice of search method, it is necessary to expand the data set for training and retraining neural networks to improve the quality of detection and classification of defects. But special attention should be paid to the issue of organizing competent lighting of the PCB and registering their images. These factors directly affect the defect search quality.

III. Discussion

In the first part of the experiments, the YOLOv8 model of size nano, pre-trained on the COCO dataset, was further trained and tested on the DeepPCB image set. Training was performed in the Google Colab environment using the Tesla T4 GPU. The training parameters of the YOLOv8n model: the number of epochs is 50, the batch size is 16, the image size is 640×640, the optimization method is AdamW, and the weight of the box loss component in the loss function is 7.5.

In this part of the experiments, the reference-based PCB inspection algorithm uses the Otsu binarization and morphological operations of opening and closing with a circular structuring element of sizes 3×3 and 5×5. This algorithm also uses a semantic filter that removes defects smaller than 20 pixels.

The experimental results, presented in Table I, show that the minimum number of missed defects, namely 16, is achieved using the hybrid algorithm. The neural network model demonstrates high accuracy in detecting PCB defects (the mAP50 metric is 0.98 on the test dataset). Herewith, on the test set for this model, the proportion of false positives is 11.9 % relative to the total number of defects, and the proportion of false negatives is 2.8 %. With respect to all defects, the worst value of the proportion of false positives corresponds to the “open” class and is 21.9 %, and the worst value of the proportion of false negatives corresponds to the “short circuit” class and is 5.2 %.

TABLE I. PCB Defect Detection Results Obtained with Proposed Methods and DeepPCB Data Set

Method	Support	Evaluation metric			
		Precision	Recall	F1-score	Accuracy
YOLOv8n	11 768	0,768	0,847	0,805	0.847
Reference-based algorithm	11 712	0,718	0,755	0,731	0,755
Hybrid algorithm	14 359	0,625	0,767	0,685	0,767

Fig. 1 shows an example of the PCB defects detection with the proposed hybrid approach in images from the DeepPCB data set.

The obtained accuracy of PCB defect detection is comparable to the best world results (Table II):

- SSD (Single Shot MultiBox Detector) is an object detection method that performs detection and classification in a single neural network pass without a region proposal generation step [2]. The mean average precision (mAP) is 95.9 %.

- YOLO (You Only Look Once) is one-stage object detection method, in which a convolutional network

(CNN) simultaneously predicts bounding boxes and class probabilities directly from full images in one evaluation [3]. The mAP is 92.6 %.

- Faster R-CNN is an object detection architecture based on the collaboration of the Region Proposal Network (RPN), which is fully-convolutional, and the feature extraction detector Fast R-CNN [4]. The mAP is 97.6 %.

- neural network model Cascade R-CNN with Attentive Context and Semantic Enhancement Module (ACASEM) PCB defect detection with two-stage and multi-stage object detectors [5]. The mAP50-95 is 79.5%.

- Uncertainty-Aware Unsupervised Defect Detection on PCB Images Using Reconstructive and Discriminative Models (U^2D^2PCB) based on two U-Net networks to serve as the reconstructive sub-network and the discriminative sub-network [6]. The mAP is 95.78 %.

- Group Pyramid Pooling (GPP) module, which extracts features of a large range of resolutions, which are merged by group to predict PCB defect of corresponding scales [7]. The highest mAP is 98.6 %.

TABLE II. PCB DEFECT DETECTION RESULTS OBTAINED WITH DEEPPCB DATA SET

Model	Result evaluation	Evaluation metric
SSD [2]	95.9	mAP
YOLO [3]	92.6	mAP
Faster R-CNN [4]	97.6	mAP
Faster R-CNN + ACASEM [5]	79.5	mAP50-95
U2D2PCB [6]	95.78	mAP
GPP with average pooling [7]	97.1	mAP
GPP with max pooling [7]	98.6	mAP
YOLOv8n (ours)	98.0	mAP

In the second part of the experiments, the YOLOv8 model of size nano, pre-trained on the DOTAv1 dataset [8], was further trained and tested on the PCB Defect Dataset. The training was performed using the NVIDIA GeForce RTX 3060 GPU. Some training parameters of the YOLOv8n OBB model: the number of epochs is 200, the batch size is 16, the optimization method is Adam, and the weight of the box loss component in the loss function is 7.5.

In this part of the experiments, the reference-based PCB inspection algorithm uses global binarization – the RGB value range from (0, 20, 0) to (45, 85, 45) corresponds to white, and the rest of the range is black. The Scale Invariant Feature Transform (SIFT) [9], the Brute-Force descriptor matching [10], and the nearest neighbor interpolation [11] are used to align a tested image with a reference. Morphological opening and closing operations with a 5×5 circular structuring element are used to smooth the results of binarization and alignment.

Fig. 2 shows an example of the PCB defects detection with the proposed YOLOv8n OBB model in images from the PCB Defect Dataset.

Comparison with the results available in the open press is given in Table III. It shows that the trained YOLOv8n OBB model shows the best accuracy in PCB defect detection.

TABLE III. PCB DEFECT DETECTION RESULTS OBTAINED WITH PCB DEFECT DATASET

Method	Evaluation metric		
	mAP50, %	Precision, %	Recall, %
Faster R-CNN [12]	84.5	87.3	92.7
YOLOv5 [12]	92.5	88.1	93.6
YOLOv7 [12]	94.7	89.3	94.3
YOLOv8s [12]	94.5	92.6	95.1
RT-DETR [12]	95.6	93.5	95.9
YOLO-BFRV [12]	98.4	96.9	98.2
YOLOv3 [13]	96.1	97.3	92.7
YOLOv5 [13]	97.7	98.8	95.5
YOLOv8 [13]	97.6	98.2	95.4
GCC-YOLO [13]	98.2	99.0	97.3
SCF-YOLO [14]	92.9	92.5	90.2
CDI-YOLO [15]	98.3	97.1	96.4
YOLOv8 [16]	97.6	98.6	94.7
YOLOv9 [16]	97.8	98.1	95.4
YOLOv10 [16]	98.0	98.9	94.4
YOLOv11 [16]	97.6	98.9	94.6
YOLO-SSW [16]	98.4	99.2	95.5
Faster R-CNN + ACASEM [5]	98.6	—	—
YOLOv8n OBB (ours)	99	99.5	98.8
Reference-based PCB inspection algorithm (ours)	85.8	86.8	85.8

Table III presents data for the following neural network models:

- Faster R-CNN [4] and Real-Time DEtection TRansformer (RT-DETR) [17] are state-of-the-art architectures for object detection in computer vision. DETR uses a transformer architecture that models global relationships between objects and image context without the need for predefined relationships.

- YOLO-BFRV is a network model based on the improved YOLOv8 framework to identify PCB defects [12]. The main components of this architecture are a bidirectional feature pyramid network (BIFPN) which expands the receptive field of each feature level and enriches the semantic information to improve the feature extraction capability; a lightweight FasterNet backbone network, reducing the computational load while improving the detection accuracy of minor defects; the high-speed re-parameterized detection head (RepHead) which reduces inference complexity and boosts the detection speed without compromising accuracy; the VarifocalLoss which enhances the detection accuracy for densely distributed PCB defects.

• GCC-YOLO is a model which uses a global contextual attention module (GC) combined with a C3 module, in order to suppress the background noisy information and further enhance the feature extraction capability, and a bi-directional weighted feature pyramid (BiFPN) feature fusion structure, in order to reduce the loss of shallow feature information due to the deepening of network layers [13].

• SCF-YOLO is a lightweight defect detection model which utilizes the more compact and lightweight MobileNet as the feature extraction network, which effectively reduces the number of model parameters and significantly improves the inference speed. SCF-YOLO utilizes the SCF (Synthesis C2f) module which facilitates the efficient fusion of superficial, detailed features with profound semantic information [14].

• CDI-YOLO is the PCB defect detection model based on the lightweight YOLOv7-tiny network [15]. One of the main features of the CDI-YOLO is the Coordinate Attention (CA) mechanism. The CA module can adjust feature weights based on location importance, improving the model's ability to capture spatially structured information. This mechanism enhances the model's accuracy in perceiving and understanding important spatial locations in computer vision tasks. Part of the common convolution is replaced by the Depthwise Separable Convolution (DSConv), i.e. the traditional convolution is replaced by two components to reduce model complexity and improve detection speed without significant quality loss. CDI-YOLO uses Inner-CIoU as the bounding box regression loss function instead of CIoU, leading to faster and more efficient regression results.

• YOLO-SSW (YOLO-SPD-SimAM-WIoU) is a network, based on an improved YOLOv8 algorithm [16]. This architecture includes the following key features. Non-strided Convolution with Space-to-Depth (Conv-SPD) is a module which allows the model to effectively capture details in low-resolution images and small objects. Simple Attention Module (SimAM) is a mechanism that enhances feature refinement, while maintaining computational efficiency, and significantly improves the model's accuracy in detecting tiny objects within complex backgrounds. Wise Intersection over Union (WIoU) is a loss function which is adopted to dynamically adjust gradient gains, reducing the impact of low-quality examples, thereby enhancing localization accuracy.

IV. Conclusion

There is a global trend towards the use of one-stage detectors (YOLO, SSD) and their lightweight versions (e.g. SCF-YOLO, CDI-YOLO, YOLO-SSW), which provide a balance between accuracy and speed, which is important for real production with product inspection on the pipeline. Such models use compact backbone networks (MobileNet, FasterNet), lightweight convolutions, and optimized loss functions. To increase sensitivity to small and complex defects, spatial and coordinate attention modules (SimAM, CA) are being actively implemented, as well as pyramid structures for combining features at different scales (BiFPN, SPD). This allows models to work effectively with defects of various sizes and with a complex background. Transformer-based architectures (DETR, RT-DETR) are beginning to outperform classical CNN in accuracy and speed in defect detection tasks, especially when it is necessary to take into account complex relationships between objects in the image.

The proposed YOLOv8n model, further trained on specialized datasets, demonstrates the mAP50 values of 0.98 and 0.99 on the corresponding test sets, which is comparable or exceeds the best global results.

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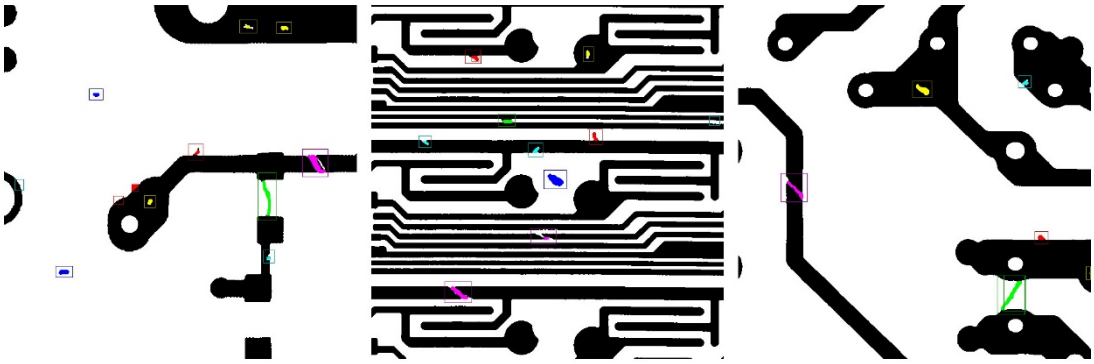

Fig. 1. PCB defects detection with the hybrid approach in images from the DeepPCB data set

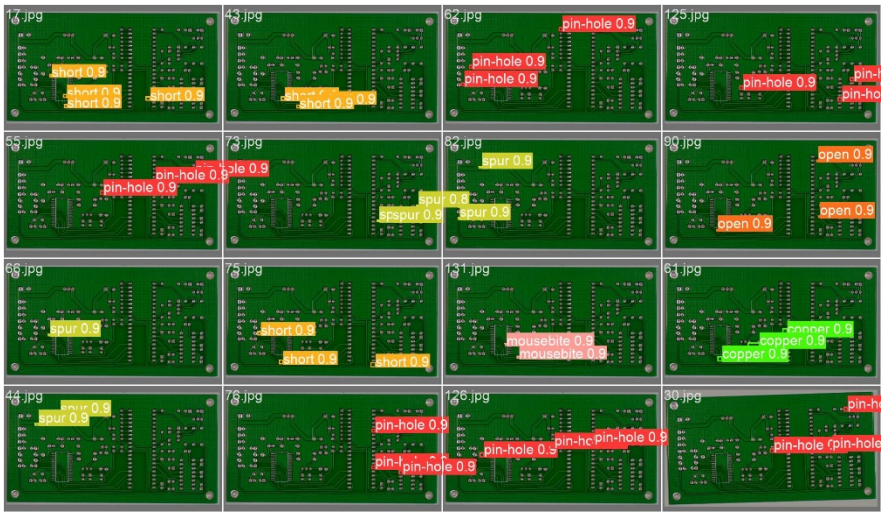

Fig. 2. PCB defects detection with the YOLOv8n OBB model in images from the PCB Defect Dataset

Parameter Estimation for Arbitrary Order MMPP

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Abstract. **The problem of the parameter estimation for the hyperexponential distribution is considered. The method of moments and the maximum likelihood method are combined for estimating the minimum intensity parameter in the case of an arbitrary number of parameters of a hyperexponential distribution. The obtained estimators are used in the cumulative sum algorithm to estimate the intensity parameters of the Markov modulated Poisson process.**

Keywords: **hyperexponential distribution, Markov-modulated Poisson process, method of moments, maximum likelihood method**

I. INTRODUCTION

Stochastic processes with changing parameters, in particular, processes with change-points, are widely used for approximating real non-linear processes in different applications. such as economics, finance, medicine, psychology, geology, literature, and so on, and even in our daily lives. From the statistical point of view, a change point is a place or time point such that the observations follow one distribution up to that point and follow another distribution after that point. Multiple change points problems can also be defined similarly [1]. Processes with a single change point are usually used to simulate a withdraw from stable conditions or an equipment error; whereas processes with multiple change points describe real processes with several states, where switches between states occur in unknown instants. The mentioned above book [1] is devoted to parametric change-point detection with applications to genetics, medicine, and finance and contains a number of classical and recent results in this field for some commonly used distributions.

Paper [2] provides an overview with a huge number of references of time-varying queues, both many-server queues, which arise in large-scale service systems, such as in customer contact centers and hospital emergency departments, and single-server queues with time-varying arrivals, which arise in some settings, such as airplanes coming to land at an airport, cars coming to a traffic intersection and medical staff waiting for the availability of special operating rooms in a hospital.

Markovian arrival processes (MAP) when the process parameters are controlled by a Markov chain is a popular tool for modeling arrival processes of stochastic systems such as queueing systems, reliability systems and telecommunications networks. Papers [3], [4] and [5] contain some examples of MAPs describing real processes with changing behavior.

To estimate the MAP parameters, usually (for example, in [6], [7]) different modifications of EM (expectation-minimization) algorithm based on the maximum likelihood estimators are used. The positive aspects of these algorithms are due to the fact that they are based on the maximum likelihood method, which guarantees the consistency and asymptotic efficiency of estimates. However, a number of works note the shortcomings of EM algorithms. Namely, the convergence of the EM algorithm is proven under the mandatory condition of the boundedness of the logarithm of the likelihood function. Also, the presence of a large number of local maximum values of the logarithm likelihood function leads to instability with respect to the initial approximation and the original data [8]. In addition, the iterative nature of the algorithms leads to a large number of calculations, the volume of which increases with a large number of parameters [9]. In this regard, alternative approaches to estimating the parameters of distribution mixtures are being developed.

In this paper, we construct the combined estimates for the two-state process using the method of moments and the maximum likelihood method. As we use the maximum likelihood method to estimate probabilities, our estimate is free from the problems mentioned above as the estimated parameter is bounded and to find maximum we can calculate the likelihood function values with the appropriate step. For the process with an arbitrary number of states, we iteratively estimate the minimum intensity parameter and then exclude the values that obey the distribution with that parameter from the sample.

II. PROBLEM STATEMENT

We consider a Markov modulated Poisson process (MMPP) if the event rate $\lambda(t)$ can take one of n values $\lambda_1 < \lambda_2 < \cdots < \lambda_n$. The value n is assumed to be unknown. We assume that the state of the process $S(t)$ at time t is j if $\lambda(t) = \lambda_j$. The initial state of the process

$S(0)$ is a random variable and has the distribution $q_j = P(S(0) = j)$. The sojourn time in state j is a random variable that has an exponential distribution with parameter $\alpha_j, j = 1, \dots, n$. The transition probability from state j, to state $i \neq j$ in determined by the transition probability matrix P_{ij}, $P_{ij} = 0$, $i, j = 1, \dots, n$. The moments of change in the process state are unobservable. The parameters $\{\lambda_j, \alpha_j\}$ are unknown. Thus, the intensity of the Poisson process is a piecewise constant random process. It is necessary to estimate the order of process n based on observations of instants $\{\tau_j\}$ when the process events occur.

The problem can be stated as the problem of the parameters estimation for the hyperexponential distribution. The density of the hyperexponential distribution has the form:

$$f(x) = \sum_{i=1}^{n} p_i \lambda_i e^{-\lambda_i x}. \quad (1)$$

It is assumed that the parameters satisfy the following conditions:

$$p_i > 0, \qquad \sum_{i=1}^{n} p_i = 1, \qquad \lambda_1 < \lambda_2 < \cdots < \lambda_n. \quad (2)$$

The problem is to estimate the parameters $\{p_i, \lambda_i\}$ based on a sample $\{\tau_j\}$ from the distribution.

III. Combined Estimates for Mixed Exponential Distribution

Let us first consider the problem of estimating the parameters for the mixed exponential distribution with the density function (1) if $n = 2$. Since $p_1 + p_2 = 1$, we estimate three parameters: $\{\lambda_1, \lambda_2, p\}$, where $p = p_1$.

Let us construct estimates using the method of moments and the maximum likelihood method. First, using the first two moments, we construct estimates for $\{\lambda_1, \lambda_2\}$ as functions of the parameter p. Next, we find the estimate of the parameter p using the maximum likelihood method.

For the first two moments, we have the following equations

$$\begin{cases} m_1 = \dfrac{p}{\lambda_1} + \dfrac{1-p}{\lambda_2}; \\ m_2 = \dfrac{p}{\lambda_1^2} + \dfrac{1-p}{\lambda_2^2}. \end{cases} \quad (3)$$

Solving the system, we come to the estimates:

$$\begin{cases} \hat{\lambda}_1 = \left(m_1 + \sqrt{\dfrac{1-p}{p}} \sqrt{m_2 - m_1^2} \right)^{-1}; \\ \hat{\lambda}_2 = \left(m_1 - \sqrt{\dfrac{p}{1-p}} \sqrt{m_2 - m_1^2} \right)^{-1}. \end{cases} \quad (4)$$

The estimates exist if

$$m_2 - m_1^2 > 0, \qquad p < \frac{m_1^2}{m_2}. \quad (5)$$

As the parameter p is bounded, we use the maximum likelihood method to estimate it. The logarithm of the maximum likelihood function has the following form:

$$\sum_{j=1}^{n} \log\left(p\lambda_1 e^{-\lambda_1 \tau_j} + (1-p)\lambda_2 e^{-\lambda_2 \tau_j}\right). \quad (6)$$

Substituting their estimates (4) for the parameters $\{\lambda_1, \lambda_2\}$ and calculating the logarithm of the likelihood function with an acceptable step for $0 < p < m_1^2/m_2$, we obtain an estimate that provides the maximum of function (6); we then use this estimate in (4).

IV. Estimate of MMPP Intensities for Arbitrary Number of Parameters

Let us now construct an estimate of the minimum intensity parameter for a hyperexponential distribution with an arbitrary number of parameters, determined by equations (1, 2). It is proposed to use the estimates of the parameters of the process with two intensities constructed above; thus, we use estimate $\hat{\lambda}_1$ from (4) where $\hat{p}$ is calculated as the argument of the minimum of function (6) for λ_1.

It has been established that if the estimates obtained under the assumption $n = 2$ are used to estimate the parameters of a hyperexponential distribution with an arbitrary value $n > 2$, then the estimate $\hat{\lambda}_1$ of the minimum parameter λ_1 will be close to its true value. This allows us to identify intervals in the observed sequence $\{\tau_i\}$ where the process intensity parameter $\lambda(t) = \lambda_1$. For this purpose, the cumulative sum (CUSUM) procedure for detecting the moment of change of the exponential distribution parameter from one known value μ_1 to another known value $\mu_2 > \mu_1$ is used.

Define the statistics

$$z_i = \ln\left(\frac{\mu_2}{\mu_1}\right) - (\mu_2 - \mu_1)\tau_i. \quad (7)$$

Then set the thresholds $h^{(1)} > 0, h^{(2)} > 0$ and define a sequence of cumulative sums:

$$S_i^{(1)} = \max\left(S_{i-1}^{(1)} + z_i, 0\right), i = 1,2, \dots; \; S_0^{(1)} = 0; \quad (8)$$

$$S_i^{(2)} = \max\left(S_{i-1}^{(1)} - z_i, 0\right), i = 1,2,\ldots;\ S_0^{(2)} = 0.$$

A decision on the change-point is made if $S_i^{(l)} > h^{(l)}$; at this moment, the cumulative sum again starts with zero to repeat the procedure and to detect the next change-point. Let the sequence $\left\{\sigma_m^{(l)}\right\}_{m\geq 0}$ be the sequence of the instants when the cumulative sum in the l-th procedure reaches the threshold $h^{(l)}$, i.e.,

$$\begin{gathered}\sigma_0^{(l)} = 0;\\ \sigma_m^{(l)} = \min\left\{t_j > \sigma_{m-1}^{(l)} : S_{j-1}^{(l)} + z_j^{(l)} \geq h^{(l)}\right\};\\ l = 1,2.\end{gathered} \qquad (9)$$

These are the instants of the controlling chain state detection. Consider a sequence $\left\{n_m^{(l)}\right\}_{m\geq 0}$ associated with the sequence $\left\{\sigma_m^{(l)}\right\}$ as follows

$$n_m^{(l)} = \max_j\left\{t_j < \sigma_m^{(l)} : S_{j-1}^{(l)} = 0, S_j^{(l)} > 0\right\}. \qquad (10)$$

Thus the instant $n_m^{(l)}$ is the instant when the cumulative sum exceeds zero to reach then the threshold. Fig. 1 illustrates the construction of the sequences.

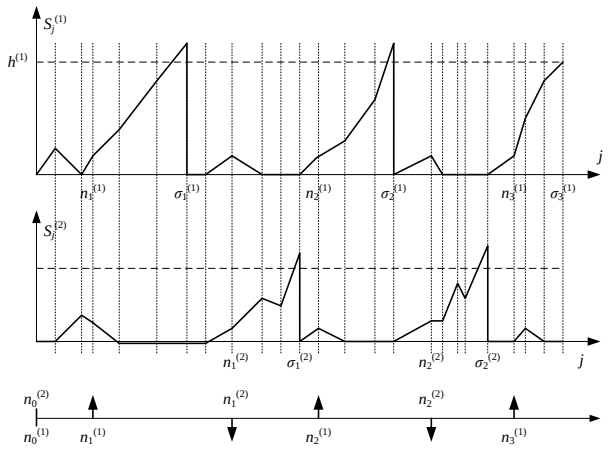

Fig. 1. Construction the sequences $\left\{\sigma_m^{(l)}\right\}$ and $\left\{n_m^{(l)}\right\}$

The instants of occurrences t_j are marked by vertical dotted lines. The diagram above demonstrates an example of the sum $S_j^{(1)}$ behavior with the instants $\sigma_m^{(1)}$ and $n_m^{(1)}$ marked out. The diagram in the middle shows a similar example for the sum $S_j^{(2)}$. We consider the instants $n_m^{(1)}$ as the estimators for the instants when the exponential distribution parameter increases. They are pointed by up arrows at the diagram below. In turn the instants $n_m^{(2)}$ are considered as the estimators for the instants when the exponential distribution parameter decreases. They are pointed by down arrows at the diagram below.

When implementing the procedure it is possible to encounter false alarm situations, i.e. the situations when the cumulative sum exceeds the threshold while the intencity does not change. We shall record all the exceeding the thresholds by either first or the second cumulative sum. If the same sum reaches threshold several times in a row, we only record the first occurrence and consider the next instants in the row as false alarms.

Thus, the procedure for estimation of instants of intensity switching is described as follows. Calculate two cumulative sums given by equations (8). Then construct the sequences $\sigma_m^{(l)}$ and $n_m^{(l)}$ defined by equations (9), (10). If $n_1^{(1)} < n_1^{(2)}$, then the initial value of the intensity is equal to μ_1. Define the sequence

$$\begin{gathered}q_0 = 0;\\ q_{2m+1} = \min\left\{n_j^{(1)} : n_j^{(1)} > q_{2m}\right\};\\ q_{2m+2} = \min\left\{n_j^{(2)} : n_j^{(2)} > q_{2m+1}\right\};\\ m \geq 0.\end{gathered} \qquad (11)$$

The values q_1, q_2,…, are calculated using formula (11) while it is possible. If

$$\left\{n_j^{(1)} : n_j^{(1)} > q_{2m}\right\} = \varnothing \quad \left(\left\{n_j^{(2)} : n_j^{(2)} > q_{2m+1}\right\} = \varnothing\right)$$

then we set $q_{2m+1} = N$ $\left(q_{2m+2} = N\right)$, where N is the instant of the last occurrence. Here the odd instants q_{2m+1} are the estimators of the instants when the intensity changes from μ_1 to μ_2, and the even instants q_{2m+2} are the estimators of the instants when the intensity changes from μ_2 to μ_1.

Fig. 2 demonstrates the construction of the sequence $\{q_j\}$. The diagram above presents the sequence $n_m^{(l)}$ constructed as it is described earlier. The diagram below presents the sequence$\{q_j\}$. The estimators for the instanses of the control chain states swithing from μ_1 to μ_2 are marked by up arrows (because it means the increase of the intensity), and the estimators for the instanses of the control chain states swithing from μ_2 to μ_1 are marked by down arrows (because it means the decrease of the intensity). The number of the supposed state of the controlling chain is also shown above the axis.

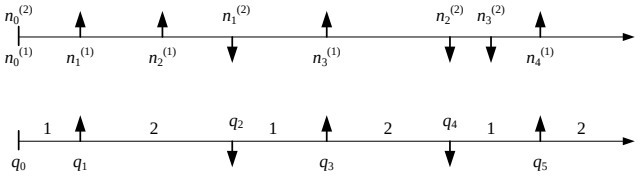

Fig. 2. Construction the sequences $\{q_j\}$

Now let us described the iterative parameter estimation algorithm. First, set the step number $M = 1$. For μ_1 we select the estimate $\hat{\lambda}_1$, for μ_2 it is proposed to select the value $c\hat{\lambda}_1$, where the coefficient $c > 1$ is determined based on the minimum expected difference between two adjacent intensity parameters. Statistics (7) have the following form:

$$z_i = \ln(c) - (c-1)\hat{\lambda}_1\tau_i. \qquad (12)$$

As a result of applying the CUSUM procedure, subsequences in the sequence $\{\tau_i\}$ will be identified where $\lambda(t) = \lambda_1$ These subsequences are excluded from the sample $\{\tau_i\}$. The value M is increased by 1. At the second stage, for the remaining observations, we again find the estimate of the minimum intensity parameter and use the CUSUM procedure to identify the subsequences where the process intensity parameter $\lambda(t) = \lambda_2$ and exclude these subsequences from the sample.

After $n-1$ steps of estimating the minimum intensity parameter and applying the CUSUM procedure, preliminary estimates of the parameters $\hat{\lambda}_j, j = 1, \dots, n$ will be obtained.

V. Results of Simulation

The developed algorithm was applied to MMPP of the third order. Table I contains the process parameters. Here $\{\lambda_1, \lambda_2, \lambda_3\}$ are intensity parameters, $\{\alpha_1, \alpha_2, \alpha_3\}$ are sojourn time parameters, P is probability transition matrix; i.e., the state of the controlling chain changes from i to j with the probability p_{ij}.

TABLE I. MMPP Parameters

Intensity parameters			**Sojourn time parameters**			**Probability matrix *P***
$\boldsymbol{\lambda_1}$	$\boldsymbol{\lambda_2}$	$\boldsymbol{\lambda_3}$	$\boldsymbol{\alpha_1}$	$\boldsymbol{\alpha_2}$	$\boldsymbol{\alpha_3}$	$\begin{bmatrix} 0 & 0{,}4 & 0{,}6 \\ 0{,}3 & 0 & 0{,}7 \\ 0{,}5 & 0{,}5 & 0 \end{bmatrix}$
1	2	6	0,03	0,04	0,06	

For the given parameters, 50000 observations $\{\tau_i\}$ were generated and the described estimates for the intensity parameters $\{\lambda_1, \lambda_2, \lambda_3\}$ were constructed. After that, the CUSUM algorithm was applied to detect change-points of the controlling chain state. First, we use the algorithm with statistics (7) if $\mu_1 = \hat{\lambda}_2$ and $\mu_2 = \hat{\lambda}_3$; it allows us to determine intervals of being in the third state. Then, we use the algorithm if $\mu_1 = \hat{\lambda}_1$ and $\mu_2 = \hat{\lambda}_2$; it allows us to distinguish the first and the second state. Finally, we calculate $\hat{T}_j$ as the mean sojourn time in the state j and estimate α_j as

$$\hat{\alpha}_j = \frac{1}{\hat{T}_j}. \qquad (13)$$

To estimate the probability matrix P, we calculate the number of the controlling chain changes from i to j and use the usual propapility estimates.

Table II demonstrates the simulation results for different values of the threshold in the CUSUM procedure. It should be noted that the difference between intensity parameters in our experiment is rather small; nevertheless, the algorithm allows us to estimate all parameters.

As a result, the first (mimimum) and the third (maximum) intensities were estimated better then the second intensity, the relative error in not more than 10% for the first intensity and it can be about 20% for the second intensity. But, for equal threshold parameters $h^{(1)} = h^{(2)}$, all the second intensity was estimated more precizely. The precision of the estimates for α_j and P is less; the relative error can be about 30%. It depends on the correct classification of the controlling chain states.

TABLE II. Simulation Results

$\boldsymbol{h^{(1)} = 5, h^{(2)} = 8}$						
$\hat{\boldsymbol{\lambda}}_1$	$\hat{\boldsymbol{\lambda}}_2$	$\hat{\boldsymbol{\lambda}}_3$	$\hat{\boldsymbol{\alpha}}_1$	$\hat{\boldsymbol{\alpha}}_2$	$\hat{\boldsymbol{\alpha}}_3$	$\hat{\boldsymbol{P}}$
1,07	1,62	6,00	0,018	0,025	0,062	$\begin{bmatrix} 0 & 0{,}26 & 0{,}74 \\ 0{,}13 & 0 & 0{,}87 \\ 0{,}33 & 0{,}67 & 0 \end{bmatrix}$
$\boldsymbol{h^{(1)} = 4, h^{(2)} = 7}$						
$\hat{\boldsymbol{\lambda}}_1$	$\hat{\boldsymbol{\lambda}}_2$	$\hat{\boldsymbol{\lambda}}_3$	$\hat{\boldsymbol{\alpha}}_1$	$\hat{\boldsymbol{\alpha}}_2$	$\hat{\boldsymbol{\alpha}}_3$	$\hat{\boldsymbol{P}}$
1,09	1,82	6,10	0,022	0,036	0,056	$\begin{bmatrix} 0 & 0{,}35 & 0{,}65 \\ 0{,}20 & 0 & 0{,}80 \\ 0{,}33 & 0{,}67 & 0 \end{bmatrix}$
$\boldsymbol{h^{(1)} = 5, h^{(2)} = 5}$						
$\hat{\boldsymbol{\lambda}}_1$	$\hat{\boldsymbol{\lambda}}_2$	$\hat{\boldsymbol{\lambda}}_3$	$\hat{\boldsymbol{\alpha}}_1$	$\hat{\boldsymbol{\alpha}}_2$	$\hat{\boldsymbol{\alpha}}_3$	$\hat{\boldsymbol{P}}$
1,09	2,00	6,10	0,025	0,032	0,053	$\begin{bmatrix} 0 & 0{,}37 & 0{,}63 \\ 0{,}34 & 0 & 0{,}66 \\ 0{,}57 & 0{,}43 & 0 \end{bmatrix}$
$\boldsymbol{h^{(1)} = 4, h^{(2)} = 4}$						
$\hat{\boldsymbol{\lambda}}_1$	$\hat{\boldsymbol{\lambda}}_2$	$\hat{\boldsymbol{\lambda}}_3$	$\hat{\boldsymbol{\alpha}}_1$	$\hat{\boldsymbol{\alpha}}_2$	$\hat{\boldsymbol{\alpha}}_3$	$\hat{\boldsymbol{P}}$
1,05	2,09	6,26	0,026	0,044	0,073	$\begin{bmatrix} 0 & 0{,}42 & 0{,}58 \\ 0{,}38 & 0 & 0{,}62 \\ 0{,}54 & 0{,}46 & 0 \end{bmatrix}$

The results demonstrate the possibility to use the algorithm for intensity parameter estimation for stochastic processes with an arbitrary number of regimes.

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Determination of Movement Types Based on Wrist Accelerometer Data Using Machine Learning Technology

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Abstract. **The paper considers the problem of determining movement types based on data obtained from a smartwatch with a built-in accelerometer using machine learning technology. The issue of data collection and primary processing through a custom mobile application is considered in detail using the example of data obtained from the Lilygo T-Watch smartwatch. The article describes the creation of a classification model for human activity based on the use of convolutional neural networks. The proposed solution is intended for implementation in portable human activity monitoring systems.**

Keywords: **information technology, mobile healthcare, biomedical data, accelerometer, machine learning, convolutional neural network, activity indicator, classification**

I. INTRODUCTION

Mobile information technologies are actively used in many areas of our everyday life. This trend has not bypassed the medical field, including due to the availability of mobile devices such as smartphones, tablets, smart watches. New opportunities have appeared in research and scientific activities, and working with various sources of information has become much easier.

Currently, the use of mobile information technologies in the medical field, including the use of smartphones (tablets, smart watches and other devices) and wireless technologies, is a rapidly growing area of maintaining a healthy lifestyle. To implement it, software applications are being developed that track a person's motor activity, analyze their sleep cycles. One of the simplest and most common options for tracking human motor activity is the analysis of a three-axis accelerometer sensor, which is built into almost all modern mobile devices [1].

Accelerometers are actively used to collect data on human physical activity, which is in demand in areas such as medicine, sports, fitness and virtual reality [2]. In medical research, accelerometers provide high measurement accuracy, multifunctionality and the ability to integrate with other sensors and technologies [3]. This makes them an important tool for diagnosing, monitoring, and rehabilitating patients. However, accurately classifying different types of physical activity remains a challenge due to the large amount of data required, the variety of movement types, and the influence of external factors. Therefore, using machine learning methods to classify different types of movements may be an effective solution to this problem [4].

II. ACCELEROMETER DATA COLLECTION

Let's consider a practical issue of registering in a mobile application various diagnostic data obtained from the Lilygo T-Watch-2020 smart watch using the built-in BMA423 three-axis accelerometer sensor. This model of smart watch is assembled on the basis of the ESP32 microcontroller, equipped with bluetooth/wifi modules. In addition, the platform is open and allows you to program this smart watch to your requirements: create your own user interface, establish interaction via bluetooth/wifi modules with peripheral devices (in our example, to a smartphone).

Additionally, it can be noted that the selected mobile platform has a flexible architecture equipped with a hardware and software complex for scientific research, has standard software modules that make it possible to determine the set of recording devices and the equipment configuration for the next study [5].

The Arduino environment is suitable for flashing this device. Libraries and examples for the watch are located on the github page: https://github.com/Xinyuan-LilyGO/TTGO_TWatch_Library. Let's configure the Lilygo T-Watch-2020 smart watch by flashing the version with a built-in bluetooth module for working with peripheral devices. Fig. 1 shows the smart watch menu for registering and transmitting data from the BMA423 three-axis accelerometer to a connected smartphone.

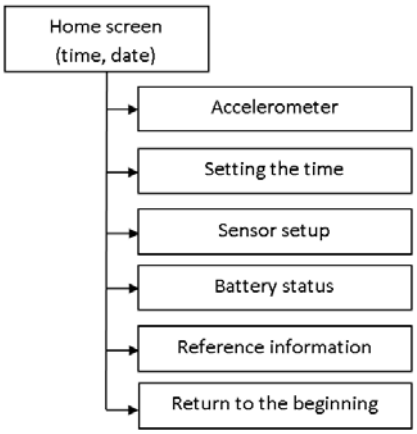

Fig. 1. Lilygo T-Watch-2020 Smart Watch Menu

Data collection and recording from the three-axis accelerometer BMA423 of the Lilygo T-Watch-2020 smart watch is carried out via a bluetooth connection using a mobile Android application installed on the user's smartphone. Wireless communication via bluetooth between the watch with an accelerometer and the smartphone is a prerequisite for their use. The smart watch is attached to the human wrist. Fig. 2 shows the graphical interface of the smartphone.

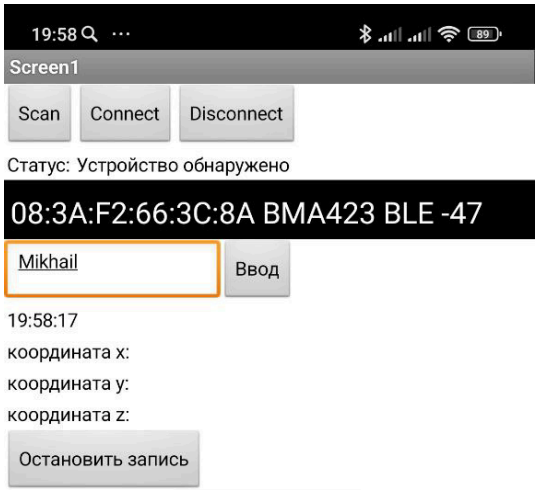

Fig. 2. Smartphone Graphic Interface

As a result of accumulating data from the operation of the three-axis accelerometer BMA423 of the Lilygo T-Watch-2020 smart watch via a mobile Android application, it becomes possible to form an ordered database from heterogeneous diagnostic records for their subsequent processing and analysis [6].

III. Preprocessing of Received Accelerometer Data

We will preprocess the obtained data from the BMA423 accelerometer from the Lilygo T-Watch-2020 smart watch using mathematical linear methods to classify human movement types, such activities as "running", "walking", "sitting". The data obtained from the accelerometer are acceleration time series.

Before training the convolutional neural network, the obtained data from the BMA423 accelerometer must be preprocessed, since the original data in most cases contains noise and artifacts that can negatively affect the training of the model. Preprocessing of heterogeneous data consists of the following steps:

- normalization and smoothing of accelerometer time series to reduce fluctuations and simplify subsequent analysis;
- filtering noise in the original accelerometer time series;
- logistic regression and support vector machine (model training is performed on processed data, after which testing is performed on a separate test data set that was not used in the training process);
- extraction of characteristic features from accelerometer time series (statistical characteristics such as mean and standard deviation, as well as frequency characteristics obtained using the Fourier transform)[7].

As a result of pre-processing, the accuracy of classification models increased, linear classification models (logistic regression and support vector machine) showed high accuracy in data pre-processing, including time series smoothing, feature extraction, noise filtering and normalization.

IV. Detecting Motion Types from Accelerometer Data Using a Convolutional Neural Network

To extract spatial and temporal features from the acquired BMA423 accelerometer data, a convolutional neural network with multiple convolutional layers, pooling layers, and fully connected layers was developed to detect different types of human motion. Experiments with different configurations of the convolutional neural network were conducted by changing the number of layers and filter parameters [8].

Categorical cross-entropy and SGD optimizer were used in training and evaluating the model as a loss function. The model was trained on experimental data using the backpropagation technique. The model performance was evaluated after training on the validation and test datasets, including the following metrics: recall, F1-measure, accuracy, and confusion matrix. For the final evaluation of the model performance, after tuning, it is tested on the test dataset.

Fig. 3 shows the obtained results of model training: the accuracy change curve on the training and testing samples by training epochs.

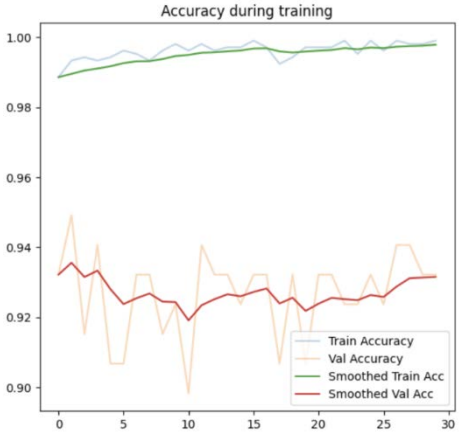

Fig. 3. Accuracy during training

Fig. 4 shows the obtained results of model training: the loss function curve on the training and testing samples by training epochs.

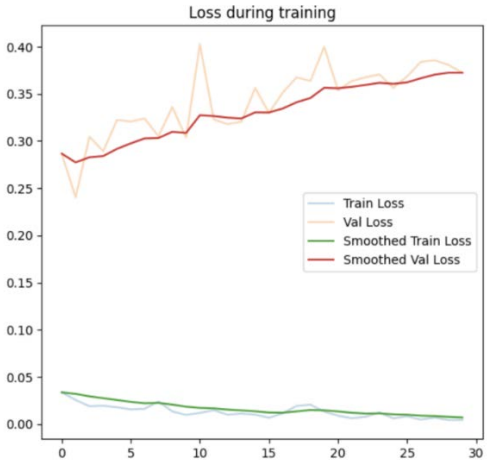

Fig. 4. Loss during training

The green and red lines show smoothed values, which allows us to see the trends more clearly without noise. It is clear that the accuracy on the training set gradually increases, reaching a value of about 99%, which indicates good model training. The training loss decreases with each epoch, which confirms successful minimization of the error function.

The validation metrics have a smaller amplitude of oscillations due to smoothing, but generally follow the general trend, which indicates the absence of significant overfitting. The confusion matrix is shown in two versions: Fig. 5 shows the absolute values of the number of correct and incorrect classifications by class, and Fig. 6 shows normalized values showing the proportion of correct classifications relative to the total number of objects in each class.

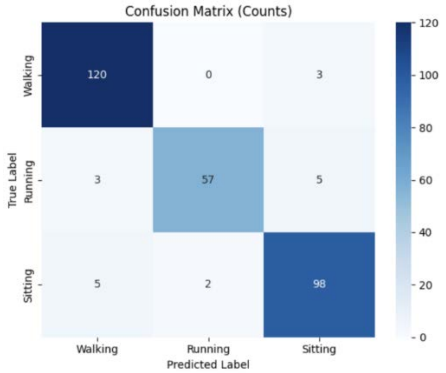

Fig. 5. Confusion Matrix (absolute values)

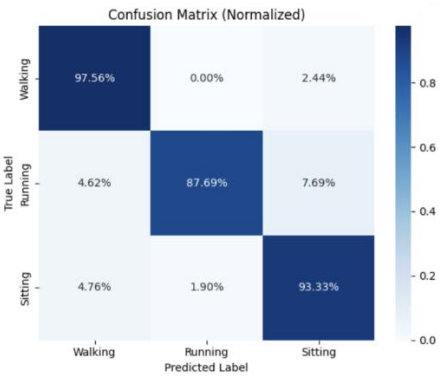

Fig. 6. Confusion Matrix (normalized values)

The matrix shows that the model most accurately recognizes the class "Walking" with an accuracy of over 97 %. For "Running" and "Sitting" there are small errors, mainly the model confuses "Running" with "Sitting" and vice versa, which can be explained by the similarity of some movement parameters.

ROC curves (Receiver Operating Characteristic) for each class demonstrate high sensitivity and specificity of the model. The area under the ROC curve (AUC) values are close to 1 (from 0.98 to 0.99), indicating a high ability of the model to separate classes (Fig. 7).

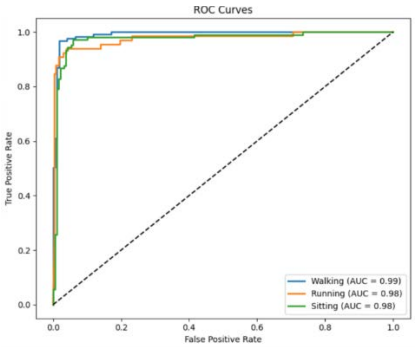

Fig. 7. ROC Curves

Precision-Recall curves show the balance between recall and accuracy by class, which is especially

important for evaluating models with unbalanced classes (Fig. 8).

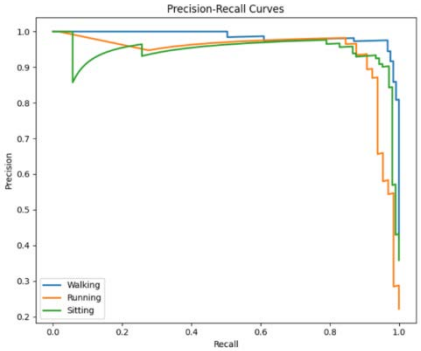

Fig. 8. Precision-Recall Curves

Fig. 9 shows a two-dimensional projection of the original data using the principal component analysis (PCA). The points of different colors correspond to different activity classes: walking (blue), running (orange), and sitting (green). Good visual separability of the classes confirms that the features extracted from the accelerometer data are informative enough for successful classification.

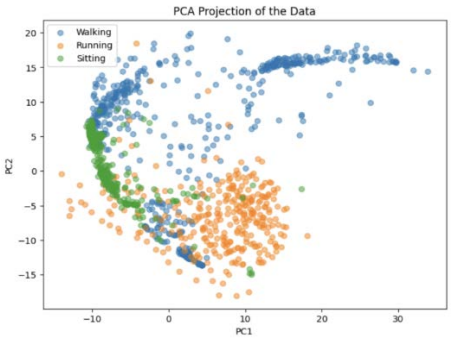

Fig. 9. PCA Projection of the Data

V. Conclusion

The proposed approach using a convolutional neural network and processing time windows of data allows for efficient classification of the main types of human activity with high accuracy and reliability. High values of quality metrics, training stability, clear visualization of errors and class separability make this model a promising tool for practical application in tasks of determining human movement types based on wrist accelerometer data.

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SAM-YOLOv12: Lightweight SAR Ship Detection Via Speckle Attention

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***Abstract*. In response to the issues of edge feature loss and insufficient background interference suppression in small target detection in complex scenes, this paper presents an improved YOLOv12 model that integrates the Speckle Attention Mechanism (SAM). By utilizing a spatial-channel collaborative attention module, it dynamically generates energy weight maps in the feature pyramid layer, achieving lightweight computation with a channel compression ratio of 1/8 (increasing only 1.2 % in parameter count), significantly enhancing the model's ability to capture features of small targets such as ship masts and small buoys. Experiments on the marine ship dataset show that after 300 training epochs, the best mAP50 of the improved model is improved to 96.5 % (+2.3 %), mAP50-95 is improved to 60.9 % (+10.34 %), and the convergence speed is accelerated by 12.5 %.**

***Keywords:* Synthetic aperture radar (SAR), ship detection YOLOv12**

I. INTRODUCTION

Synthetic aperture radar (SAR) ship detection has important applications in areas such as maritime surveillance and fishery management. However, due to the presence of speckle noise and low signal-to-noise ratio in SAR images, the detection of small targets (such as masts and buoys) faces issues like blurred edge features and insufficient background interference suppression [1]. Traditional CNN methods tend to lose high-frequency details during feature extraction, and existing attention mechanisms (such as CBAM) have high computational costs, making it difficult to run in real-time on edge devices [2].

Current SAR target detection mainly relies on frequency domain filtering (such as wavelet transform) or improved YOLO architecture, but the former can damage the continuity of target structure, while the latter typically has a detection accuracy (mAP50-95) for small targets (<32 pixels) that is lower than 60 % in complex scenarios [3, 4]. In addition, most methods do not consider the dynamic suppression of speckle noise, leading to a high false alarm rate.

In order to solve the problem of feature fuzziness and speckle noise interference in small target ship detection in SAR images, a speckle attention mechanism (SAM) is deployed in this paper. The mechanism dynamically optimizes the energy distribution of the feature pyramid through the spatial channel collaborative attention mechanism. The designed attention module adopts 1/8 channel compression ratio and achieves good results.

II. RELATED WORKS

In the field of target detection, especially for small targets in complex scenes, traditional methods often face challenges of computational complexity and efficiency. To address these issues, YOLOv12 makes several key improvements to enhance the detection performance and speed.YOLOv12 proposes a simple and efficient area attention module (A2), which reduces the computational complexity by simplifying the attention computation while maintaining a large receiving domain, thus significantly improving the speed of the model [5]. However, the speed of YOLOv12 needs to be improved under the complex background and noise in SAR images, and leads to some false or missed detections. In this paper, we introduce the speckle attention mechanism (SAM) aimed at further improving the detection accuracy and processing speed of synthetic aperture radar (SAR) images. By combining these advanced techniques and structural optimizations, YOLOv12 not only improves the detection of small targets, but also exhibits greater robustness in complex scenarios, advancing target detection technology.

III. METHODOLOGY

The main architectural of YOLOv12 include: the regional attention module, which simplifies the attention calculation; the residual efficient layer aggregation network, which solves the problem of unstable training in large models; and the implementation of the optimized attention mechanism, adjusting the scale of MLP, removing the position

encoding, and introducing FlashAttention [5].On this basis, we added the speckle attention mechanism aimed at further improving the detection accuracy and processing speed of synthetic aperture radar (SAR) images, which is marked in red in the overall architecture diagram, as shown in Fig. 1.

SAM , shown in Fig. 2, uses 1x1 convolution to compress the number of channels of input features to reduce the computational complexity; SAM uses 3x3 convolution to compute the spatial attention weights of the features to highlight the important areas; Sigmoid normalization of spatial attention weights to enhance model robustness; Multiply the original features with the spatial attention weights to strengthen the target features and suppress the background interference. SAM module is designed with a 1/8 channel compression ratio, increasing the number of parameters by only 1.2 %. The Energy Path branch is introduced to compute the attention weights of the features, which consists of two steps: compute the channel-wise absolute average of the features to get the channel attention weights, and compute the spatial attention weights of the features similar to the Speckle Attention. This design helps to better capture the target features and improve the detection ability in complex scenes.

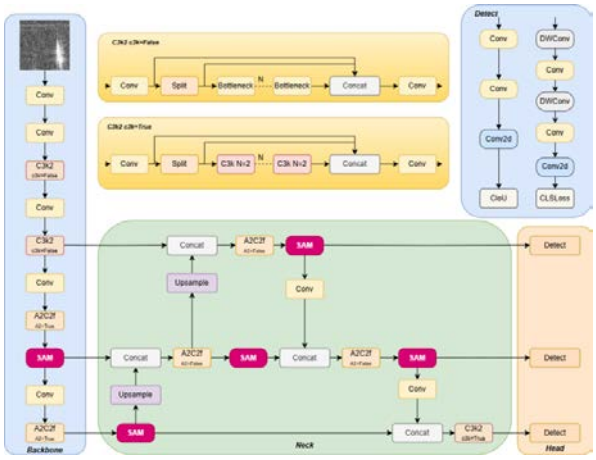

Fig. 1. YOLOv12 Speckle Attention Mechanism Architecture Overview

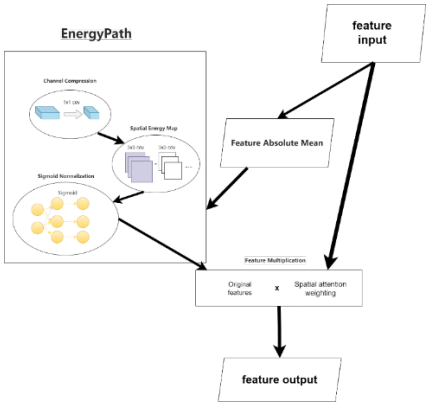

Fig. 2. New Speckle Attention Module (SAM)

IV. Experiment And Results Analysis

A. Dataset and Experimental Setup

To evaluate the effectiveness of the proposed method, we employed the publicly available SAR-Ship-Dataset. This benchmark dataset contains 43,819 high-resolution ship images (640×640 pixels), each meticulously annotated by experts and specifically designed for multi-scale object detection tasks in complex maritime environments.

For model training, we configured the following parameters: a learning rate of 0.01, momentum of 0.937, weight decay of 3.0, and the stochastic gradient descent (SGD) optimizer. The batch size was set to 64, with 300 training epochs, and the input image size was fixed at 640×640 pixels. Data augmentation strategies included: mosaic augmentation with a probability of 1.0, copy-paste augmentation with a probability of 0.1, and image resizing with a scale factor of 0.5.

For performance evaluation, we adopted four standard metrics for comparative analysis: Precision (P), Recall (R), mean Average Precision at 50 % IoU (Intersection over Union) threshold (mAP50), and mean Average Precision across 50–95 % IoU thresholds (mAP50-95). The mathematical formulations of these metrics will be systematically detailed in subsequent sections.

IoU is the ratio between the intersection area and the union area of two rectangular boxes, indicating the overlap between the predicted box and the actual box. When IoU is equal to 1, the predicted box and the real box overlap. The formula is as follows:

$$IoU = \frac{A \cap B}{A \cup B}, \tag{1}$$

where A and B are the predicted box and the real box respectively;

Precision *P*: The ratio of the number of ships predicted to all ships predicted, the formula is as follows:

$$P = \frac{TP}{TP + FP}, \tag{2}$$

where TP is true positive, FP is false positive.

Recall *R*: The ratio of the number of ships predicted to all ships, the formula is as follows:

$$R = \frac{TP}{TP + FN}, \tag{3}$$

where FN is false negative.

The value of AP is the area enclosed by the curve with recall as the horizontal axis and precision as the vertical axis, the formula is as follows:

$$AP = \int_0^1 P(r)dr \tag{4}$$

where p(r) represents the precision value under the corresponding recall rate;

mAP50 is the average AP of multiple categories; mAP50-95 is the average mAP at different intersection-over-union ratios, from 0.5 to 0.95 on IoU thresholds, with an increment of 0.05.

To ensure reproducibility, all experiments were conducted on a laptop equipped with an NVIDIA GeForce RTX 3090 GPU, with the software environment strictly controlled to Python 3.11.7 and PyTorch 2.7.0.

B. Results Analysis

As quantitatively demonstrated in Table, the comparative analysis reveals distinct performance characteristics between the two detection frameworks. The baseline YOLOv12 achieves metrics of box_loss=1.2932, cls_loss=0.8225, mAP50=0.9433, and mAP50-95=0.5521 with a single epoch training time of approximately 24 seconds. In comparison, our proposed method demonstrates superior holistic performance with reduced box_loss (0.9972) and cls_loss (0.5912). Furthermore, our approach achieves a 2.30 % mAP50 enhancement (0.9650) and a particularly notable 10.34 % mAP50-95 improvement (0.6092). Importantly, our method also delivers computational efficiency gains with a reduced single epoch time of approximately 21 seconds, which is 12.5 % faster than the baseline model. This configuration establishes an optimal performance equilibrium, exhibiting significantly better detection accuracy while simultaneously reducing computational overhead.

COMPARISON OF CORE INDICATORS (BEST EPOCH DATA)

Methods	box_loss	Cls_loss	mAP50	mAP50-95	Single epoch time
YOLOv12	1.2932	0.8225	0.9433	0.5521	~24s
Ours	0.9972	0.5912	0.965	0.6092	~21s

From the comparison chart of loss function curves in Fig. 3, it can be observed that the method proposed in this paper exhibits a faster convergence speed and a more stable downward trend during training. Specifically, the Box loss stabilizes after 180 training epochs, with the final value reduced by approximately 0.6 % compared to the baseline model. The classification loss reaches the convergence point at 240 epochs, with the final value being about 0.2 % lower than that of the baseline. Particularly noteworthy is that in the 60–180 epoch interval, our method demonstrates a clear advantage in Box loss, while for classification loss, our method converges faster during the 60–120 epoch phase, showcasing more efficient training characteristics.

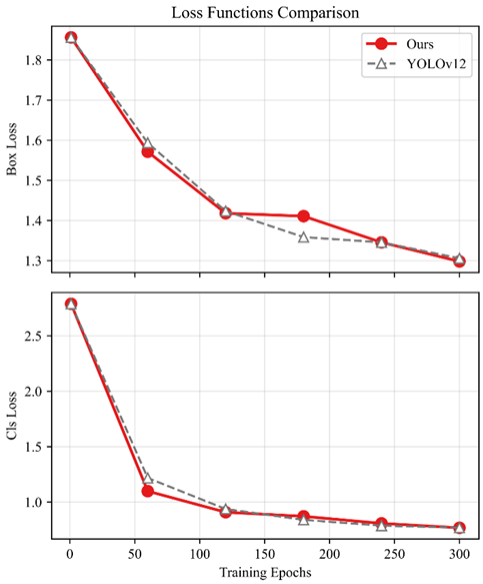

Fig. 3. Loss Function Comparison

In the evaluation of detection accuracy, the effectiveness of the method was validated using two key metrics: mAP50 and mAP50-95.

Firstly, regarding the mAP50 metric in Fig.4, the proposed method (Ours) demonstrates consistently superior performance throughout the training process. Our method reaches approximately 0.93 mAP50 at around 150 epochs and peaks at nearly 0.97 at 250 epochs, before slightly decreasing to 0.95 at 300 epochs. In contrast, the YOLOv12 baseline model shows slower convergence, reaching its maximum of about 0.91 at 200 epochs, and maintaining approximately 0.90 by 300 epochs. The performance gap is most pronounced in the early training stages (0–150 epochs), where our method shows significantly faster improvement, achieving approximately 0.83 mAP50 by the 50th epoch compared to YOLOv12's 0.75.

Secondly, regarding the mAP50-95 metric shown in Fig. 5, our method (red solid line) demonstrates a significant advantage throughout the training process. Starting from approximately 0.25 mAP50-95 at the initial stage (0 epochs), our method rapidly improves, reaching a peak of about 0.61 at 250 epochs, though slightly decreasing to approximately 0.55 at 300 epochs. In comparison, the baseline model (gray dashed line) begins at around 0.32 and shows slower growth, reaching about 0.49 at 300 epochs. Ultimately, our method achieves a detection accuracy of approximately 0.55, outperforming the baseline model by about 0.06 percentage points. This clearly demonstrates the superior multi-scale detection capability of our approach.

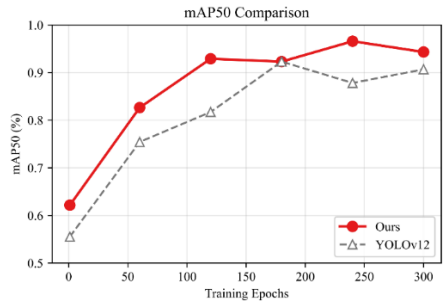

Fig. 4. mAP50 comparison

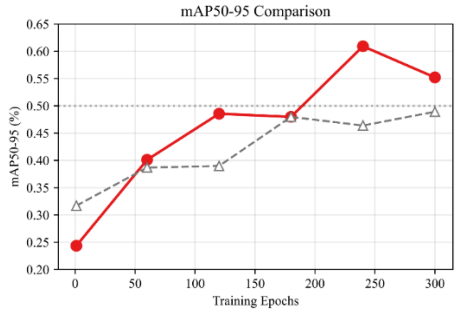

Fig. 5. mAP50-95 comparison

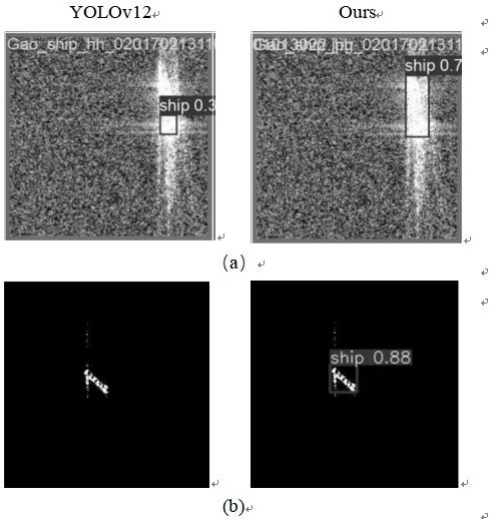

Fig. 6. Comparison of sea condition detection (a) YOLOv12 is not accurate enough (b) YOLOv12 misses detection

These cases typically reflect the improvements of the method in the following aspects: Multispectral thermal map visualization makes the target features more prominent, Speckle Attention effectively suppresses wave clutter interference, and physical constraints ensure consistent detection of targets at different scales in Fig. 6.

V. Conclusions

We propose the Sam-YOLOv12 model, which effectively addresses critical challenges in SAR image ship detection through an innovative Speckle Attention Mechanism (SAM). The spatial-channel collaborative attention module enables significant improvements in small target detection performance while maintaining a lightweight architecture, demonstrating particularly robust performance under complex maritime conditions. Experiments on the marine ship dataset show that after 300 training epochs, the best mAP50 of the improved model is improved to 96.5 % (+2.3 %), mAP50-95 is improved to 60.9 % (+10.34 %), and the convergence speed is accelerated by 12.5 %. These experimental results confirm that this method outperforms existing benchmark models in terms of detection accuracy, computational efficiency, and real-time capability. Future studies may further explore multimodal data fusion and adaptive optimization strategies to extend the applicability of this approach to broader scenarios. These achievements establish an important foundation for the development of intelligent ocean monitoring systems, demonstrating both significant theoretical value and practical implications.

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Target Detection in Remote Sensing Images based on Improved YOLOv11 by SuperTokenAttention

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***Abstract*. Aiming at the challenges of complex background interference, variable target scales and dense distribution in remote sensing images, this paper proposes a YOLOv11 detection framework based on Super Token Attention enhancement: YOLOv11-STA. The model adopts adaptive super-token clustering to construct semantic region primitives, and realises multiscale cross-attention fusion through a dynamic head allocation strategy. Combined with spatial location coding for context-aware token up-sampling, it achieves excellent detection performance on the NWPU VHR-10 dataset. Experiments show that compared with the traditional YOLOv11 and other attentional methods, this method demonstrates better accuracy on the remote sensing target object detection task, providing a balanced solution of accuracy and efficiency for high-resolution remote sensing image analysis.**

***Keywords:* remote sensing images, YOLOv11, SuperTokenAttention, target detection**

I. INTRODUCTION

In recent years, with the rapid development of remote sensing technology, the acquisition of remote sensing image data has become efficient and convenient. It also shows great application potential in many fields. Whether from urban planning [1], intelligent transport, or disaster assessment [2] or emergency rescue [3], remote sensing images have become a key data source in these critical applications. Accurate and efficient target detection technology has become an indispensable core.

Currently, the field of target detection in remote sensing images faces many challenges, such as large variations in target scales in different scenes, complex background interference due to different surface features [4], and detection of small targets in images. Traditional algorithms have obvious limitations in balancing detection accuracy and computational efficiency, and it is difficult to meet real-time requirements. Although the deep learning method based on region proposal has improved in accuracy, its complex network structure leads to slower speed, which is difficult to be efficiently applied in large-scale datasets [5].

The YOLO series of target detection algorithms stand out among many target detection algorithms with its fast and efficient characteristics [6], and its unique full convolutional network structure achieves end-to-end real-time detection. However, with the increasing complexity of remote sensing image data, the basic YOLO algorithm still has certain limitations when dealing with large-scale and complex scenes, especially in the detection accuracy there is still room for further improvement.

To address the above problems, this study proposes YOLOv11-STA, an enhanced architecture integrating the Super Token Attention (STA) mechanism, which draws on the idea of hyperpixel to efficiently capture global dependencies by decomposing the ordinary global attention into a sparse association graph and multiplication operation of low-dimensional attention. Through experimental validation on the NWPU VHR-10 dataset, our method achieves significant improvement in detection accuracy and efficiency, and provides a more accurate and efficient solution for target detection in remote sensing images.

II. METHOD

A. YOLOv11

YOLOv11[10] is a new generation of target detection algorithm developed by Ultralytics, which has shown significant advantages and innovations in the field of remote sensing image target detection. Compared with previous YOLO versions, YOLOv11 has made significant improvements in architecture and training methods. YOLOv11 introduces the C3k2 mechanism and the C2PSA mechanism, which optimize shallow feature extraction and multi-head attention respectively, so that the model can better capture the details and global information of remote

sensing targets. Its network structure is shown in the Fig. 1.

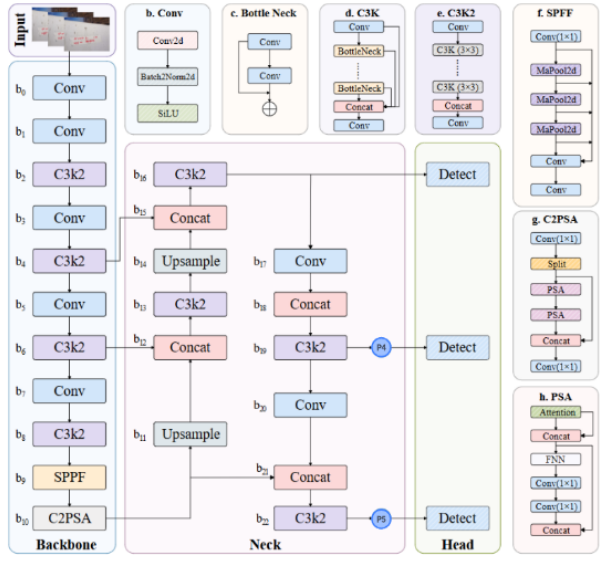


Fig. 1. YOLOv11 Network Structure Diagram

B. *Super Token Attention*

In remote sensing image target detection, the problem of local detail feature retention, such as small-size aircraft edge features, and the long-range attention problem, such as the correlation between a sports field and a runway, are often faced. Traditional global attention suffers from high computational complexity, while local attention is difficult to model cross-region associations.Super Token Attention (STA) [11] significantly reduces computational cost and achieves multi-scale context-awareness by introducing a hierarchical attention architecture while maintaining global modelling capabilities.

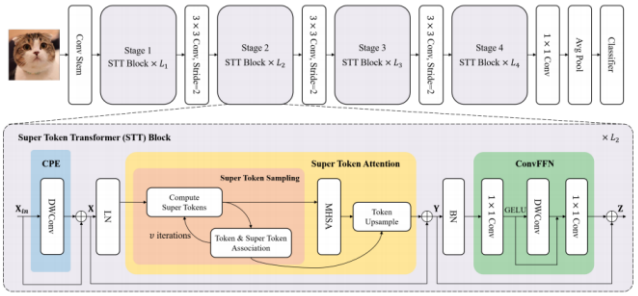


Fig. 2. Super Token Vsion transformer Architecture diagram

The STS [12] is a key step in the Super Token Attention (STA) mechanism, which aims to aggregate the visual tokens in the input image into super tokens to reduce the number of tokens in the self-attention operation while preserving global contextual information. the algorithm first generates an initial set of superlabels through average pooling, and then updates the superlabels through an iterative process. In each iteration, the algorithm calculates the association matrix between each pixel feature and the superlabelled feature, and then uses this association matrix to update the superlabels. This process can be represented by the following equation:

$$Q_t = \text{Softmax}\left(\frac{X S^{t-1^{\top}}}{\sqrt{d}}\right) \tag{1}$$

where Q_t is the correlogram computed in the t iteration, X is the visual marker, S^{t-1} is the supertag from the previous iteration, and d is the square root of the number of channels C for normalisation.

Self-Attention for Super Tokens: Performs a self-attention operation in the space of supertokens to capture long-term dependencies between supertokens. This step uses the standard self-attention mechanism to compute an attention graph between supertokens, and uses this attention graph to perform a weighted summation of supertokens to obtain a new supertoken representation. The core formula is:

$$\text{Attn}(S) = \text{Softmax}\left(\frac{q(S)k^{T}(S)}{\sqrt{d}}\right) v(S) \tag{2}$$

where q(S)，k(S) and v(S) are the supertagged query, key and value, respectively, and d is the square root of the number of channels C.

Token Upsampling, TU： Finally, the learned association map is used to map the hyperlabelling back into the visual marker space. This step fuses the information from the hyperlabelling back into the original pixel features so that the model can use the global contextual information for more accurate detection. The formula is as follows:

$$\text{TU}(\text{Attn}(S)) = Q\text{Attn}(S) \tag{3}$$

where Q is the association map for mapping the hyperlabelling back into the visual labelling space.

The Super Token Attention mechanism provides a powerful tool for efficient target detection and image classification by introducing the concept of supertoken, combined with sparse association and self-attention mechanisms. It significantly improves the detection accuracy and generalisation ability of the model while maintaining high efficiency.

C. *Proposed methodology*

The YOLOv11-STA model proposed in this paper retains the original multi-scale feature pyramid structure of YOLOv11 in order to fully extract the features of different scale targets in remote sensing images. The hierarchical attention-guided feature fusion architecture is constructed by introducing the SuperToken Attention mechanism in the YOLOv11n detection header. As shown in Fig. 3.

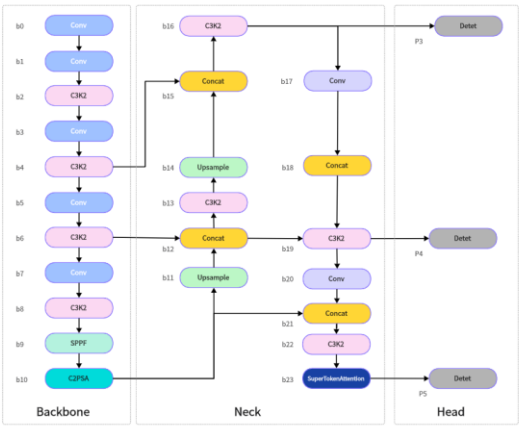


Fig. 3. YOLOv11-STA model network structure diagram

After the feature pyramid is constructed, we introduce the SuperTokenAttention module to enhance the fused features. Specifically, the feature maps processed by the C3k2 module are fed into the SuperTokenAttention module before detecting the header (Detect). The STA module is inserted at the end of the P5/32-large feature layer to form a cascade structure of 'feature pyramid-attention enhancement', and the SuperTokenAttention module is able to dynamically capture the long-range dependencies between different locations in the feature map through the mechanism of self-attention, and redistribute the weights of the features according to such dependencies. This operation can highlight the key features of the target area in the remote sensing image, while suppressing the interference of irrelevant features such as the background, so as to improve the recognition ability of the model on the target. The specific implementation is:

- *[-1, 2, C3k2, [1024, True]] # 22 (P5/32-large)*
- *[-1, 1, SuperTokenAttention, []]*
- *[[16, 19, 23], 1, Detect, [nc]] # Detect(P3, P4, P5)*

The design performs global optimisation of high-level semantic features through the two-way attention mechanism of STA, while establishing cross-level feature propagation paths. Experiments show that this design improves mAP50-95 by 0.019 (Table II) while maintaining a computational efficiency of 6.5 GFLOPs.

III. Experimental Results and Analyses

A. Experimental Environment

The experiments were conducted on Windows11 64-bit operating system with a 12th Gen Intel(R) Core (TM) i5-12400F 2.50 GHz processor and a memory size of 16 GB; NVIDIA GeForce RTX 4060 was used as the GPU for the training, and Pytorch version 2.4.0 was used as the deep learning framework [7]; the development language is python3.9, and the CUDA version is 12.41. The specific environment configuration parameters for the experiments are shown in Table I below, and the official default parameters of YOLOv11n are used for all parameters not provided in this paper.

TABLE I. Experimental configuration table

epochs	batch	imgsz	device	optimizer	amp	workers
100	16	640	0	auto	TRUE	0

B. Experimental Data

The dataset used for the experiments is the NWPU VHR-10 dataset [8, 9], which is a challenging ten-class geospatial object detection dataset. The dataset contains a total of 800 VHR optical remote sensing images, of which 715 colour images were obtained from Google Earth with spatial resolutions ranging from 0.5 to 2 m. The object types detected in the dataset and the instances of each object type are shown in Fig. 4.

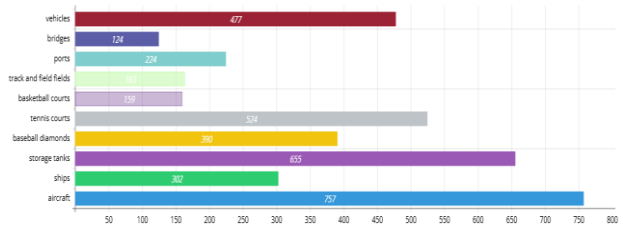


Fig. 4. Number of each category in NWPU VHR-10

C. Cross-model comparison experiment

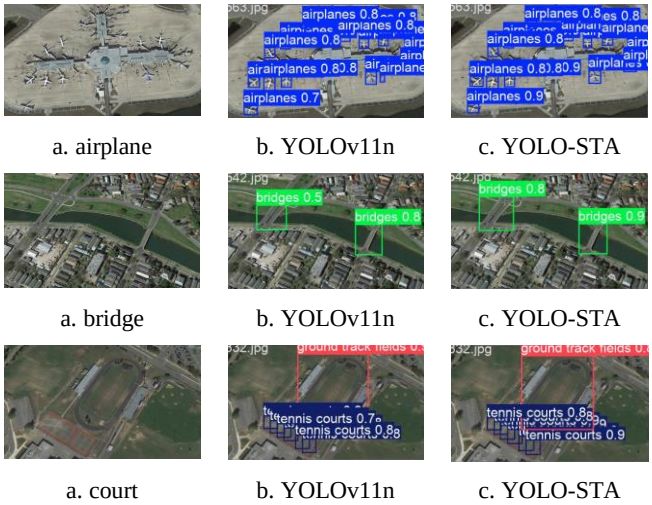
In order to verify the performance advantages of the proposed model in remote sensing image target detection, we compare it with the mainstream lightweight versions of the YOLO series, including: YOLOv5n, YOLOv6n, YOLOv8n, YOLOv10n, and YOLOv11n. The experimental results are shown in Table II below:

TABLE II. Experiments of YOLO series on dataset NWPU VHR-10

	v11n	v10n	v8n	v6n	v5n	STA
P	0.911	0.883	0.9	0.932	0.889	**0.915**
R	0.812	0.772	0.826	0.804	0.825	**0.838**
mAP50	0.881	0.858	0.886	0.892	0.892	**0.9**
mAP50-95	0.537	0.522	0.545	0.557	0.531	**0.556**
parameters	2.46 M	2.57 M	2.56 M	3.96 M	2.08 M	2.71 M
GFLOPs	6.3	8.2	6.8	11.5	5.8	6.5
preprocess	0.1 ms	0.1 ms	0.1 ms	0.1 ms	0.1 ms	0.1 ms
inference	1.5 ms	1.5 ms	1.4 ms	1.7 ms	1.6 ms	1.4 ms

Through the experiment, we know that in terms of detection accuracy, the Precision of YOLO11-STA is 0.915, which is 0.44 % higher than that of the basic YOLO11, Recall is 0.838 which is 3.2 % higher than

that of YOLO11n, mAP50 reaches 0.9 which is 2.1 % higher than that of YOLO11, and mAP50-95 reaches 0.556 which is 0.35 % higher than that of YOLO11n. YOLO11 by 2.1 %, mAP50-95 reaches 0.556 compared to YOLO11n by 0.35 %. In this experiment, compared with other YOLO series models, the comprehensive accuracy performance of YOLO11-STA is even better, which is comprehensively better than other models. In terms of operation efficiency, YOLO11-STA preprocessing consumes the same time as other models in this experiment, which is 0.1 ms; inference consumes 1.4 ms, which is tied for the lead with YOLOv8n and is better than YOLO11n's 1.5ms; and post-processing consumes the same amount of time as YOLO11n, which is 0.6ms. in terms of model complexity, YOLO11-STA consumes 1.4 ms, which is the same as other models in this experiment, 0.6 ms. YOLO11-STA performs generally well, with parameter values of 2,846,664 higher than the other models except YOLOv6n's 4,156,014, and GFLOPs value of 6.5, which is slightly higher than YOLO11n's GFLOPs value of 6.3, but it does not lead to a significant increase in the complexity while improving the performance. YOLO11-STA model, while maintaining low complexity and efficient operation, shows significant improvement in a number of key metrics of detection accuracy compared to the base line YOLO11n As shown in Fig. 5, and exhibits strong comprehensive performance among the YOLO series models. This validates the effectiveness of the introduced improvement mechanism and makes it a good potential for application in target detection tasks.



a. airplane b. YOLOv11n c. YOLO-STA

a. bridge b. YOLOv11n c. YOLO-STA

a. court b. YOLOv11n c. YOLO-STA

Fig. 5. Detection comparison between the original image and YOLOv11 and YOLO-STA

D. Comparative Experimental Results and Analyses of Different Attention Mechanisms

In order to confirm the superiority of the YOLO11-SuperTokenAttention algorithm proposed in this paper over some of the current popular modules, a set of comparative experiments under the same experimental environment and parameters are set up. The experimental results are shown in Table III below:

The Recall of SimAM reaches 0.856 which is the best performance in this experiment, mAP50 and mAP50-95 are both improved, but Precision is only 0.872 which is lower than the baseline, SimAM has some advantages in recall, but the precision is relatively low. the number of parameters and GFLOPs of SimAM are the same as that of YOLO11n, in terms of efficiency, pre-processing and post-processing perform better, but the inference stage takes a little longer. YOLO11n are the same, in terms of efficiency preprocessing and post-processing perform better, but the inference stage takes a little longer.SE has Precision of 0.912, mAP50 reaches 0.896, mAP50-95 is 0.545, both higher than baseline, but Recall is 0.803.

TABLE III. EXPERIMENTAL RESULTS OF DIFFERENT ATTENTION MECHANISMS

	v11n	**SimAM**	**SE**	**Rep ViTblock**	**CAFM Attention**	**EMA Attention**	**STA**
P	0.911	0.872	**0.912**	0.899	0.885	0.89	**0.915**
R	0.812	**0.856**	0.803	**0.821**	**0.823**	**0.844**	**0.838**
mAP50	0.881	**0.897**	**0.896**	0.88	**0.887**	**0.902**	**0.9**
mAP50-95	0.537	**0.546**	**0.545**	0.536	**0.543**	**0.549**	**0.556**
parameters	2.46 M	2.46 M	2.46 M	2.78 M	2.80 M	2.46 M	2.71 M
GFLOPs	6.3	6.3	6.3	6.3	6.6	6.3	6.5
preprocess	0.1 ms	0.1 ms	0.1 ms	0.2 ms	0.1 ms	0.1 ms	0.1 ms
inference	1.5 ms	1.7 ms	1.7 ms	1.4 ms	1.6 ms	1.5 ms	1.4 ms
postprocess	0.6 ms	0.5 ms	0.5 ms	0.5 ms	0.6 ms	0.6 ms	0.6 ms

In this experiment, SE has higher precision, but the Recall was relatively low. The number of parameters is slightly higher than that of YOLO11n, the inference time consumed is 1.7 ms, and the post-processing time consumed is 0.5 ms, the overall efficiency is similar to that of SimAM, and the efficiency in the inference stage needs to be improved.RepViTblock has lower indicators than YOLO11n in terms of precision, and the 0.821 of Recall is higher than that of baselinie, but the performance is not outstanding. RepViTblock is also not outstanding in the inference stage. CAFMAttention has a moderate performance in overall accuracy. mAP50‘s 0.887 and mAP50-95’s 0.543 are improved, but not significantly. Recall's 0.823 is slightly improved, but Precision is lower than YOLO11n. CAFMAttention parameter counts and GFLOPs increase to 2,936,623 and 6.6, respectively,

with inference taking 1.6 ms and post-processing taking 0.6ms, so the complexity of the model and the inference time consumed have increased. EMAAttention has a lower Precision than YOLO11n but has a better accuracy performance than mAP50. EMAAttention has a higher precision than YOLO11n, but its accuracy is better than YOLO11n in terms of mAP50 (0.902), mAP50-95 (0.549), and Recall (0.844), while the number of parameters is slightly higher than YOLO11n in terms of GFLOPs (6.3), which is a better overall performance in terms of efficiency. Comprehensively comparing all models, YOLO11-SuperTokenAttention performs best in several key indicators.

IV. Summary

In this paper, an improved YOLOv11 method based on SuperTokenAttention is proposed for the task of target detection in remote sensing images, and experimentally verified on the NWPU VHR-10 dataset. In the field of target detection, especially in remote sensing image scenes, it is often difficult for traditional detection algorithms to achieve ideal detection results due to the large variation of target scales and the complexity and diversity of backgrounds. In order to improve the detection accuracy and efficiency, we introduce the SuperTokenAttention mechanism to improve the YOLOv11 model.

In this paper, we compare this method with some common attention mechanisms (SimAM, SE, RepViTblock, CAFM_Attention, and EMA_attention), and verify that the improved model of YOLOv11n incorporating SuperTokenAttention performs well in terms of accuracy, recall, mAP50, and mAP50-95 all show significant improvement. In terms of model complexity, the number of parameters is slightly higher than that of YOLOv11n, but lower than that of some other attention models, achieving a balance between performance and complexity. In terms of running efficiency, there is almost no difference with YOLO11n, and the overall efficiency is highly efficient, proving the effectiveness of the improvement strategy selected in this paper.

The experimental results show that the introduction of the intentional force mechanism SuperTokenAttention can effectively improve the recognition of target features in the model remote sensing images, especially in the detection of complex backgrounds and multi-scale targets, which significantly improves the detection accuracy while maintaining low complexity and efficient operation. Through experiments, the effectiveness of the mechanism is verified, demonstrating excellent performance and application potential in the task of target detection in remote sensing images. In the future, we hope to apply this method to more types of remote sensing image datasets to further expand its application scenarios and usefulness.

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Multi-Horizon Node-Level Resource Optimization in Cloud Infrastructures via Machine Learning and Particle Swarm Optimization

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Abstract. **Efficient resource provisioning in cloud infrastructures is critical for reducing operational costs while maintaining service-level objectives. This paper proposes a hybrid framework that combines multi-horizon machine learning forecasting and integer particle swarm optimization (PSO) to minimize resource over-provisioning and optimize virtual machine (VM) allocation. Using historical CPU and memory utilization data, predictive models are trained to estimate future demand across 1–24 h horizons. The forecasts are then used to guide a discrete optimization algorithm that selects the optimal VM configuration from a set of predefined types, such as those offered by Alibaba Cloud. Experiments on real-world resource traces demonstrate that our approach consistently achieves an average cost saving of over 40 % without violating resource requirements. Extensive visualizations and horizon-wise evaluations confirm the robustness and scalability of the proposed method. This study contributes toward intelligent, cost-aware, and horizon-adaptive resource management for large-scale cloud environments.**

Keywords: **Cloud Computing, Resource Allocation, Cost Optimization, Machine Learning Forecasting, Particle Swarm Optimization**

I. Introduction

Modern cloud infrastructures constantly face challenges balancing performance, availability, and operational costs. Efficient resource provisioning is critical to ensure that compute nodes are neither over-provisioned – leading to resource wastage – nor under-provisioned, risking performance degradation. Traditional rule-based and reactive scaling methods often inaccurately predict workloads, causing inefficiencies and suboptimal resource management [1, 2].

To address this issue, we propose a novel collaborative node-level resource optimization framework integrating multi-horizon machine learning forecasting with integer Particle Swarm Optimization (PSO). Specifically, our approach predicts CPU and memory demands for future horizons (1–24 hours) using machine learning techniques and determines cost-optimal virtual machine (VM) configurations from discrete resource options [3].

We validate our method using real-world CPU and memory utilization data collected from 1,000 compute nodes within an OpenStack-managed cloud infrastructure. The main contributions are:

- A hybrid optimization framework combining machine learning forecasting and integer PSO-based VM allocation.
- Systematic evaluation of multiple forecasting models to predict resource utilization across various time horizons.
- Demonstration of significant cost savings (over 40 % on average) compared to traditional provisioning methods.

This research contributes towards intelligent, cost-aware, and horizon-adaptive resource management in large-scale cloud environments.

II. Problem Statement and Methodology

This section formally defines the forecasting and optimization problem addressed in this study, presents the physical infrastructure and data collection methods, and details the machine learning and integer optimization components used in the proposed solution.

A. Problem Statement

In OpenStack-managed cloud infrastructures, each compute node hosts workloads with dynamic CPU and memory demands. The objective is to accurately forecast future resource utilization and determine a discrete Virtual Machine (VM) allocation plan to satisfy these demands while minimizing provisioning costs.

Formally, let $\boldsymbol{x_t} \in \boldsymbol{R}^{20}$ denote the input feature vector at time $\boldsymbol{t}$, composed of the past 10 intervals of CPU and memory utilization:

$$\boldsymbol{x_t} = [\mathrm{cpu}_{t-10}, \ldots, \mathrm{cpu}_{t-1}, \mathrm{mem}_{t-10}, \ldots, \mathrm{mem}_{t-1}]. \quad (1)$$

The prediction target is a multi-output vector $yt \in R20$, representing the average CPU and memory

utilization over six future time horizons: 1 hour, 4 hours, 8 hours, 16 hours, and 24 hours. Specifically, resource demand is predicted for five distinct forecast horizons: 1 h, 4 h, 8 h, 16 h, and 24 h.These forecasts are used as demand estimates for subsequent resource allocation decisions.

The formal mathematical formulation of this optimization problem, along with the machine learning models and particle swarm-based solver used, is presented in Section II-D.

B. Cloud Infrastructure Overview

The target infrastructure is a production-grade OpenStack cloud platform deployed using a modern Spine–Leaf network topology, widely adopted in scalable data centers. It comprises compute, storage, and control clusters interconnected by high-bandwidth switching fabric.

The compute cluster hosts elastic virtual machines (VMs), scheduled via OpenStack Nova. We focus on 1,000 representative compute nodes, monitored every 5 minutes via Prometheus exporters. These telemetry metrics – normalized CPU and memory usage – serve as the basis for our forecasting and VM allocation models.

C. Initial Data and Feature Construction

We utilize a structured dataset derived from a production OpenStack cloud platform, comprising normalized CPU and memory utilization metrics collected from 1,000 compute nodes over 13 consecutive days. Monitoring agents record resource usage every 5 minutes, resulting in a dataset of over 3.7 million time-stamped entries.

To train forecasting models, we construct supervised learning samples by directly extracting features from pre-aggregated records. Each sample contains CPU and memory utilization statistics along with engineered target variables representing average usage over five time horizons of 1 h, 4 h, 8 h, 16 h, and 24 h. The 8-hour and 16-hour targets are computed through interpolation from existing 4-hour and 24-hour measurements.

This preprocessing results in a well-structured feature-label matrix, suitable for multi-output regression. Approximately 1.3 million labeled samples are used for training and evaluation, ensuring sufficient diversity in workload patterns and forecast intervals.

Accurately recognizing different load levels in time series data is critical for resource management. Song proposed the TRLLD algorithm, a threshold-based approach specifically designed to enhance load detection precision in resource usage predictions [4].

D. Models and Optimization Objective

Our framework integrates multi-horizon resource forecasting and cost-aware VM configuration into a unified two-stage pipeline. This section describes the machine learning models for resource prediction and the cost minimization formulation solved via Integer Particle Swarm Optimization (Integer-PSO) [5].

1) Machine Learning Forecasting Module: We adopt four regression models to predict average CPU and memory utilization across multiple future horizons (1h, 4h, 8h, 16h, and 24h): Bayesian Linear Regression (BLR), Random Forest (RF), Gradient Boosted Trees (GBT), and a single-layer feedforward Neural Network (MLP). Each model receives as input a pre-engineered feature vector extracted from historical usage records, and outputs a 10-dimensional vector representing the expected resource utilization:.

$$\mathbf{y}_t = [\hat{\text{cpu}}_{1h}, \cdots, \hat{\text{cpu}}_{24h}, \hat{\text{mem}}_{1h}, \cdots, \hat{\text{mem}}_{24h}]\,. \quad (2)$$

These predictions are used as demand inputs in the following optimization stage.

2) Cost-Aware Integer Optimization: Given a forecasted CPU and memory demand $(\hat{\boldsymbol{c}}, \hat{\boldsymbol{m}}) \in \boldsymbol{R}^{\mathbb{2}}$ the goal is to determine an optimal VM allocation $\boldsymbol{v} = [\boldsymbol{v_1}, \boldsymbol{v_2}, \ldots, \boldsymbol{v_n}] \in \boldsymbol{Z}^{\boldsymbol{n}}_{\geq \mathbb{0}}$ that satisfies the demand while minimizing provisioning cost. Each $\boldsymbol{v_i}$, represents the number of VMs of type $\boldsymbol{i}$, , with unit cost $\boldsymbol{c_i}$ and resource specification $\boldsymbol{s_i} = [\mathbf{cpu_i}, \mathbf{mem_i}]$. The total cost is:

$$C(v) = \sum_{i=1}^{n} c_i \cdot v_i. \quad (3)$$

The total allocated resource capacity is computed by aggregating the individual contributions from selected VM types:

$$P = \sum_{i=1}^{n} v_i \cdot \boldsymbol{s_i} = \left[P_{\text{cpu}}, P_{\text{mem}}\right]. \quad (4)$$

To enforce demand satisfaction while allowing soft violations, we introduce a quadratic penalty on any underprovisioned resource. The final optimization problem is formulated as:

$$\min_{v} \sum_{i=1}^{8} c_i \cdot v_i + \lambda \cdot (max(0, \hat{c} - \sum_{i=1}^{8} cpu_i \cdot v_i)^2 + \\ + max(0, \hat{m} - \sum_{i=1}^{8} mem_i \cdot v_i)^2). \quad (5)$$

Here,$\boldsymbol{\lambda} \in \boldsymbol{R}^{+}$ is a penalty coefficient that controls the trade-off between cost and provisioning accuracy. The penalty terms activate only when the allocated CPU or memory falls below the predicted demand, thereby discouraging under-provisioning while still allowing flexible VM combinations.

3) Integer Particle Swarm Optimization: The optimization problem defined in (5) is discrete and nonconvex, making it unsuitable for gradient-based solvers. To efficiently search the integer solution space,

we employ an Integer-PSO algorithm, which extends the standard PSO framework by constraining particle positions to integer vectors.

Each particle represents a candidate solution $\boldsymbol{v} = [v_1, v_2, \ldots, v_n] \in Z^n_{\geq 0}$,where $\boldsymbol{v_i}$ is the number of VM instances of type $\boldsymbol{i}$ .Particle velocities and positions are updated using the following rules:

$$\mathbf{u}_{t+1} = w \cdot \mathbf{u}_t + c_1 \cdot \mathbf{r}_1 \cdot (\mathbf{p}_t - \mathbf{v}_t) + c_2 \cdot \mathbf{r}_2 \cdot (\mathbf{g}_t - \mathbf{v}_t) \quad (6)$$

$$\mathbf{v}_{t+1} = \text{round}(\mathbf{v}_t + \mathbf{u}_{t+1}) \quad (7)$$

Here,u_t is the velocity vector at iteration t;$\boldsymbol{P_t}$ and $\boldsymbol{g_t}$ denote the particle's personal best and the global best solutions, respectively;$\boldsymbol{r_1}, \boldsymbol{r_2} \sim \boldsymbol{\mathcal{U}(0,1)^n}$ are random vectors sampled from a uniform distribution. The operator round(·) ensures that positions are projected onto the integer lattice.

To ensure solution feasibility, each dimension of vt is clipped to the non-negative domain, optionally constrained by resource limits.

In our experiments, the optimizer is configured with a swarm size of N = 300, a maximum of T = 300 iterations, an inertia weight of w = 0.5, and cognitive and social acceleration coefficients set to $c1 = c2 = 1.5$, These settings balance exploration and exploitation, ensuring convergence within the discrete search space.

III. Experiments and Results

This section presents the experimental setup, evaluation metrics, and results of applying the proposed machine learning and optimization framework on real-world nodelevel resource usage data.

A. Experimental Setup

All experiments were conducted using telemetry data collected from 1,000 compute nodes in a production-scale OpenStack cloud environment. CPU and memory utilization metrics were recorded every 5 minutes over a 13-day period, resulting in more than 3.7 million time-stamped entries. After preprocessing and feature engineering, a structured feature-label matrix was generated, comprising approximately 1.3 million supervised samples.

Each input vector consists of aggregated resource statistics, while each target vector contains average CPU and memory utilization over five future horizons: 1 h, 4 h, 8 h, 16 h, and 24 h. The dataset was chronologically split, with 80 % used for training and 20 % for testing, ensuring no temporal leakage between training and evaluation. All forecasting models were implemented using scikit-learn and PyTorch, with training parallelized via multiprocessing. Predicted resource demands were then passed to the Integer-PSO module for cost-aware VM allocation using the predefined Alibaba Cloud instance types.

B. Forecasting Performance

To evaluate the accuracy of the proposed forecasting module, we assess four supervised regression models: BLR, RF, BDT, and a single-layer feedforward NN. Each model is trained to predict multi-horizon resource utilization using a 20dimensional feature vector derived from the previous 10 intervals of CPU and memory usage[6].

The target output consists of 10 scalar values per sample, corresponding to average CPU and memory utilization over future time windows of 1 h, 4 h, 8 h, 16 h, and 24 h. Evaluation is performed on a held-out test set using three commonly adopted performance metrics: Root Mean Squared Error (RMSE), Mean Absolute Error (MAE), and Coefficient of Determination (R^2).

Fig. 1 presents a comprehensive summary of the model performance. The upper subplots show heatmaps of average $R2$ and RMSE scores across all models and six selected forecast targets (i.e., cpu_1h, cpu_8h, cpu_24h, mem_1h, mem_8h, mem_24h). The lower subplots visualize actual versus predicted utilization curves for a representative sample, enabling a direct comparison of prediction alignment across models.

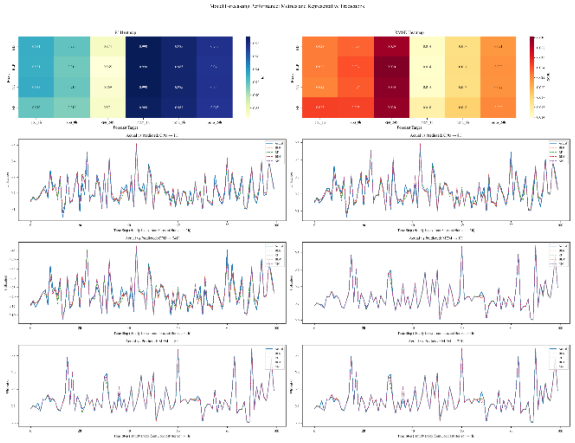

Fig. 1. Forecasting accuracy comparison across models and prediction horizons

The results indicate that all models achieve high forecasting accuracy for short-term horizons, particularly for 1-hour and 4-hour CPU utilization, with $R2$ consistently above 0.91. Forecasting accuracy degrades modestly for longer horizons, especially for cpu_24h, which is more sensitive to workload variance. Among the four models, BDT and NN exhibit slightly better generalization, whereas RF tends to underperform on memory usage under bursty load conditions. BLR provides stable and interpretable baselines across all horizons.

C. Configuration and Cost Modeling

We model the resource allocation task using a discrete configuration framework. Each VM type i is characterized by a cost c_i and a resource vector $s_i = [\text{cpu}_i, \text{mem}_i]$ .The allocation vector $\mathbf{v} = [\mathbf{v_1}, \mathbf{v_2}, \ldots, \mathbf{v_n}] \in \mathbf{Z}^{\mathbf{n}}_{\geq 0}$ defines the number of VMs of each type. The total provisioned CPU and memory are given by:

$$P = v \cdot S = [P_{\text{cpu}}, P_{\text{mem}}], \tag{8}$$

where $\mathbf{S} \in R^{n \times 2}$ is the specification matrix, and the total cost is:

$$C(v) = \sum_{i=1}^{n} v_i \cdot c_i = v \cdot c. \tag{9}$$

To balance cost and sufficiency, the optimization objective includes a penalty for under-provisioning as defined in (5). We further define per-unit cost efficiency as:

$$\text{eff}_i = \frac{c_i}{\text{cpu}_i + \text{mem}_i}, \tag{10}$$

which reflects the relative economic value of each VM type. This metric guides priority selection in heuristic or greedy baselines.

To assess provisioning effectiveness, we compute the resource waste ratio:

$$R = \frac{1}{T}\sum_{t=1}^{T} (u_t - p_t) \cdot \mathbb{I}(u_t > p_t), \tag{11}$$

where $\boldsymbol{u_t}$ and $\boldsymbol{p_t}$ denote the actual provisioned and predicted usage at time t , respectively, and $I(u_t > p_t) = 1$ when over-provisioning occurs, 0 otherwise.

This modeling framework provides a flexible foundation for applying discrete optimization methods, such as Integer-PSO, under real-world infrastructure constraints.

D. Resource Optimization and Cost Reduction

We evaluate the effectiveness of our forecasting-driven optimization framework across five prediction horizons: 1 h, 4 h, 8 h, 16 h, and 24 h. For each time step and predicted demand pair $(\hat{\boldsymbol{c}}, \hat{\boldsymbol{m}})$, the Integer-PSO algorithm selects a cost-optimal combination of VM types from the predefined Alibaba Cloud portfolio.

Fig. 2 illustrates a representative 1-hour prediction result. The upper subplots show predicted versus allocated CPU cores and memory (in GB), demonstrating close alignment with forecasted demand. The bottom subplot compares total costs, where shaded regions highlight the savings achieved by our method over a static over-provisioned baseline.

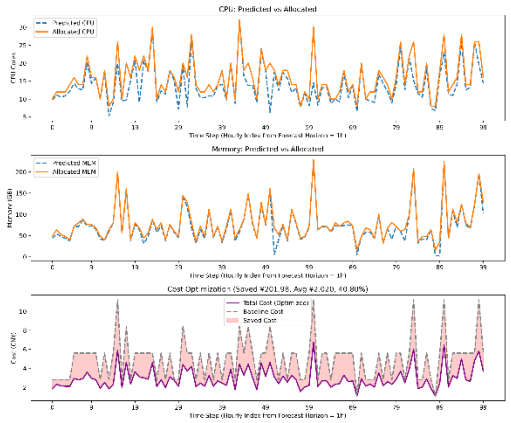

Fig. 2. Resource allocation and cost reduction results

On average, our method achieves a cost saving of ¥201.98 per 100 hourly decisions, corresponding to a mean saving rate of 40.80 %, while maintaining adequate resource provisioning. These results confirm that integrating short-term forecasts with cost-aware VM selection can significantly reduce unnecessary over-provisioning.

To assess robustness under different forecast granularities, Fig. 3 presents the optimization performance across all five prediction horizons. The stacked bars display the decomposed costs (optimized provisioning and saved cost), and the overlaid line illustrates the corresponding saving rate. The 8-hour horizon achieves the highest absolute savings, while saving rates consistently exceed 40 % across all horizons, demonstrating the adaptability of our method to diverse workload anticipation scenarios.

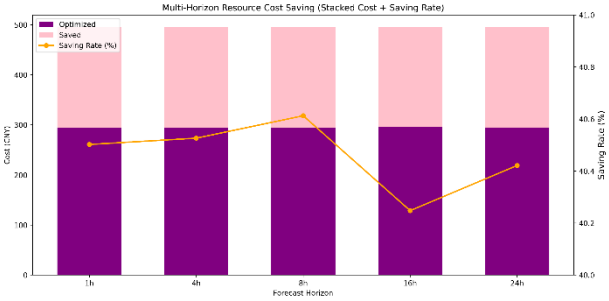

Fig. 3. Multi-horizon resource cost saving comparison

IV. Conclusion and Future Work

This paper presents a hybrid resource optimization framework for cloud infrastructures, integrating multi-horizon machine learning forecasting with integer-constrained Particle Swarm Optimization (Integer-PSO). By predicting CPU and memory demands over multiple future intervals and selecting cost-efficient VM configurations from a real-world portfolio, the proposed method significantly reduces over-provisioning and operational cost.

Experimental results on production-scale OpenStack telemetry demonstrate consistent cost reductions of approximately 40% across forecast horizons from 1 to 24 hours. The framework maintains alignment between allocated and forecasted resources, confirming its effectiveness in workload-aware provisioning. Furthermore, the method exhibits strong adaptability across varying prediction granularities, as shown by stable saving rates and optimal allocation patterns.

Future work will proceed along three key directions. First, we aim to extend the optimization model to incorporate additional resource dimensions such as I/O throughput and storage bandwidth. Second, we plan to integrate uncertainty-aware forecasting techniques to enhance robustness under volatile workload conditions. Third, we intend to deploy the proposed framework within real-time orchestration systems (e.g., Kubernetes, OpenStack Heat) to evaluate its effectiveness in dynamic, online scheduling scenarios.

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Combining Hierarchical Clustering and Multi-Stage Feature Selection to Identify Drug Resistance–Associated Single Nucleotide Polymorphisms in Mycobacterium Tuberculosis

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Abstract. **Feature selection is a key step in genomic data analysis. However, traditional global selection strategies often fail to capture lineage- or subpopulation-specific signals due to high cross-cluster variability. To overcome this limitation, we propose a novel framework that combines the hierarchical clustering with a multi-stage feature selection procedure to effectively balance global and local genetic patterns. Evaluation of the proposed method carried out on a genomic dataset including 4,044 samples of *Mycobacterium tuberculosis* strains for predicting their drug resistance to 13 antituberculosis drugs showed that the prediction accuracy of this procedure outperforms the one of the traditionally used tool TB-profiler for four of the five first-line drugs, and for the one drug, Pyrazinamide, the prediction data are close. At the same time, the results for prediction accuracy obtained using the compared approaches are equally distributed among the eight second-line drugs. These findings suggest that incorporating hierarchical clustering methods into feature selection can enhance the identification of meaningful genetic markers, providing a promising direction for genomic data analysis.**

Keywords: **GWAS, SNPs, Feature selection, M. tuberculosis, Drug Resistance**

I. INTRODUCTION

The COVID-19 pandemic seriously undermined the progress achieved in the fight against tuberculosis (TB) around the world, and the mortality rate from this disease increased for the first time in more than ten years [1]. However, after the end of the COVID-19 pandemic, TB still continues to be an extremely life-threatening infectious disease remaining in the top ten causes of death worldwide (https://deathmeters.info) and is the leading cause of death in patients with HIV and diabetes mellitus. The main reason for this is the emergence of drug-resistant strains of *Mycobacterium tuberculosis* (*Mtb*), especially in TB-endemic regions, making TB drug resistance a global public health problem. In this regard, genome-wide association studies on relationships between genomes and phenotypes that can provide a productive framework for the development of novel effective therapeutic agents against drug-resistant TB are of great scientific and practical importance.

When examining large genomic datasets in bioinformatics, one often confronts high complexity and heterogeneity, a scenario likewise prevalent in *Mtb* strain diversity. To capture the overall characteristics at a macro level, many studies still favor global models that optimize predictive performance across the entire dataset. However, such approaches often overlook underlying local structures. To account for complex local relationships, global models typically require increased complexity, such as the incorporation of nonlinear functions or deep networks, which not only substantially raises computational costs but also increase the risk of overfitting, ultimately compromising model performance in real-world applications [2]. In the context of *Mtb*, different lineages or sub lineages can exhibit distinct resistance profiles, which global models can easily overlook [3]. Alongside the challenge of capturing local structure, an equally pressing issue is the selection of relevant single nucleotide polymorphism (SNP) features, particularly as the number of candidate mutations can be immense [4]. Among various feature selection approaches, Incremental Feature Selection (IFS) and greedy algorithm have been widely used in previous studies [4, 5]. However, greedy strategies often result in locally optimal solutions, and IFS often leads to a large number of selected features, which may introduce redundancy and reduce the model interpretability [6].

Our approach differs from the conventional methods in two key aspects. First, by applying hierarchical clustering before feature selection, we mitigate cross-

cluster variability and enhance the detection of lineage-specific genetic markers that might otherwise be masked in global selection strategies. Second, we introduce a multi-stage feature selection pipeline that combines random forest-based feature importance, maximal information coefficient (MIC) evaluation, and backward selection, balancing predictive performance with computational efficiency.

II. Materials And Methods

A. Data

The original data sets used in this study included the drug susceptibility test data (DST) and whole genomes corresponding to these cases. These data were taken from the TB portal [7] presenting an excellent platform for investigations on drug-resistant TB. The DST data provide the verified information on resistance or sensitivity of the *Mtb* samples to the considered drugs. The data set *S* contained 4,044 samples and test data on their resistance to 13 drugs, including 5 first-line drugs, namely Ethambutol (EMB), Isoniazid (INH), Pyrazinamide (PZA), Rifampin (RIF), Streptomycin (SM), and 8 second-line drugs, such as Amikacin (AMK), Capreomycin (CM), Ethionamide (ETO), Kanamycin (KM), Levofloxacin (LFX), Moxifloxacin (MFX), Ofloxacin (OFX), Para-aminosalicylic acid (PAS).

B. GWAS problem

For a GWAS problem, we represent the SNPs in genomes of the dataset *S* as a matrix

$$X = (x_{i,j})_{m\times p}.$$

Here $\mathbf{x}_i = (x_{i,1}, x_{i,2}, \ldots, x_{i,p})$ is the *i*-th row of the matrix *X*, $x_{i,j} \in \{0,1\}$, which represents SNPs in the *i*-th sample of the dataset. The value $x_{i,j} = 0$ means that the sample does not contain the *j*-th mutation. If $x_{i,j} = 1$, then the sample contains the *j*-th mutation. Column *j* of the matrix *X* denoted as $\mathbf{x}_{0,j} = (x_{1,j}, x_{2,j}, \ldots, x_{m,j})^t$ represents a SNP s_j and demonstrates the *j*-th mutation in all samples of the dataset. Given drug *d*, the class label $\mathbf{y}_d = (y_1, y_2, \ldots, y_m)^t$, $y_k \in \{0,1\}, k = 1,2,\ldots,m,$ indicates the drug resistance status of the samples in the data set, 0 represents sensitive and 1 represents resistant.

C. Sample clustering

The first step is to compute the pairwise distance between all samples:

$$d(\mathbf{x}_i, \mathbf{x}_j) = \| \mathbf{x}_i - \mathbf{x}_j) \|_2 = \sqrt{\sum_{k=1}^{p} (x_{i,k} - x_{j,k})^2}, \quad \forall i, j \in \{1,2,\ldots,m\}.$$

The resulting distance matrix $D \in \mathbf{R}^{m\times m}$ is symmetric, with elements $d(\mathbf{x}_i, \mathbf{x}_j)$.

The hierarchical clustering process starts by treating each data point as its own cluster. Clusters are merged iteratively based on a linkage criterion. The Ward.D2 method [8] minimizes the total within-cluster variance (WSS, Within-Cluster Sum of Squares) at each step.

The hierarchical clustering process produces a dendrogram but does not specify the optimal number of clusters. To determine the best partition, the silhouette coefficient [9] is used as the evaluation metric. For each vector $\mathbf{x}_i$, the silhouette coefficient $s(i)$ is defined as:

$$s(i) = \frac{b(i) - a(i)}{\max\{a(i), b(i)\}},$$

where $a(i)$ is the average distance of $\mathbf{x}_i$ to all other vectors in the same cluster, $b(i)$ is the minimum average distance of $\mathbf{x}_i$ to all vectors in any other cluster.

Given a partition of vectors into *k* clusters, the silhouette coefficient of the partition is calculated as:

$$sc_k = \frac{1}{m}\sum_{i=1}^{m} s(i).$$

The optimal number of clusters k^* is chosen as:

$$k^* = \arg\max_k sc_k.$$

D. Feature selection

The Mean Decrease Accuracy (*MDA*) for a feature s_j is calculated by measuring the difference between the classification accuracy of the random forest model when s_j is included into consideration and when its values, i.e. the values of the vector $\mathbf{x}_{0,j}$ are changed randomly. Specifically, it is defined as:

$$MDA(s_j) = Acc_o(s_j) - Acc_c(s_j),$$

where $Acc_o(s_j)$ is the accuracy of the model computed for the validation set using only one feature s_j, and $Acc_c(s_j)$ is the accuracy after changing randomly the values of s_j. Features with $MDA(s_j) < 0$ are considered to have no significant contribution to the classification task.

Maximal Information Coefficient (*MIC*) [10] is a nonparametric exploration method of maximal information. For two continuous random variables *X* and *Y*, the mutual information is defined as

$$I(X;Y) = \int_x \int_y p(x,y) \log \frac{p(x,y)}{p(x)p(y)} dxdy,$$

where: $p(x,y)$ is the joint probability density function, $p(x)$ and $p(y)$ are the marginal probability density functions of X and Y, respectively.

Mutual information measures the statistical dependency between X and Y, with higher values indicating stronger dependency. The Maximal Information Coefficient is defined as the normalized maximum mutual information:

$$MIC(X,Y) = \max_{m,n} \frac{I_{m,n}(X;Y)}{\log \min\{m,n\}},$$

where $I_{m,n}(X;Y)$ is the mutual information calculated for a grid with m rows and n columns, $\log \min\{m,n\}$ is the normalization factor ensuring that the MIC values lie in the range [0, 1].

E. Algorithm of feature Selection workflow

In this study, we present a new feature selection workflow to get a reduced feature subset containing SNPs.

In Step 1, the entire set *M* of SNPs is entered into a random forest model, and the value of *MDA* is calculated for each SNP s_i. SNPs with *MDA* values less than or equal to 0 are considered non-informative or detrimental to the performance of the model and are removed from further consideration. The filtered SNP set M_f is represented as:

$$M_f = \{s_i |\ MDA(s_i) > 0\}.$$

Here M_f contains the SNPs that passed the *MDA* filtering step.

In Step 2, for each SNP $s_i \in M_f$, represented by the vector $\mathbf{x}_{0,i}$, the *MIC* value is calculated with respect to the cluster label. *MIC* shows the strength of the association between the SNP and the target label. The SNPs are ranked according to their *MIC* values in descending order, and the top *k* SNPs are selected. The resulting set of important SNPs M_{f_1} is denoted as:

$$M_{f_1} = \{s_1, s_2, \ldots, s_k |\ MIC(s_i),\ i = 1,2,\ldots k,\ \text{are among the top } k \text{ values}\}.$$

In Step 3, all possible SNP pairs (s_i, s_j) are generated for $s_i \in M_{f_1}$ and $s_j \in S$. For each pair such pair (s_i, s_j), the random forest model is trained using s_i and s_j as the only features. The F1-score of the model is calculated to evaluate the predictive power of the SNP pair.

The top n pairs with the highest F1-scores are selected for each s_i. Let us denote by M_{sel} the set of different SNPs belonging to these sets of selected pairs.

In the final step, remove from the selected set of SNPs M_{sel} some redundant features while retaining predictive performance. Starting with the initial feature subset $F_0 = M_{sel}$ a backward selection process is applied iteratively including the following steps:

1. Training a random forest model using the current feature subset F_t.
2. Calculating the F1-score of the model.
3. Identifying the least significant SNP in F_t based on either its importance or its contribution to the F1 score.
4. Removing the least significant SNP from the set F_t, resulting in the updated subset of characteristics F_{t+1}.

This process is repeated until the best prediction performance of the model is achieved, resulting in a final subset F^* of features:

$$F^* = \arg\max_t \text{F1-score}(F_t),$$

that contains an informative subset of SNPs obtained by the above procedure.

F. Performance evaluation

Several evaluation metrics, including the Recall, Precision, Accuracy, and F1-score, were used to evaluate the model performance.

$$\text{Precision} = \frac{TP}{TP+FP},\ \text{Recall} = \frac{TP}{TP+FN},$$
$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN},$$
$$\text{F1-score} = \frac{2 \times \text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}.$$

III. RESULTS

A. Characterization of the dataset

Table I presents the distribution of sensitive and resistant samples for each drug in the dataset.

TABLE I. CHARACTERIZATION OF THE DATASET

Drug	Resistance	Sensitive	Drug	Resistance	Sensitive
EMB	1459	2009	INH	2358	1343
PZA	652	623	RIF	2219	1474
SM	1631	715			
AMK	371	1237	CM	523	1714
ETO	164	180	KM	736	988
LFX	386	798	MFX	213	821
OFX	896	1400	PAS	150	1179

In this study, we performed 5-fold cross-validation (5-CV). To do this, all the microbe-disease associations were randomly divided into 5 equal portions, of which 4 portions were used to train the model, and the remaining portion 1 was used for testing. Additionally, the Synthetic Minority Over-sampling Technique (SMOTE) was used to balance the data for each training set of fold, while not altering the test set of fold.

B. Determination of the Optimal Number of Clusters (k)

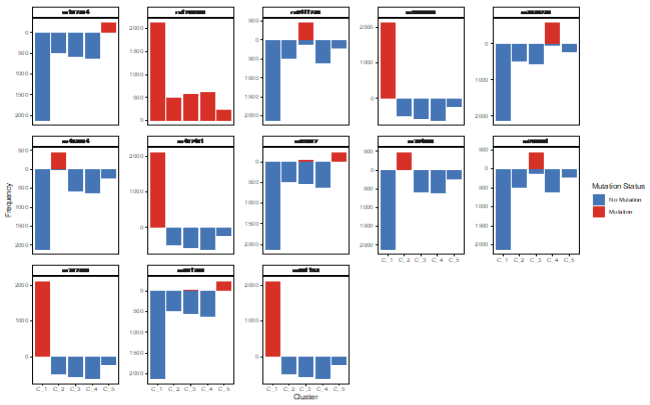
To find the optimal number of clusters k^*, the dendrogram was cut at different levels to produce clusters with $k = 2,3,\ldots,k_{\max}$ and the silhouette coefficient sc_k for each k was then calculated. The optimal number of clusters 5 was chosen as described in Section C. Sample clustering and Table II.

TABLE II. SILHOUETTE COEFFICIENT ANALYSIS FOR CLUSTER VALIDATION

Number of Clusters (*k*)	Silhouette Coefficient	Number of Clusters (*k*)	Silhouette Coefficient
2	0.463	7	0.305
3	0.429	8	0.294
4	0.472	9	0. 267
5	0.506	10	0.262
6	0.314		

The Silhouette Coefficient ranges from 0 to 1, where higher values indicate better-defined clusters. The optimal number of clusters is $k = 5$ with the highest coefficient of 0.506

As follows from Figure, 13 SNPs selected by feature selection exhibit different mutation patterns in the five clusters, supporting their usefulness as predictive markers for cluster classification. The average prediction accuracy of the model reached 98.3 % with 13 SNPs when a 5-fold cross-validation strategy was employed in the training process.



Distribution of mutation frequencies of 13 selected SNPs in five clusters. Each panel represents one SNP, with blue bars indicating the frequency of wild type (no mutation) and red bars indicating the frequency of mutation. The y-axis indicates the frequency of each variant type, while the x-axis indicates the cluster number (1–5). These 13 SNPs were identified through feature selection as predictive markers for cluster classification

C. Comparison with competitive baselines

We compared the efficiency of the developed algorithm with that of TB-Profiler [11] frequently used to process whole genome sequencing data to predict lineage and drug-resistance of *Mtb*. The prediction results of TB-Profiler v5.0.1 and the proposed algorithm for 13 drugs using the same dataset are given in Table III and IV. For four of the five first-line drugs, the developed method outperforms TB-profiler in accuracy of drug-resistance prediction, and for the one drug, Pyrazinamide (PZA), the prediction data are close (Table III). At the same time, analysis of the data from Table IV shows that the results for prediction accuracy obtained using the compared approaches are equally distributed among the eight second-line drugs.

TABLE III. COMPARISON OF THE DEVELOPED ALGORITHMS WITH TB-PROFILER TOOL FOR PREDICTION OF RESISTANCE TO FIRST-LINE ANTI-TB DRUGS

Drug	Recall	Precision	F1	Accuracy	Method
EMB	85.7 %	75.5 %	80.3 %	82.3 %	Our method
	78.3 %	76.9 %	77.6 %	80.9 %	Tb-profiler
INH	94.9 %	98.5 %	96.6 %	95.8 %	Our method
	82.2 %	98.1 %	89.4 %	87.6 %	Tb-profiler
PZA	85.9 %	72.6 %	78.7 %	76.2 %	Our method
	67.8 %	83.1 %	74.7 %	76.5 %	Tb-profiler
RIF	94.9 %	95.0 %	94.9 %	93.9 %	Our method
	84.8 %	98.0 %	90.9 %	89.8 %	Tb-profiler
SM	90.7 %	93.7 %	92.1 %	89.3 %	Our method
	86.5 %	95.3 %	90.7 %	87.6 %	Tb-profiler

TABLE IV. COMPARISON OF THE DEVELOPED ALGORITHMS WITH TB-PROFILER TOOL FOR PREDICTION OF RESISTANCE TO SECOND-LINE ANTI-TB DRUGS

Drug	Recall	Precision	F1	Accuracy	Method
AMK	68.5 %	85.2 %	75.9 %	90.0 %	Our method
	72.5 %	71.5 %	72.0 %	87.0 %	Tb-profiler
CM	56.0 %	74.0 %	63.8 %	85.1 %	Our method
	67.7 %	78.1 %	72.5 %	88.0 %	Tb-profiler
ETO	61.6 %	62.7 %	62.2 %	64.2 %	Our method
	77.4 %	55.9 %	65.0 %	60.2 %	Tb-profiler
KM	71.5 %	75.9 %	73.6 %	78.1 %	Our method
	76.6 %	78.3 %	77.5 %	81.0 %	Tb-profiler
LFX	60.4 %	75.2 %	67.0 %	80.6 %	Our method
	88.9 %	75.7 %	81.8 %	87.1 %	Tb-profiler
MFX	37.6 %	62.5 %	46.9 %	82.5 %	Our method
	88.3 %	50.5 %	64.3 %	79.8 %	Tb-profiler
OFX	66.2 %	82.4 %	73.4 %	81.3 %	Our method
	91.2 %	84.6 %	87.8 %	89.8 %	Tb-profiler
PAS	36.7 %	59.1 %	45.3 %	90.0 %	Our method
	25.3 %	30.2 %	27.5 %	85.0 %	Tb-profiler

IV. CONCLUSION

In this study, we proposed a novel workflow that combines hierarchical clustering with a multi-stage SNP selection procedure to predict phenotypes of interest and used this approach for prediction of drug-resistant phenotypes of *Mtb*. In the proposed method,

hierarchical clustering is used to assign each isolate to a specific cluster based on the whole genome information, and the effective SNPs are found by the feature selection algorithm for random forest to identify the cluster to which the sample belongs. A multi-tier feature selection strategy is then applied in which mean descent accuracy in random forest is used to filter out SNPs with noise or misleading information followed by ranking the remaining SNPs via the Maximum Information Coefficient. The top-ranked k SNPs expanded by pairing each SNP with up to n additional SNP partners form an extended set M_{sel}. Finally, a backward selection procedure prunes redundant or weakly contributing SNPs, leading to a compact yet highly discriminative feature subset. The developed model achieves better prediction accuracy with fewer SNPs compared to the generally used TB-profiler tool, facilitating easier interpretation and follow-up potential studies on the biological relevance of the identified markers.

ACKNOWLEDGMENT

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Design and Verification of a Centralized Multi-Agent Visual SLAM System Based on Cloud-Native Architecture

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Abstract. **Addressing the challenges of map topology fragmentation, cumulative pose drift,and edge computing resource bottlenecks in multi-robot collaborative visual SLAM systems, this paper proposes a cloud-native multi-agent collaborative SLAM architecture. By offloading computationally intensive tasks such as ORB feature extraction and g2o pose graph optimization to cloud-based heterogeneous computing nodes, we constructed a dual-robot collaborative mapping system with ROS-based communication and conducted simulation experiments. Experimental results prove that compared with the traditional ORB-SLAM3 framework, the proposed architecture enhances pose estimation stability and map fusion performance in dynamic environments while reducing dependence on edge device computing resources. This architecture provides a high-precision solution for missions such as UAV swarm cooperative reconnaissance, meeting real-time requirements for SWaP-constrained platforms in complex environments.**

Keywords: **Cloud-native architecture, Multi-agent SLAM, Map fusion**

I. INTRODUCTION

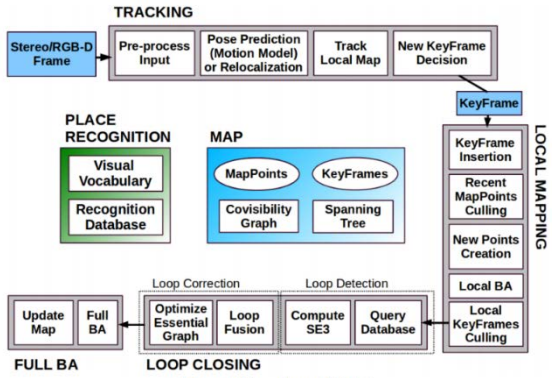
Simultaneous Localization and Mapping (SLAM) serves as the fundamental technology enabling autonomous navigation for mobile robots. By capturing environmental information through cameras for real-time localization and map construction, V-SLAM offers advantages such as cost-effectiveness and rich information [1–3]. However, single-robot SLAM systems face limitations in computational resources and cumulative localization drift when processing large-scale complex environments, hindering their efficiency for demanding tasks. The global map construction in multi-robot collaborative SLAM relies on the fusion of local maps from individual robots – a process involving intricate data association and optimization computations [4]. This approach suffers from high computational resource consumption, low mapping efficiency, and insufficient real-time performance. To address these challenges, this paper proposes a cloud server-based multi-robot collaborative SLAM framework. By optimizing video streaming protocols and cloud-based map fusion algorithms, the framework enables efficient, low-latency collaborative localization and mapping.

II. RESEARCH ACTUALITY

A. ORB-SLAM

ORB-SLAM, as a feature-based visual SLAM system, has continuously advanced in algorithmic robustness and precision optimization in recent years. It innovatively constructs a multi-layered optimization framework incorporating a Covisibility Graph and an Essential Graph. The backend integrates loop closure detection results through pose graph optimization, effectively reducing computational complexity while suppressing error drift.

The latest iteration, ORB-SLAM3, further extends into a multi-modal system supporting monocular, stereo, and RGB-D cameras. It introduces an enhanced bag-of-words-based loop closure detection module, significantly improving relocalization capabilities in complex scenes.



(a) System Threads and Modules.

Fig. 1. ORB SLAM2 System flowchart

B. *Multi-Robot Collaborative Localization Algorithms*

The core challenges in multi-robot collaborative localization lie in communication architecture and data fusion strategies. The CoSLAM system proposed by Zou et al. [5] achieves monocular camera group collaboration through scene overlap detection. However, it requires enforced synchronization and unified scene initialization, limiting individual autonomy and relying on GPU acceleration, which hinders scalability for multi-mobile robot applications. The C2TAM system developed by Riazuelo's team [6], based on the PTAM framework, adopts a centralized architecture for keyframe fusion but lacks loop closure mechanisms. Moreover, expanding map scales inevitably impose bandwidth pressure due to server-side global map retransmission, diminishing its practical utility. Morrison et al.'s MOARSLAM [7] supports independent multi-device mapping but restricts the server to map storage and sharing without global map fusion, failing to fully leverage collaborative localization advantages. These systems share a critical limitation: the inability to construct a globally consistent, shared map in real time.

C. *Multi-robot collaborative mapping algorithm*

Multi-robot collaborative mapping requires solving the challenges of map alignment and fusion. Early approaches achieved partial map stitching through robot encounter detection, but low scene overlap rates resulted in insufficient fusion efficiency [9]. Scene recognition algorithms based on bag-of-words models (e.g., DBoW2 [10]) improved loop closure detection accuracy through visual word matching, yet their neglect of spatial feature relationships made them prone to mismatches. Recent studies propose enhanced solutions, such as employing point-line word pair models to strengthen scene discriminability and integrating ICP algorithms to optimize pose transformation matrices, effectively improving map fusion accuracy. Additionally, dense point cloud-based mapping methods generate global maps through keyframe tracking models and filtering algorithms, but their high computational resource consumption still necessitates real-time performance optimization.

In summary, while existing research has advanced multi-robot collaborative SLAM in architecture design and algorithmic optimization, balancing communication efficiency, fusion accuracy, and real-time performance remains challenging. The cloud-based collaborative framework proposed in this paper offers a novel solution through lightweight communication protocols and efficient optimization strategies.

III. System Architecture Documentation

A. *Cloud-edge collaborative computing frameworks*

This study innovatively constructs a cloud-native architecture-driven multi-agent visual SLAM system, overcoming the deployment limitations of traditional SLAM technologies on resource-constrained edge devices through an end-cloud-end heterogeneous computing architecture. The system establishes a real-time collaborative mechanism between edge devices and cloud services, leveraging containerization technology to achieve elastic modular encapsulation of core SLAM algorithms. In architectural design, terminal nodes focus on real-time sensor data acquisition and feature preprocessing, while the cloud platform decouples SLAM tasks via dynamic computational resource scheduling and delivers pose estimation feedback through standardized data interface protocols. The three-layer heterogeneous computing architecture of the system is structured as follows:

- Edge Perception Layer: Built on the TurtleBot4B mobile robot platform integrated with Intel OAK-D Pro depth vision sensors, it runs lightweight visual odometry processes for real-time ORB feature detection and local keyframe sequence maintenance.
- Data Transmission Layer: Utilizes ROS topic-based communication to establish video data channels.
- Cloud Processing Layer: Deploys NVIDIA A100 computing node clusters to execute multi-dimensional ORB feature matching, cross-robot pose graph optimization, and global map fusion, constructing a distributed nonlinear optimization engine based on the g2o framework.

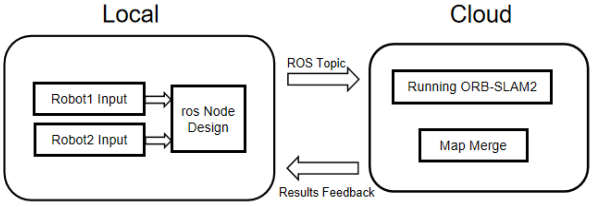


Fig. 2. Flowchart of multi-agent SLAM system based on cloud-native architecture

B. *Map fusion computing framework*

The map fusion computational framework system achieves efficient conversion from 3D point clouds to 2D occupancy grids through customized ROS nodes. These nodes subscribe to dense point cloud data streams (PCD) in real time, perform data compression and grid processing, and publish standardized occupancy grid maps under a unified namespace. The algorithm design follows these principles:

1) Dynamic probabilistic modeling: Grid cells are initialized to an unknown state (probability value 0.5), with state values dynamically updated based on valid point cloud density.

2) Incremental optimization: A streaming data processing mode replaces global recomputation with localized updates, effectively reducing time complexity.

This approach utilizes orthographic projection for dimensionality reduction from 3D to 2D, significantly reducing data throughput while maintaining obstacle recognition accuracy. The system architecture supports dynamic scalability, enabling collaborative operations for additional robots by adding ROS node instances.

The system implements real-time map fusion through distributed ROS nodes, with its core consisting of a coordinate transformation module and a grid merging module. The mapping relationship between Robot 1's local coordinates and the global coordinates is achieved through inverse transformation matrices:

$$\begin{pmatrix} x \\ y \\ 1 \end{pmatrix} = \begin{pmatrix} \cos\theta & \sin\theta & -x_0\cos\theta - y_0\sin\theta \\ -\sin\theta & \cos\theta & x_0\sin\theta - y_0\cos\theta \\ 0 & 0 & 1 \end{pmatrix} \begin{pmatrix} x' \\ y' \\ 1 \end{pmatrix}. \quad (1)$$

The map fusion process is as follows.

Algorithm: Merge Maps Algorithm

Input: OccupancyGrid grid1, grid2 // Maps from two robots

Output: OccupancyGrid grid // Final merged map

```
1. grid.header ← grid1.header
2. grid.info ← grid1.info
3. for i ← 0 to grid1.data.size do
4.    if grid1.data[i] ≠ 0.5 ∧ grid2.data[i] = 0.5 then
5.       grid.data[i] ← grid1.data[i]
6.    else if grid1.data[i] = 0.5 ∧ grid2.data[i] ≠ 0.5 then
7.       grid.data[i] ← grid2.data[i]
8.    else if grid1.data[i] = 0.5 ∧ grid2.data[i] = 0.5 then
9.       grid.data[i] ← 0.5
10.   else
11.      grid.data[i] ← (grid1.data[i] + grid2.data[i]) / 2
12.   end if
13. end for
```

IV. Experiment and Results.

A. *Authors and Affiliations*

This section verifies the performance effectiveness of the SLAM system based on the cloud-native architecture by building a cloud robot experimental platform. The experimental platform is built as follows: The cloud node is configured with an Intel Core i9-13900H processor (32GB memory, Ubuntu 18.04 LTS system), and the local end adopts an AMD Ryzen 5 4600H mobile processor (8GB memory, the same version of the operating system). The mobile robot platform selects the TurtleBot4 intelligent vehicle. Due to the limitations of the site and equipment, the TurtleBot4 simulation environment was built using Gazebo. The test environment selects typical indoor structured feature scenarios to evaluate the robustness of the system.

Fig. 3. Simulation experiment 3D map

B. *Experimental result*

After the cloud architecture based on SLAM was completed, we tested the operation effect of the system. The operation process of the test results is shown in the Figure.

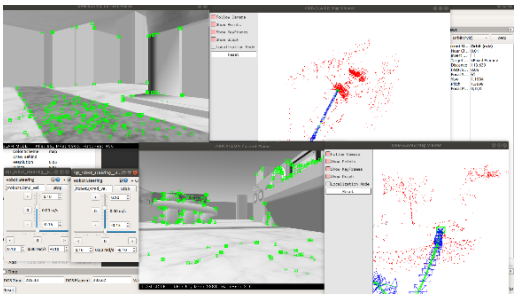


Fig. 4. SLAM Operation Diagram of the Simulated Experiment

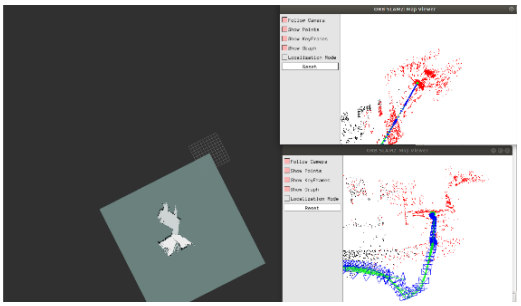


Fig. 5. Map Fusion Operation Diagram of the Simulated Experiment

The experimental results demonstrate that the system successfully achieved real-time collaborative mapping functionality for multiple robots, effectively validating the technical advantages of the centralized cloud-based architecture in reducing edge-side computational load and enhancing the robustness of collaborative systems. To further verify the universality of the experimental conclusions, this study conducted comparative experiments between cloudless architecture systems and cloud-based architecture systems. Data indicates that while both architectures meet basic real-time requirements, their performance differs significantly: the cloudless architecture system maintained only approximately 20 FPS in adaptive mode during simulations, whereas the cloud-based architecture system operated stably above 60 FPS. Notably, constrained by local memory capacity, the cloudless architecture system experienced memory overflow and process termination in three independent trials when keyframes reached 1,100 frames. In contrast, the cloud-based architecture system not only completed mapping tasks successfully but also accumulated keyframes stably to around 2,500 frames.

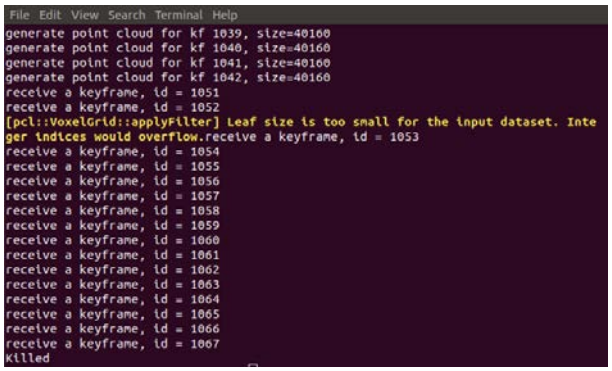


Fig. 6. Number of Keyframes at the Terminal in the Cloudless Architecture System

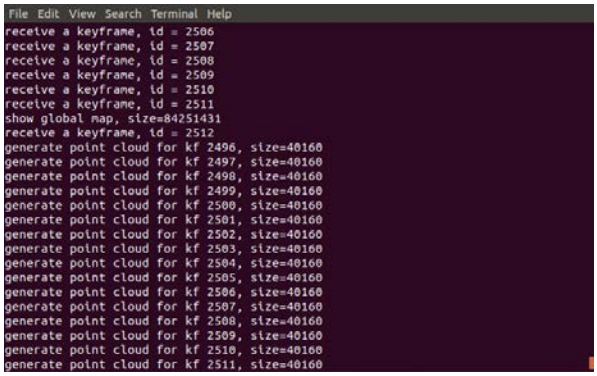


Fig. 7. Number of Keyframes at the Terminal in the Cloud-Based Architecture System

V. CONCLUSION

This study addresses the core challenges of traditional visual SLAM systems – insufficient computational power, poor real-time performance, and weak environmental adaptability in resource-constrained devices (e.g., small unmanned platforms) – by proposing a collaborative computing framework based on a cloud-native architecture. Through the establishment of an "edge-cloud" heterogeneous computing paradigm, hierarchical decoupling and dynamic scheduling of multi-agent SLAM tasks are achieved. Preliminary experiments validate the feasibility of the proposed approach.

The engineering significance of this research lies in providing scalable, lightweight SLAM solutions for mobile platforms such as UAVs and ground reconnaissance robots. By leveraging cloud computing empowerment, edge devices only need to handle data acquisition and decision execution, thereby enhancing deployment flexibility for unmanned systems in mission-critical scenarios like battlefield reconnaissance and disaster response operations.

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Joint Range-Angle Unambiguous Estimation Based on DAPSO-OMP for FDA-MIMO Radar

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***Abstract*. Radar systems typically adopt one-dimensional measurement methods for range and angle detection, meaning that range and angle estimation are usually performed separately. This approach lacks the capability for real-time integrated processing within a unified joint framework, thereby limiting the radar's ability to achieve rapid and precise positioning in complex multi-target environments. In contrast, FDA-MIMO radar systems can utilize both range and angle dimensions embedded in steering vectors to realize joint range-angle estimation, thereby delivering more comprehensive and accurate target localization in multi-target scenarios.**

This paper proposes a Double-precision Adaptive Particle Swarm Optimization (DAPSO) combined with Orthogonal Matching Pursuit (OMP) algorithm tailored for FDA-MIMO radar systems. The proposed DAPSO-OMP algorithm aims to overcome the limitations of subspace-based algorithms under small snapshot sizes and low signal-to-noise ratio (SNR) conditions. By integrating DAPSO's global optimization capability with OMP's sparse representation advantages, our method achieves significantly enhanced efficiency and unambiguous joint range-angle estimation.

***Keywords:* FDA-MIMO radar, joint range-angle estimation, DAPSO-OMP algorithm, unambiguous range**

I. INTRODUCTION

Subspace-based algorithms are a classical category of radar parameter estimation methods. Early subspace-based algorithms are constrained by the Rayleigh limit, resulting in limited resolution within a radar beamwidth and difficulty in estimating multiple targets within the same beam [1], 2]. Additionally, the performance of subspace-based algorithms relies on the number of snapshots, requiring sufficient snapshots to accurately estimate the covariance matrix, thereby effectively decomposing the signal subspace and noise subspace [3]. However, in limited observation time windows, radars often struggle to acquire a large number of snapshots simultaneously. This leads to insufficient accuracy in covariance matrix estimation, hindering effective separation of the signal and noise subspaces, and ultimately degrading the final estimation precision.

Compared with subspace-based algorithms, compressed sensing methods demonstrate superior advantages in processing high-dimensional redundant echo data from FDA-MIMO radar systems, providing a novel approach for joint range-angle estimation [4]. Compressed sensing leverages signal sparsity to achieve signal reconstruction at sampling rates below the Nyquist criterion, i.e., the signal can be represented by a small number of non-zero coefficients in a specific basis or transform domain [5]. This characteristic enables accurate reconstruction of high-dimensional signals using only limited measurements. Consequently, compressed sensing significantly reduces the required sampling data volume and

eliminates covariance matrix computations of echo data, making it particularly suitable for real-time monitoring and rapid imaging applications [6].

This paper proposes a DAPSO-OMP (Double-precision Adaptive Particle Swarm Optimization-Orthogonal Matching Pursuit) algorithm for FDA-MIMO radar. We derive the range ambiguity-resolved signal model for FDA-MIMO radar. Based on this signal model, the proposed DAPSO-OMP algorithm adopts a dual-precision iterative strategy to enhance convergence speed and global optimal solution search capability, thereby accelerating the optimization process of OMP while reducing computational complexity. Finally, through simulation experiments, we verify that the proposed DAPSO-OMP algorithm improved estimation accuracy, and enhanced robustness compared to PSO-OMP and conventional OMP algorithms.

II. Signal Model

A. Signal Model of FDA-MIMO Radar

The geometric configuration of FDA-MIMO radar is illustrated in Fig. 1. Consider a colocated FDA-MIMO radar system with M transmitting elements and N receiving elements, where both the transmitter and receiver employ half-wavelength spaced uniform linear arrays. Each transmitting element operates at a frequency offset increment Δf_m relative to the carrier frequency.

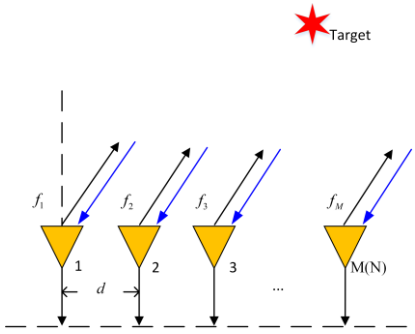


Fig. 1. The geometric configuration of FDA-MIMO radar

Consequently, the transmit frequency of the m-th element can be expressed as

$$f_m = f_0 + (m-1)\Delta f_m, m = 1, 2, \cdots, M, \quad (1)$$

where f_0 denotes the reference carrier frequency, the transmit signal of the m -th transmitting element is

$$s_m(t) = \sqrt{\frac{E}{M}}\mathrm{u}\left(\frac{t}{T_p}\right)\phi_m(t)\,\mathrm{e}^{j2\pi f_m t}, \quad (0 \le t \le T_p)$$
$$\mathrm{u}\left(\frac{t}{T_p}\right) = \begin{cases} 1, & 0 < t < T_p \\ 0, & else \end{cases} \quad (2)$$

where E represents the total transmitted energy, T_p denotes the pulse width, $\phi_m(t)$ indicates the complex envelope form of the transmitted signal from the m-th antenna array element. To ensure that the transmitted signals meet specific orthogonality requirements, $\phi_m(t)$ adopts code-division multiplexing orthogonal waveforms. Under the condition of orthogonal transmitted waveforms, after scattering from a point target (R,θ) in the far-field by the signals emitted from M transmitting array elements, the echo signal arriving at the n -th receiving array element is

$$\begin{aligned} x_n(t) &= \xi_d \sum_{m=1}^{M} \phi_m(t-\tau_{m,n})\,\mathrm{e}^{j2\pi f_m(t-\tau_{m,n})} \\ &\approx \xi_d \sum_{m=1}^{M} \phi_m(t-\tau_0)\,\mathrm{e}^{j2\pi f_m(t-\tau_{m,n})} \\ &= \xi_d\,\mathrm{e}^{j2\pi f_0(t-\tau_0)}\,\mathrm{e}^{j2\pi\frac{d}{\lambda_0}(n-1)\sin\theta} \times \\ &\quad \sum_{m=1}^{M} \phi_m(t-\tau_0)\,\mathrm{e}^{j2\pi(m-1)\Delta f_m(t-\tau_0)}\,\mathrm{e}^{j2\pi\frac{d}{\lambda_0}(m-1)\sin\theta} \end{aligned} \quad (3)$$

where ξ_d denotes the complex scattering coefficient of the point target, $\tau_{m,n} = [2R - d(n-1)\sin\theta - d(m-1)\sin\theta]/c$ represents the round-trip propagation delay of the transmitted signal from the m -th transmitting array element scattered by the target to the n -th receiving array element, c is the speed of light, d is the array element spacing, $\lambda_0 = c/f_0$ denotes the wavelength, and $\tau_0 = 2R/c$ indicates the common delay time. Under the far-field narrowband assumption, $\phi_m(t-\tau_{m,n}) \approx \phi_m(t-\tau_0)$. Since $f_0 \gg \Delta f_m$, the echo signal from the n -th receiving array element is processed through matched filtering, yielding the following expression

$$\begin{aligned} y_{m,n} &= \xi\phi_{m,n}\,\mathrm{e}^{-j4\pi\frac{\Delta f_m}{c}(m-1)R}\,\mathrm{e}^{j2\pi\frac{d}{\lambda_0}(m-1)\sin\theta} \\ &\quad \times \mathrm{e}^{j2\pi\frac{d}{\lambda_0}(n-1)\sin\theta} \end{aligned} \quad (4)$$

where $\xi = \xi_d\,\mathrm{e}^{-j4\pi R/\lambda_0}$ denotes the post-matched-filtering complex scattering coefficient of the point scatterer, $\phi_{m,n}$ representing the output of the n -th array element matched with the m -th transmitted waveform. For a colocated FDA-MIMO radar, the matching waveform on the receiving array element is the transmitting waveform, and the echo signals received by each receiving array element througth matched filter, represented as

$$\begin{aligned} \mathbf{Y} &= \left[y_{11}, y_{12}, \cdots, y_{1N}, y_{21}, \cdots, y_{MN}\right]^T \\ &= \xi \cdot \mathbf{\Phi} \odot \mathbf{b}(\theta) \otimes \mathbf{a}(R,\theta) \end{aligned} \quad (5)$$

where $\mathbf{\Phi}=\left[\phi_{1,1},\phi_{1,2},\cdots,\phi_{M,N}\right]^T\in\mathbb{C}^{MN\times 1}$ represents the waveform output through the matched filter, $\otimes$ denotes the Kronecker product. $\mathbf{a}(R,\theta)\in\mathbb{C}^{M\times 1}$ and $\mathbf{b}(\theta)\in\mathbb{C}^{N\times 1}$ are respectively defined as the transmit steering vector and receive steering vector, given by

$$\begin{aligned}\mathbf{a}(R,\theta)&=\mathbf{a}_R(R)\odot\mathbf{a}_\theta(\theta)\\&=\left[1,\mathrm{e}^{-j4\pi\frac{\Delta f_2}{c}R},\cdots,\mathrm{e}^{-j4\pi\frac{\Delta f_m}{c}(M-1)R}\right]^T\odot\\&\quad\left[1,\mathrm{e}^{j2\pi\frac{d}{\lambda_0}\sin\theta},\cdots,\mathrm{e}^{j2\pi\frac{d}{\lambda_0}(M-1)\sin\theta}\right]^T\end{aligned}\tag{6}$$

$$\mathbf{b}(\theta)=\left[1,\mathrm{e}^{j2\pi\frac{d}{\lambda_0}\sin\theta},\cdots,\mathrm{e}^{j2\pi\frac{d}{\lambda_0}(N-1)\sin\theta}\right]^T\tag{7}$$

where $\odot$ denotes the Hadamard product, $\mathbf{a}_R(R)\in C^{M\times 1}$ and $\mathbf{a}_\theta(\theta)\in C^{M\times 1}$ respectively represent the transmit range and angle steering vectors. Compared to MIMO radar and FDA radar, the transmit steering vector of FDA-MIMO radar simultaneously incorporates both range and angle dimensional information of target, endowing FDA-MIMO radar with the capability to distinguish targets at different ranges and angles in the transmit dimension. When uniform weighting is applied to the receiving array, the range-angle two-dimensional receive beampattern of the FDA-MIMO radar can be expressed as

$$Y(R,\theta)=\sum_{n=1}^{N}\sum_{m=1}^{M}\xi\,\mathrm{e}^{-j4\pi\frac{(m-1)\Delta f_m}{c}R}\,\mathrm{e}^{j2\pi\frac{d(m-1)\sin\theta}{\lambda_0}}\,\mathrm{e}^{j2\pi\frac{d(n-1)\sin\theta}{\lambda_0}}\tag{8}$$

When the frequency offset between transmitting array elements is configured as a linear frequency increment $\Delta f_m=(m-1)\Delta f$, the expression can be further simplified to

$$Y(R,\theta)=\xi\,\frac{\sin\left[M\pi\left(\frac{2\Delta f}{c}R-\frac{d}{\lambda_0}\sin\theta\right)\right]}{\sin\left[\pi\left(\frac{2\Delta f}{c}R-\frac{d}{\lambda_0}\sin\theta\right)\right]}\,\frac{\sin\left(N\pi\frac{d}{\lambda_0}\sin\theta\right)}{\sin\left(\pi\frac{d}{\lambda_0}\sin\theta\right)}\tag{9}$$

Analyzing the above expression, in the FDA-MIMO radar receive beampattern, since the angle parameter θ independently appears in the final term of the expression, the angle is uniquely determined. Consequently, the range and angle parameters are decoupled in the second term. However, a periodic ambiguity arises in the range dimension, with the range ambiguity interval defined as $R_u=c/2\Delta f$.

When each transmitting array element of the radar applies a random nonlinear frequency offset Δf_m to the carrier frequency, the transmitted frequency of the m-th transmitting array element is formulated as

$$\begin{aligned}f_m&=f_0+(m-1)\Delta f_m\\&=f_0+(m-1)\Psi(a_m)\Delta f,\ m=1,2,\cdots,M\end{aligned}\tag{10}$$

where $\boldsymbol{\alpha}_m=[a_1,a_2,\cdots,a_M]^T$ denotes a random vector variable, the scalar component $a_1,a_2,\cdots,a_M$ follows a uniform distribution, and Ψ represents a logarithmic nonlinear operator. Under the condition of random nonlinear frequency offsets, Equation (8) can be expressed as

$$Y(R,\theta)=\sum_{n=1}^{N}\sum_{m=2}^{M}\xi^{\dagger}\,\mathrm{e}^{j2\pi\frac{d(n-1)}{\lambda_0}\sin\theta}\,\mathrm{e}^{-j2\pi(m-1)\left[\frac{2\Delta f_m}{(m-1)c}R-\frac{d}{\lambda_0}\sin\theta\right]}\tag{11}$$

Analysis of the above expression demonstrates that the maximum unambiguous range R_u grows significantly as the number of transmitting array elements M is increased. Theoretically, R_u can extend to infinity, thereby achieving complete range ambiguity resolution

B. DAPSO-OMP Algorithm

The Double-Precision Adaptive Particle Swarm Optimization Orthogonal Matching Pursuit (DAPSO-OMP) algorithm improves the velocity and position update equations of the Adaptive Particle Swarm Optimization (APSO) method by introducing a dual-precision iterative strategy. This enhancement significantly increases the convergence rate and global optimum search capability of the algorithm. The modified velocity and position update equations are formulated as

$$\begin{cases}w_d^n=w_{d,\max}-(w_{d,\max}-w_{d,\min})\times n/T\\v_i^{n+1}=w_d^n v_i^n+c_{d,1}\gamma_1(pbest_i^n-s_i^n)+c_{d,2}\gamma_2(gbest_i^n-s_i^n)\\s_i^{n+1}=s_i^n+v_i^{n+1}\end{cases}\tag{12}$$

where v_i^n denotes the velocity of the i-th particle at the n-th iteration, s_i^n represents the position of the i-th particle at the n-th iteration, and w_d^n indicates the inertia weight under the d-th precision level at the n-th iteration. $w_{d,\max}$ and $w_{d,\min}$ respectively denote the maximum and minimum values of the inertia weight under the d-th precision level. $c_{d,1}$ and $c_{d,2}$ are the learning factors corresponding to the d-th precision level. γ_1 and γ_2 represent random numbers within the

interval [0,1]. $pbest_i^n$ signifies the personal best position of the i-th particle up to the n-th iteration, while $gbest^n$ denotes the global best position of the entire swarm up to the n-th iteration. T specifies the maximum number of iterations.

During the initial search phase, the inertia weight and learning factors of the first precision level are set to larger values, enabling particles to perform broad exploration with higher velocity and larger step sizes. At this stage, particles adaptively update their velocities and positions for coarse-grained search. Each iteration records the current best fitness value u_n, and calculates the difference Δu between the best fitness values of two consecutive iterations. When Δu falls below the tolerance threshold tol, the counter cnt is incremented by 1. If the counter reaches the predefined threshold $cnt = q$, the global particle positions contract to the neighborhood of the current best fitness $gbest^n$. Subsequently, the velocity and position updates transition to the parameter settings of the second precision level, initiating fine-grained search with reduced step sizes. The iterative process terminates when the counter $cnt = 2q$ or the iteration count $n = T$, outputting the optimal fitness value $gbest^n$ at convergence.

Compared to PSO and APSO, the DAPSO algorithm significantly enhances the global optimum search capability and accelerates the convergence rate of the OMP algorithm. This methodology enables the discovery of superior solutions within fewer iterations, effectively mitigating APSO's susceptibility to premature local convergence. By integrating DAPSO's optimization strategy, the OMP algorithm achieves more efficient residual error minimization during signal reconstruction, thereby improving reconstruction accuracy. Through its high-efficiency particle update mechanism, DAPSO reduces the computational complexity of OMP in identifying optimal atoms, substantially enhancing overall algorithmic efficiency.

III. Simulation Results

This section verifies the joint range-angle estimation performance of the DAPSO-OMP algorithm for multi-target under small snapshot counts and low SNR conditions. Based on the range ambiguity-resolved signal model, the range ambiguity resolution capability of DAPSO-OMP is further verified. The simulation parameters for the FDA-MIMO radar and grid search ranges are consistent with those listed in Table I, including a range-domain search resolution of 10 m and an angle-domain search resolution of 1º.

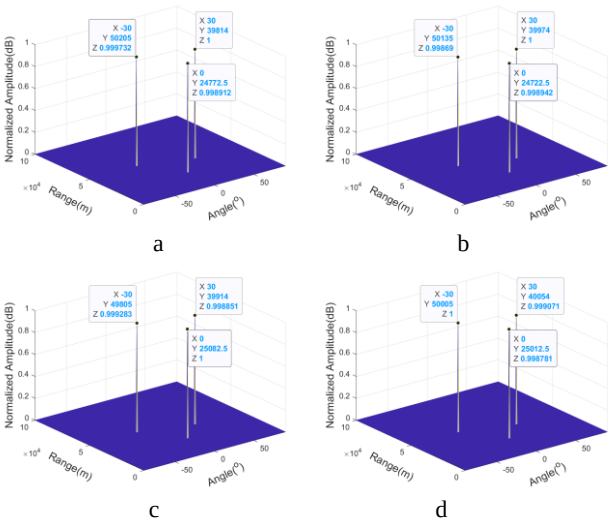
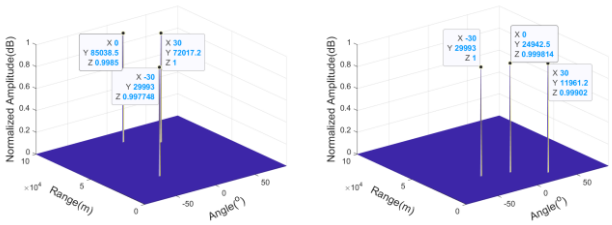


Fig. 2. Parameter estimation results of DAPSO-OMP algorithm: (1, –10 dB) (a), (1, 0 dB) (b), (20, –10 dB) (c), (20, 0 dB) (d)

Considering that there are three point targets located at (14 km, 30º), (25 km, 0º), and (50 km, –30º) in the space, in order to verify the small snapshot and low signal-to-noise ratio performance of the DAPSO-OMP algorithm, the number of snapshots and SNR for the four experiments are set to (1, –10 dB), (1, 0 dB), (20, –10 dB), and (20, 0 dB), respectively. Figs. 2 represent the estimation results of each experiment. The results show that under the condition of single snapshot and low SNR, the DAPSO-OMP algorithm can still accurately estimate the range-angle parameters of the three targets, and the estimation error gradually decreases with the increase of snapshot number and SNR. Therefore, the DAPSO-OMP algorithm has the ability to accurately detect multi-target range-angle parameters under small snapshot conditions.

TABLE I. Simulation Parameters

Parameters	Symbols	Values
transmitting elements	M	8
receiving elements	N	8
element spacing	d	0.0075 m
Range Domain Search Range	R_d	[0,100 km]
Angle Domain Search Range	Θ_d	[–90º, 90º]
carrier frequency	f_0	10 GHz
frequency offset reference	Δf	100 KHz
signal bandwidth	B	5 MHz
pulse repetition frequency	f_r	4 KHz
Sampling frequency	f_s	15 MHz



a b

Fig. 3. Parameter estimation of different frequency offset: linear frequency offset (a), random logarithmic frequency offset (b)

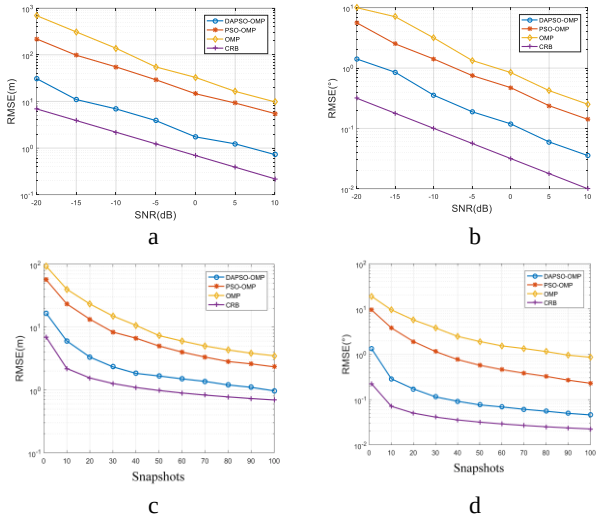
In order to verify the ability of the DAPSO-OMP algorithm based on the distance ambiguity model to solve distance ambiguity, we conducted two sets of simulation experiments with different frequency offsets. The first set of experiments used linear frequency offset, and the second set of experiments used the proposed random logarithmic frequency offset. The number of snapshots L = 1 and the SNR = 0 dB. Due to the maximum unambiguous range of the FDA-MIMO radar being 25 km, three point targets are set at (12 km, 30º), (25 km, 0º), and (30 km, –30º), and the farthest distance of the search grid is set to 100 km, covering three ambiguity intervals. The simulation results of target estimation are shown in Fig. 3, which indicate that the distance angle parameters of the target can be estimated without ambiguity based on the random logarithmic frequency DAPSO-OMP.

To verify the robustness of the algorithm to changes in SNR and snapshot count, root mean square error (RMSE) is used as the standard to measure the performance of the algorithm. The root mean square error of range and angle is defined as

$$RMSE_R = \frac{1}{K}\sum_{k=1}^{K}\sqrt{\frac{1}{I}\sum_{i=1}^{I}(\hat{R}_{k,i}-R_k)^2}\ , \qquad (13)$$

$$RMSE_\theta = \frac{1}{K}\sum_{k=1}^{K}\sqrt{\frac{1}{I}\sum_{i=1}^{I}(\hat{\theta}_{k,i}-\theta_k)^2}\ , \qquad (14)$$

where K is the target number and I is the number of Monte Carlo experiments. $\hat{R}_{k,i}$ and $\hat{\theta}_{k,i}$ are the range and angle parameters of the k-th target in the i-th experiment, respectively. R_k represents the true distance of the target, and θ_k represents the true angle of the target. The SNR interval is set to [–20 dB:5:10 dB], snapshot count interval [1, 10:10:100], and Monte Carlo experiments are conducted 300 times. The simulation results are shown in Fig. 4, which indicate that the DAPSO-OMP algorithm is more suitable for low SNR and small block snapshots conditions, and has superior robustness.



a b c d

Fig. 4. The variation of RMSE of range-angle with SNR and number of snapshots using different algorithms

IV. Conclusion

This paper proposes a range ambiguity DAPSO-OMP algorithm for FDA-MIMO radar. The receiving pattern of FDA-MIMO radar based on random logarithmic frequency offset is derived to solve range ambiguity. On this basis, the DAPSO-OMP algorithm further improves the speed and position update formulas of the adaptive particle swarm algorithm by adopting a dual precision iterative method to enhance the convergence speed and global optimal solution search ability of the algorithm, thereby accelerating the optimization process of OMP and reducing computational complexity. Finally, through complexity analysis and simulation experiments, it is verified that the DAPSO-OMP algorithm proposed in this paper has better estimation accuracy and robustness compared to the PSO-OMP and OMP algorithms.

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Hybrid Voice Activity Detection and Speaker Gender Separation Model

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Abstract. **Modern smartphones demand efficient, privacy-preserving speech processing without cloud dependency. We present a hybrid on-device model for joint voice activity detection (VAD) and speaker gender separation, optimized for mobile CPUs and NPUs. The architecture fuses temporal and spectral features via a multi-branch neural network, distilled to under 3M parameters for real-time inference. It incorporates a novel Compact Audio Embedding Network (CAEM) for learned feature extraction from raw audio, yielding 97.5 % gender accuracy on VoxCeleb1. Hardware optimizations include INT8 quantization, achieving <15 ms latency on mid-tier devices. Dynamic resource allocation adapts to battery and thermal constraints. Experiments show 95.2 % VAD F1-score in noisy conditions, with innovations like gender-biased noise suppression enhancing precision by 13 % for female voices.**

Keywords: **voice activity detection, speaker embedding, speaker identification, speaker separation, DSP, DNN**

I. INTRODUCTION

Voice activity detection (VAD) and speaker gender separation are critical for on-device applications like call screening and voice assistants, enabling personalized, privacy-focused interactions [1]. Traditional methods rely on cloud servers, raising latency, energy, and privacy concerns [2]. Scientific rationale stems from speech signal properties: VAD requires distinguishing speech from noise using temporal dynamics and spectral patterns, while gender separation exploits physiological cues like pitch (fundamental frequency, F0) and formants, where females typically exhibit higher F0 (180–250 Hz) and distinct formant distributions compared to males (80–180 Hz) [3]. Hybrid models combining neural networks with signal processing address these by integrating complementary features, improving robustness in noisy environments (SNR $\geqslant$5 dB) without enrollment [4].

We propose a hybrid model optimized for mobile SoCs (e.g., Qualcomm Hexagon, Apple Neural Engine), fusing BiLSTM for temporal modeling and CNN for spectral analysis. Feature extraction uses a novel Compact Audio Embedding Network (CAEM) to learn robust representations from raw audio, replacing traditional preprocessing. Distillation and quantization ensure efficiency, with dynamic CPU/NPU switching for resource management. This achieves high accuracy while reducing energy by 45 % versus server-based alternatives.

II. RELATED WORK

Existing VAD models like WebRTC [5] use statistical thresholds but falter in noise. Neural VADs (e.g., DNN-based [6]) improve accuracy but are computationally heavy. Gender classification often employs Gaussian mixture models on MFCCs [7] or deep embeddings [8], achieving ~95 % on clean data but degrading in noise. Joint models are rare; [9] combines VAD with diarization but requires cloud processing. Our hybrid approach advances this by on-device joint tasks, leveraging hardware-aware optimizations and learned embeddings for noisy scenarios, building on efficient audio models like SincNet [10] and wav2vec [11].

III. PROPOSED MODEL

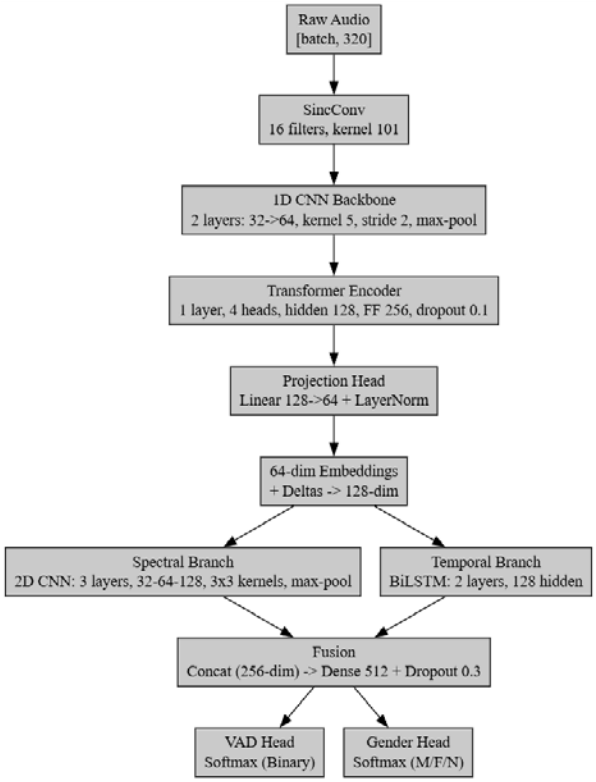
A. Compact Audio Embedding Network

The model's foundation lies in speech acoustics: VAD benefits from temporal continuity (e.g., speech bursts) and spectral energy (e.g., voiced harmonics), while gender relies on F0 and formants as biomarkers of vocal tract differences [3]. To capture these end-to-end without hand-crafted features, we propose the Compact Audio Embedding Network (CAEM), a novel lightweight model developed based on existing architectures including SincNet [10] for raw-waveform filtering, wav2vec 2.0 [11] and DistilHuBERT [12] for self-supervised embedding learning, and MiniLM [13] for compact transformers. CAEM processes raw audio into compact embeddings, implicitly encoding pitch, formants, and noise patterns, enabling gender-biased noise suppression (e.g., adaptive filtering for female voices in crowd noise via contrastive fine-tuning). All processing is on-device, ensuring privacy – no raw audio is stored or transmitted.

Total parameters for CAEM: 0.5M. Input: Raw 16 kHz audio frames (20 ms windows, 10 ms overlap; shape: [batch, 320 samples]). Output: 64-dimensional embedding vector per frame. Layers: (1) SincConv

(16 filters, kernel 101) for frequency selectivity; (2) 1D CNN backbone (2 layers, 32→64 filters, kernel 5, stride 2, max-pooling); (3) Transformer encoder (1 layer, 4 heads, hidden dim 128, feed-forward 256, dropout 0.1); (4) Projection head (linear 128→64 with LayerNorm). FLOPs: ~50 MFLOPs/frame.

The model is first pretrained in a self-supervised on LibriSpeech [14] (960 hours, unlabeled) using masked reconstruction (mask 15% frames, reconstruct spectrograms; AdamW optimizer, lr=1e-4, batch 64, 20 epochs). For fine-tuning, the model is trained on labeled data on VoxCeleb1 [15] for gender and NOISEX-92 [16] for VAD/noise (contrastive loss for gender-biasing + cross-entropy; augmentations: SNR 5–20 dB babble noise; 10 epochs, weight decay 1e-5). This yields robust, gender-discriminative embeddings with <0.5 % accuracy drop post-INT8 quantization.



Architecture of processing pipeline (including CAEM)

B. Processing Pipeline

The architecture is a multi-branch DNN with joint outputs for VAD (binary: speech/non-speech) and gender (male/female/neutral) per frame, enabling real-time separation without diarization. Input: CAEM embeddings (64-dim + delta features, forming 128-dim vectors).

- Spectral Branch: A 2D CNN (3 layers, 32-64-128 filters, 3×3 kernels) processes embeddings as pseudo-spectrograms to capture frequency patterns. Max-pooling and ReLU activations extract noise-robust spectral features (rationale: CNNs excel at local invariance [6])
- Temporal Branch: A BiLSTM (2 layers, 128 hidden units) models sequence dependencies, capturing speech continuity for VAD and pitch variations for gender (rationale: LSTMs handle long-range cues [17]).

Branches concatenate outputs (256-dim), fed to a shared dense layer (512 units) with dropout (0.3), followed by two softmax heads. Total parameters: 2.8M (including CAEM) post-distillation from a teacher (ResNet + Transformer on LibriSpeech). Knowledge distillation minimizes KL-divergence, combined with task losses. INT8 quantization with per-channel scaling. Dynamic allocation: CPU for efficiency (<20 % battery), NPU for accuracy. Inference: 15 ms/frame on Snapdragon 855 via PyTorch/ExecuTorch.

IV. Experiments and Results

We evaluated on VoxCeleb1 (gender-balanced, 1,251 speakers) [15] augmented with noise (Babble, SNR 5–20 dB from NOISEX-92 [16]). No speaker enrollment was used. Overall VAD F1-score: 95.2 % (vs. 92,4 % for Silero VAD [17]), with 13 % precision gain for females via biased suppression. Gender accuracy: 97.5 % (vs. 94 % baseline CNN [8]). Results are shown in Table.

PERFOMANCE METRICS OF PROPOSED MODEL

Metric	**Model type**			
	Proposed CAEM	***Silero VAD***	***Baseline CNN***	***MFCC + Formant***
VAD F1 (%)	95,2	90,0	89,.5	92,4
Gender F1 (%)	97,5	–	94,0	94,3

Comparison with Traditional Preprocessing: Ablating CAEM and using standard MFCCs + formant tracking (as in our initial design) yields lower performance: VAD F1-score drops to 92.4 % (–2.8 %), and gender accuracy to 94.3 % (–3.2 %), due to CAEM's superior noise robustness and learned representations (e.g., +5 % in low-SNR <10 dB conditions). On-device benchmarks on Redmi Note 13 (Snapdragon 855, PyTorch): 15 ms/frame latency, 75 MB RAM, 45 % less energy than cloud. Cross-platform via ExecuTorch.

V. Conclusion

Our hybrid model advances on-device speech processing with joint VAD and gender separation, grounded in acoustic principles and optimized for mobile hardware via the novel CAEM. Future work includes multi-speaker extensions.

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SIApp: Sea Ice Analyzer Application

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Abstract. **Sea ice information is important for a wide range of socio-economic, ecological, and scientific applications. The monitoring and analysis of sea ice are basic for safe navigation in polar regions, managing natural resources, and advancing scientific knowledge, including understanding climate change impacts. The Sea Ice Analyzer Application (SIApp), which is a robust software tool, was developed for the automated detection and monitoring of sea ice using synthetic aperture radar (SAR) imagery, particularly from Sentinel-1 and RADARSAT Constellation Mission (RCM) satellites. This paper describes the automated processing pipeline of SIApp, its pre-processing steps, performance and the dual-algorithm detection framework that incorporates both traditional backscatter-based analysis and AI-based segmentation. The presented results demonstrate that SAR image processing can be performed in less than a minute, which satisfies user requirements.**

Keywords: **sea ice, synthetic aperture radar (SAR), satellite image, AI, algorithms**

I. INTRODUCTION

Sea ice monitoring is fundamental for climate research, navigation safety, fisheries management, and ecological forecasting, especially in Arctic and Antarctic regions where dynamic ice conditions pose a risk to operational activities and infrastructure. Remote sensing using Synthetic Aperture Radar (SAR) offers an operational means of observing sea ice due to SAR's ability to operate under all weather and lighting conditions. Sentinel-1 (S1) and the RADARSAT Constellation Mission (RCM) satellites, with their C-band SAR capabilities, provide frequent and medium-resolution coverage of northern oceans, making them particularly suitable for sea ice applications.

Sea ice edge detection is one of the critical tasks in sea ice analysis, commonly used for delineating the boundary between open water and ice-covered areas. Numerous algorithms have been developed over the past decades to automate this process from SAR imagery [1–6]. Ice segmentation methods can employ various image processing and machine learning (ML) techniques, such as:

- Thresholding: These algorithms use fixed or adaptive thresholds on backscatter intensity (e.g., σ^0 values) to differentiate between sea ice and water. Examples include Otsu's method and k-means clustering. While computationally efficient, they are often sensitive to variations in incidence angle, ice type, and ocean surface conditions.
- Texture-based: These approaches analyze spatial variations in image texture to identify sea ice features. Techniques, such as Grey Level Co-occurrence Matrix (GLCM), have shown promise in capturing heterogeneous ice surfaces, but often require tuning and are susceptible to noise.
- Edge detection: Classic image processing methods like Canny, Sobel, or Laplacian filters have been used in conjunction with morphological operations (e.g., dilation, erosion) to outline ice boundaries. These methods offer precise localization but are sensitive to speckle noise, common in SAR images.
- ML and deep learning: In recent years, supervised classifiers (e.g., Support Vector Machines, Random Forests) and convolutional neural networks (CNNs) have been applied to sea ice segmentation tasks. These models require annotated datasets and computational resources but can outperform traditional methods in terms of robustness and generalization.

In our work we describe the implementation in SIApp and performance of two algorithms: classical, based on SAR backscatter analysis (BA), and Meta AI Segment Anything Model (SAM) [7].

II. ICE SEGMENTATION

A. BA Algorithm

The BA algorithm implemented in SIApp is a hybrid rule-based approach designed to extract sea ice edges from dual-polarization SAR imagery. It utilizes intensity thresholding and spatial gradient analysis of both HH and HV channels, enhanced through a series of morphological operations to improve robustness against noise and speckle.

The algorithm begins by applying a backscatter threshold to the HV (cross-polarized) channel. All thresholds were identified using a large number on images and scientific publications [8, 9] allowing to generate consistent results for different incidence

angles with minimum false features. Pixels exceeding a user-defined threshold are marked as potential ice, while land areas are excluded using a land mask generated using a coastlines shapefile. A smoothing and morphological operations are then applied to reduce noise and small-scale variability to remove small features such as speckle noise.

To enhance edge detection, the algorithm computes image gradients on both HH and HV channels using Sobel-based gradient operators helping to identify high-contrast boundaries associated with sea ice floes. The HV-based gradients are further dilated to create a buffer, within which HH gradients are selectively applied. This cross-polarization fusion ensures that gradient-based detection is spatially consistent and less sensitive to channel-specific artifacts.

The final output binary mask represents a clean, sea ice mask, with noise suppression, coastal exclusion, and internal gap filling. The result is a stable and interpretable sea ice edge suitable for both scientific analysis and operational decision support. Fig. 1 shows an example of ice edge delineated in RCM SC50 image (2024/03/15) superimposed on RGB as Red – HH; Green – HV; Blue – (2HV+HH) color composite image.

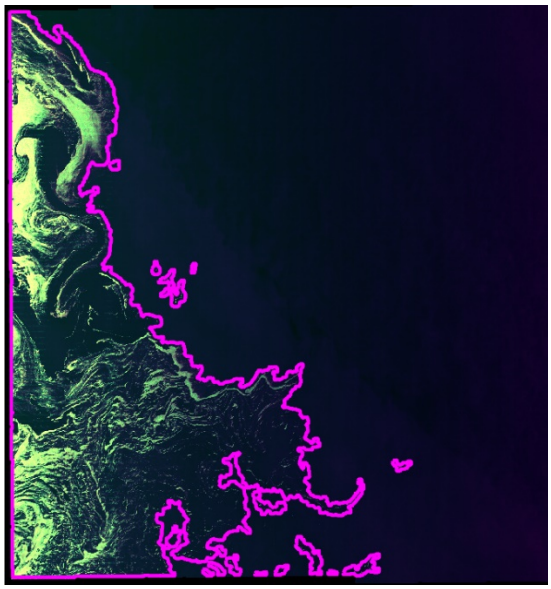

Fig. 1. Ice edge detected using BA algorithm in RCM image. RADARSAT Constellation Mission Imagery © Government of Canada (2024). RADARSAT is an official mark of the Canadian Space Agency

B. SAM

In SIApp, the SAM algorithm [7] is operationalized through a user-guided prompting mechanism that interacts with the model's embedding space. The process begins by automatically generating representative foreground (ice) and background (ocean) points (Fig. 2) from the HV-polarized SAR image. These points serve as prompts to SAM's segmentation engine. Once the points are defined, the RGB (or pseudo-RGB) SAR image is generated applying incidence angle normalization and passed through SAM's image encoder to produce an embedding, which encapsulates spatial and semantic information about the input image and serves as the foundation for the segmentation.

Then the model processes the embedding along with identified foreground and background points to generate a binary mask that segments the sea ice from open water. This approach allows the model to adapt its decision boundaries to local context, even under complex conditions such as partial ice cover, melt ponds, ocean features, or radar shadowing.

The resulting mask can be optionally overlaid on the original RGB image for visual inspection and quality assurance. This implementation does not require training on SAR data thus providing a powerful complement to the BA algorithm. Fig. 2 shows sea ice segmentation results using SAM in the same RCM image (2024/03/15).

III. Interface

SIApp supports both Graphical User Interface (GUI) and command-line modes, offering flexibility in accommodating different user preferences and operational scenarios.

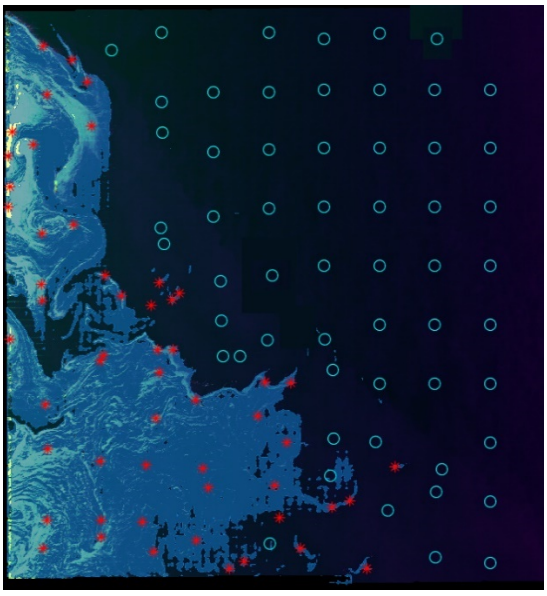

Fig. 2. Ice mask detected using SAM in RCM image based on foreground (ice is indicated as red stars) and background (ocean as blue circles) points. RADARSAT Constellation Mission Imagery © Government of Canada (2024). RADARSAT is an official mark of the Canadian Space Agency

A. GUI

The GUI of SIApp (Fig. 3) is designed to guide users through a structured workflow for processing S1 or

RCM SAR data to detect and extract sea ice edges. The interface begins with primary buttons to open SAR data which allow the user to initiate automated processing based on the satellite source. Once the appropriate button is selected, the user is prompted to choose the manifest file from an unzipped SAR product folder. This ensures that the application loads all necessary metadata and raw data components correctly. Upon selection the manifest file from an SAR product folder, SIApp automatically launches the processing pipeline and creates a new output directory one level above the SAR product folder.

Following initial processing, the GUI displays the result of the BA and SAM algorithms, highlighting detected sea ice regions. Users can interactively refine the detection results by modifying threshold values using the "Ice" button. This real-time threshold adjustment allows the user to fine-tune the algorithm's sensitivity to ice features, accommodating scene-specific variations in backscatter intensity. The QA block of the GUI enables further inspection and correction of the detected ice edge, where the "Edit" button allows manual reshaping of the extracted polygon, and the "Delete" button removes the last added or edited polygon.

For final product generation, the GUI provides tools to visualize and export the processed output. The "Product" button presents an overview image of the generated sea ice edge (Fig. 3), enabling a quick visual review before export. By pressing the "Export Shape File" button, the user can save the extracted ice edge as a shapefile in the product folder, ready for integration into GIS workflows, product delivery or further scientific analysis. Additionally, each execution of SIApp creates a timestamped log file to record processing details, errors, and debug information thus maintaining traceability and supporting continuous testing, particularly during operational deployments or multi-scene batch processing.

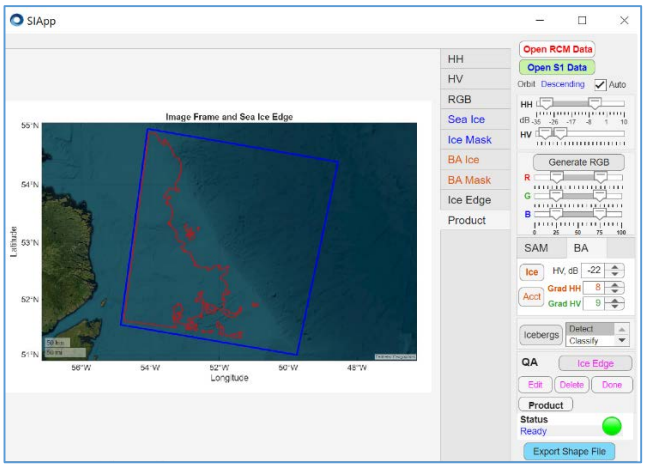

Fig. 3. SIApp GUI showing final product

B. *Command Line*

In addition to GUI operation, SIApp supports a command-line mode designed for efficient, large-scale processing. This mode is particularly advantageous for operational users who need to process multiple SAR scenes in batch without manual intervention. By specifying a root directory, users can execute fully automated workflows that include image pre-processing (sigma naught calibration and thermal noise removal), ice detection using both BA and SAM algorithms, and final product generation (shapefiles, JPEGs, and logs) for each scene. This enables seamless scaling of the application for time series analysis, regional monitoring, or archiving purposes. Fig. 4 shows multi-scene processing result for four Sentinel-1C IW images, acquired on 2025/04/01.

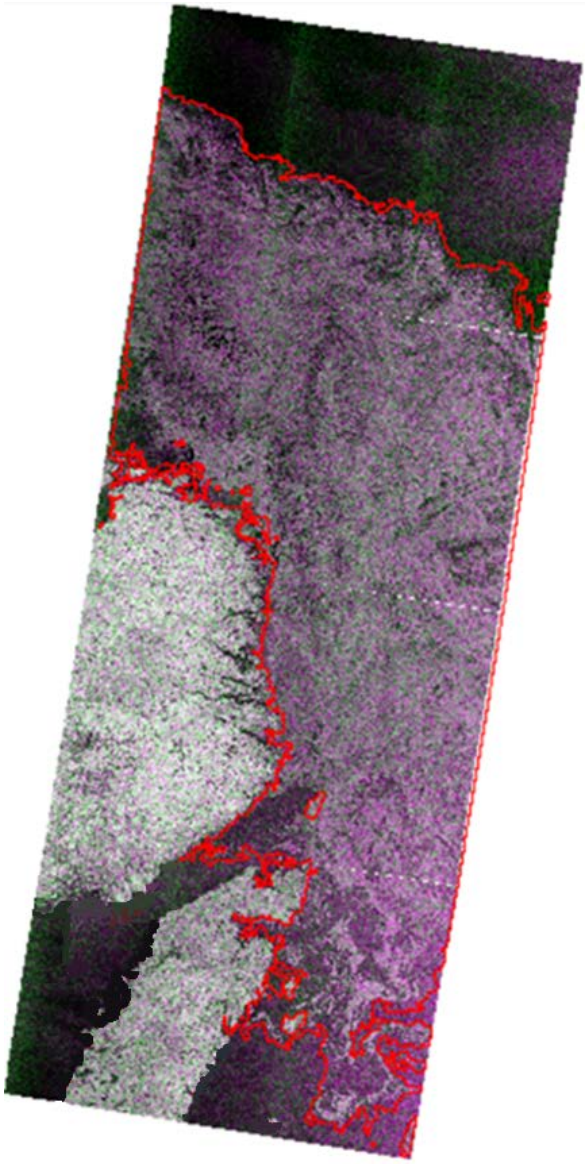

Fig. 4. Ice edge detected using BA algorithm in four Sentinel-1C images. Sentinel-1 SAR data provided by the Copernicus Programme and the European Space Agency (ESA)

Batch processing via the command line also supports parameter customization, such as adjusting backscatter thresholds or selecting algorithm modes. Processed outputs are organized into structured product folders, and a log file is created for each run to record processing details and potential errors. This automated functionality makes SIApp suitable for integration into real-time monitoring systems and large-scale climate data repositories.

IV. Implementation and Performance

The SIApp is implemented in MATLAB 2025a and operates as a self-contained application, requiring no additional software or external tools for full functionality. It simplifies installation, reduces compatibility issues, and ensures consistent behavior across platforms. Combined with its efficient architecture, SIApp can process a full RCM SC50 scene in under one minute on a standard computer or laptop. Such speed is achieved through optimized MATLAB routines, efficient use of memory, and computationally efficient morphological operations. The rapid turnaround makes SIApp well-suited for near-real-time monitoring applications and large-scale environmental projects where timely delivery of sea ice information is critical.

V. Conclusions

The SIApp integrates both classical and modern approaches for automated sea ice edge detection from Sentinel-1 and RCM SAR imagery. It introduces state-of-the-art AI capabilities into the workflow, enabling accurate sea ice mask and edge generation. The SIApp supports a fully automated processing pipeline that produces shapefile and JPEG outputs, while also allowing manual correction and QA through an interactive user interface.

Future development will focus on extending SIApp functionality to support additional sensors, such as L- and X-band SAR and multispectral data, and novel ice parameter retrieval algorithms. Furthermore, ML iceberg detection/classification and sea ice characterization will simplify QA process. These improvements aim to increase the reliability, performance, and operational readiness of SIApp. Currently SIApp serves as an efficient tool for C-CORE ice analysts and it is also an R&D prototype for rapid algorithm development and testing for its implementation in the cloud-based platform Coresight.

Acknowledgment

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Theory and Practice of Procedures Digitalization for Designing Lightweight Parts Based on Cellular Structures

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Abstract. **The use of additive manufacturing technologies allows for faster production processes and the creation of unique products made from various materials in many different fields of science and technology. This article provides an overview of the theoretical foundations for designing different cell configurations and analyzes modern approaches to creating cellular structures. It also discusses methods and models for designing lightweight parts, as well as an overview of existing software for developing complex cellular structures for three-dimensional printing. A practical example is provided of creating a cylindrical cell structure using the SolidWorks API.**

Keywords: **additive manufacturing, material consumption, cellular structure, lightweight parts, CAD**

I. Introduction

Additive manufacturing (3D printing) has opened up new possibilities for the design and manufacture of products, especially when creating complex geometric shapes, lightweight structures with different configurations of cellular structures. Unlike traditional subtractive machining technologies, the use of additive technologies implies the construction of a part by layer-by-layer build-up to obtain a finished product, and the material utilization factor (the ratio of the immediate mass of the part to the amount of raw material required for the production of this part) tends to 1.

II. The Rationale Behind the Construction of Components with Cellular Structures

One of the most crucial tasks in designing products manufactured using additive technologies is to reduce material consumption [1, 2]. The ability to modify the geometric configuration of a part, such as incorporating hollow cell areas within or on the surface, allows for optimizing material usage and enhancing production efficiency. Constructing parts with cellular structures significantly reduces their weight while altering their technical and operational properties. In certain production areas where structural rigidity and strength, particularly under compressive, bending, and impact loads, are critical, it is essential to strictly adhere to regulatory requirements and stress-strain state limits. In many cases, only a portion of the material in a part effectively contributes to its functionality. Therefore, optimization methods enable the identification of areas where material can be reduced through the replacement of solid structures with cellular ones, thereby improving overall efficiency and performance.

Cellular parts are characterized by a developed spatial geometry with a large number of channels and pores. The initial step in creating any cellular structure involves determining the configuration of the cells and filling the required volume or surface with this type of structure. Many options exist for modeling the final part, but the initial shape significantly influences the complexity of the task. Using standard geometric shapes simplifies the creation of a cellular structure, often achievable through computer-aided design (CAD) systems.

III. Modelling Methods of Cellular Structures

Applying various algorithms for filling the part's volume with cells and modifying cell shapes (Fig. 1) transforms the part's technical and operational properties. This enables predicting changes in strength characteristics and optimizing their ratios.

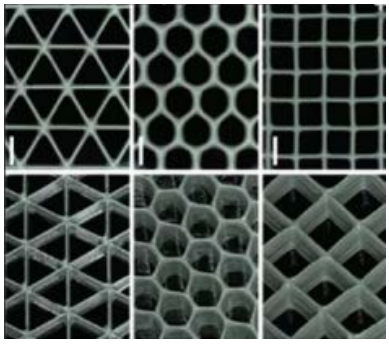

Fig. 1. The multivariance of cellular structures

The work was carried out as part of a research project on GB 21-266 "Marketing support for industrial enterprises of the Republic of Belarus in the context of regional integration and digitalization of the global economy" for 2020-2025.

A. *Designing cellular structures based on an elementary cell*

This method based on modelling of an elementary cell which involves applying a selected cell structure to an input model of any complexity after performing logical operations to repeat the elementary unit in various directions. According to the required technical and operational characteristics, cells can be combined to create the final cellular structures.

B. *The grid-based geometric modeling method*

The named method is highly effective for designing lattice structures. It allows any structure, regardless of its size, to be broken down into multiple nodes and connections between them, also known as struts or beams. These struts can have various orientations and sizes, cylindrical or cubic in shape [3], depending on the intended application. The size of the struts can remain constant or vary linearly or non-linearly.

The grid-based structure formation system begins by reading an input structure configuration file, which specifies the arrangement of nodes and struts. After reading the file, an array of nodes and struts is created. For each node, grids are generated, and a set of flat contours is defined to represent the boundaries of the node. Strut grids are then created using pairs of these boundary contours. Finally, all the cells are combined to form the complete grid of the structure.

C. *The Bi-directional Evolutionary Structural Optimization method (BESO)*

The BESO is a robust approach used in structural design to optimize the arrangement of components within a structure. The method operates by systematically removing components with low stress levels (referred to as "unloaded" components) and adding components to areas experiencing high stress levels (referred to as areas of maximum strain energy). The goal is to create a structure that meets specific functional requirements while minimizing material usage and enhancing performance. The number of elements to change is determined by meeting functional requirements (functional volumes (FVs) and functional surfaces (FSs)).

In addition to the physical specifications, the printability of a sample created using a specific technology and the capabilities of the equipment are crucial considerations. The use of computer-aided design (CAD), engineering analysis (CAE), and optimization (CAO) systems has significantly accelerated the product design and visualization process, enabled the development of components that are optimal in terms of weight and strength, and reduced costs and development time. This step is crucial for reducing material usage without compromising the structure's integrity.

IV. Overview of Software Tools in Cellular Structures Modelling

Modern design tools make it possible not only to predict the degree of deformation of a part but also to optimize its design according to specified weight and strength constraints. The process begins with creating a blank model, from which excess material is subsequently removed through a process known as topological optimization. This optimization results in a complex structure, which is then used to form a production model of the part. The resulting part meets the required strength criteria while minimizing its weight, but it can be challenging to manufacture using traditional methods. Additive manufacturing emerges as the optimal solution for such parts.

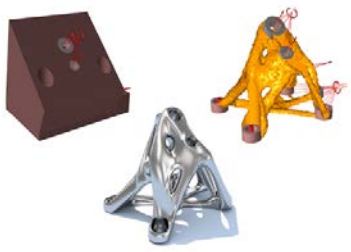

Fig. 2. Optimization of part’s structure in the Altair OptiStruct software environment

Modern software systems, such as **Altair's OptiStruct**, allow for the integration of solid-state structures with variable volumes of cavities directly within the design. These tools enable detailed analysis of the stress-strain state of hollow structures, including compression, shear, bending, and torsion, as well as the evaluation of their fatigue characteristics (Fig. 2). This comprehensive analysis helps ensure that the final design is both efficient and robust, meeting the demands of modern engineering applications.

The optimization methods of the OptiStruct system allow the designer to determine the best material distribution and the most suitable zones for the inclusion of cellular structures in two stages.

In the first stage, standard topological optimization is applied, which helps to define a certain amount of porous material with an average density. Then, these porous structure zones are transformed into explicit cellular structures, with varying volumes of material and voids.

In the second stage, the cell sizes are optimized. This results in a structure that combines solid-state zones with zones containing cellular structures, where the material volume varies.

Altair collaborates with technology partners such as **Materialise** to ensure efficient data imports directly for 3D printing.

Another software package, **3DXpert**, is designed to aid in creating lightweight, optimized designs with cellular structures and calculating part strength specifically for 3D printing. It is a comprehensive, integrated additive manufacturing software that streamlines the workflow from design to printing.

The **Autodesk Within** software system, based on topological optimization (CAO) methods, generates complex-shaped objects with cellular structures that are lighter than conventional designs while meeting specified performance criteria such as strength, rigidity, and durability (Fig. 3). Autodesk Within also addresses the challenge of preparing optimized virtual models for production through additive technologies, as these designs often cannot be manufactured using traditional multi-axis CNC machines.

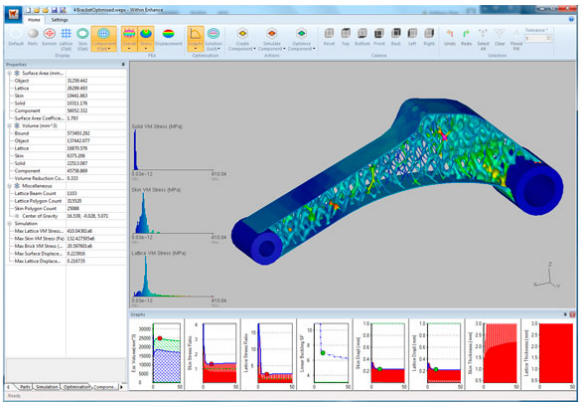

Fig. 3. An example of optimizing parts in Autodesk Within

Currently, automatic design tools for parts with cellular structures are available as components of large CAD/CAM/CAE development packages from Siemens, Dassault Systèmes, Autodesk, Ansys, Netfabb, and Solidworks. However, these software products are not considered user-friendly or cost-effective, and they do not allow for the limitation of optimization parameters, which could lead to changes in the size and shape of the object, potentially critical in various applications. Therefore, there is a need to develop a software tool that can create an internal cellular structure (specifically, cylindrical) without altering the external geometric characteristics of the object, while reducing the overall mass of the part and maintaining required technical and operational properties.

V. Empirical Experience of Modelling a Part with a Cylindrical Cellular Structure

To address practical issues in the digitalization of procedures for designing lightweight parts with cellular structures, a combination of **SolidWorks CAD** and **C#** libraries is proposed for dynamic control via the **API.** A software tool developed in **Microsoft Visual Studio** using C# and a **Windows Forms** interface is designed to digitally construct a test sample of a part in the form of a parallelepiped. This tool integrates an internal cylindrical cellular structure without changing the external geometry, aiming to reduce the overall mass of the part while maintaining necessary technical and operational properties.

The approach involves repeatedly redesigning the initial geometric model of a solid part and integrating cellular structures through engineering analysis. This iterative process is facilitated by the SolidWorks API, enabling precise control and automation of design modifications. By leveraging the power of SolidWorks and C#, the software tool streamlines the design process, enhancing efficiency and precision in creating lightweight parts with cellular structures.

The tool's functionality includes dynamic control over the geometric configuration of cylindrical cellular structures through adjustable parameters. It automatically performs engineering analysis within a CAD environment and exports the resulting data values. This capability allows for the automation of multiple studies examining the impact of geometric configurations on the stress-strain state of parts. The system also enables users to modify the number, location, and size of cells, as well as control the visualization of the structure and associated body parameters.

Moreover, during experimental testing, it became evident that the system must possess several specific features to facilitate the design digitization process. These include control over cell visualization, the ability to modify or delete bodies and cells, the capacity to create studies for analyzing the stress-strain state parameters of the part. It encompasses selection of the side of fixation, the direction and magnitude of applied forces. Additionally, the system must provide access to stress and strain data as well as other technical and operational characteristics.

Consequently, our theoretical examination and empirical tests (Fig. 4) have shown that contemporary design techniques provide a substantial benefit when employing additive manufacturing for the creation of functional components [4]. By minimizing the requirement for tooling and facilitating more adaptable material addition and removal, it becomes feasible to produce components with intricate geometries that surpass the capabilities of conventional manufacturing methods. The incorporation of a cellular structure, combined with structural analysis, enables the reduction of product weight while preserving its structural integrity, which is essential across a wide range of

industries. The variety of cellular structure forms and sizes opens up new possibilities for production and sparks interest in this area.

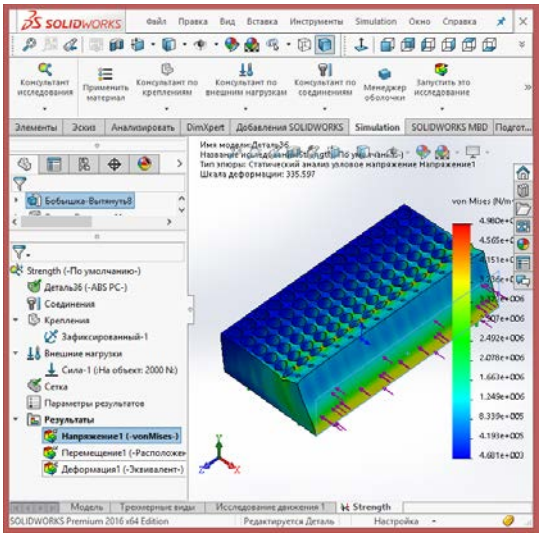

Fig. 4. Investigation of the experimental cellular structure made by authors

This is particularly important during the transition to Industry 4.0 technologies. In the process of digital transformation of the economy, we should take into account the experiences of advanced industrial countries [5] and implement these technologies to achieve sustainable economic growth.

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A SAR Ship Detection Method Enhanced by Receptive Field Attention

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Abstract. **This paper proposes a SAR (Synthetic Aperture Radar) ship detection method based on a receptive field attention mechanism, aiming to address the challenges posed by densely distributed small targets and background interference in complex marine environments for detection algorithms. By introducing Receptive Field Attention Convolution (RFAConv) into the YOLOv11 model, the method overcomes the limitations of standard convolution kernel parameter sharing and dynamically generates receptive field attention weights, thereby enhancing the perception capability for local feature significance. Experimental results demonstrate that the improved model achieves significant accuracy enhancement on ship datasets, particularly excelling in the mAP50-95 metric, while maintaining low computational overhead.**

Keywords: **SAR ship detection, YOLOv11, receptive field attention, RFAConv**

I. INTRODUCTION

Ship image detection has significant application value in areas such as marine monitoring and autonomous ships. However, challenges such as complex sea conditions, dense distribution of small targets, and background interference pose higher demands on the robustness and accuracy of detection algorithms [1]. Existing YOLO series models, despite optimizing performance through lightweight design and attention mechanisms, still exhibit notable limitations in ship image scenarios: the fixed parameter sharing mechanism of standard convolution struggles to adapt to the multi-scale variations of ship targets, traditional attention methods (such as CBAM [2]) inadequately model the differentiated spatial features within the receptive field, and the dense distribution of small targets leads to low feature extraction efficiency and high missed detection rates in existing models. Therefore, this paper proposes the introduction of Receptive-Field Attention Convolution (RFAConv) into the YOLOv11 model, breaking the limitations of convolution kernel parameter sharing by dynamically generating receptive field attention weights, thereby enhancing the ability to perceive the importance of local features. Experiments show that the improved model significantly enhances detection accuracy on ship datasets, with negligible incremental computational overhead, providing a new approach to solving ship detection issues in complex scenarios.

II. RELATED WORKS

The YOLO series is renowned for its efficient single-stage detection framework. YOLOv11 demonstrates outstanding performance in real-time detection through improvements in feature pyramids and lightweight design[3]. However, in ship images characterized by significant scale variations of targets and complex backgrounds, existing models are susceptible to noise interference, leading to frequent missed detections of small targets. The CBAM attention mechanism exhibits notable limitations in ship detection: Its spatial attention generates a single weight map through global pooling, forcing different receptive fields to share identical parameter adjustments, which struggles to adapt to local feature variations (e.g., multi-scale ships or intricate backgrounds). Simultaneously, CBAM solely focuses on pixel-level importance while lacking holistic feature interaction modeling for non-overlapping local regions, resulting in insufficient mining of contextual relationships among dense small targets and consequently high missed detection rates [4]. In contrast, RFAConv [5] significantly enhances multi-scale object detection robustness by dynamically generating non-shared local receptive field attention weights combined with lightweight grouped convolution design. Particularly in complex maritime environments, it effectively strengthens feature perception for ship edges and dense regions while reducing computational overhead, thereby substantially decreasing missed detection rates.

III. Proposed Method

In the proposed method (YOLOv11-RFAConv), we strategically replace two standard convolutional (Conv) layers in the neck with Receptive Field Attention Convolution (RFAConv) modules to overcome the limitations of static feature extraction in complex maritime detection scenarios. The neck, which is responsible for multi-scale feature fusion and refinement, originally employed standard Conv operations to process and integrate features from both the backbone and upsampling layers.

By incorporating RFAConv, the model dynamically adjusts the receptive field size and assigns spatially adaptive attention weights to feature maps, thereby achieving context-aware feature enhancement. This can significantly improves the network's ability to handle challenging marine environments while maintaining computational efficiency.

Fig. 1 shows the architecture of the proposed method and it is noticed that the RFAConv modules have been marked with red color.

RFAConv (Receptive-Field Attention Convolution) enhances the processing of spatial features within the receptive field by integrating a spatial attention mechanism with convolutional operations. It focuses on improving local feature extraction by dynamically adjusting convolutional kernel parameters through attention, addressing the limitations of parameter sharing in traditional CNNs. This approach significantly boosts the efficiency of large-kernel convolutions in handling information, thereby improving model performance.

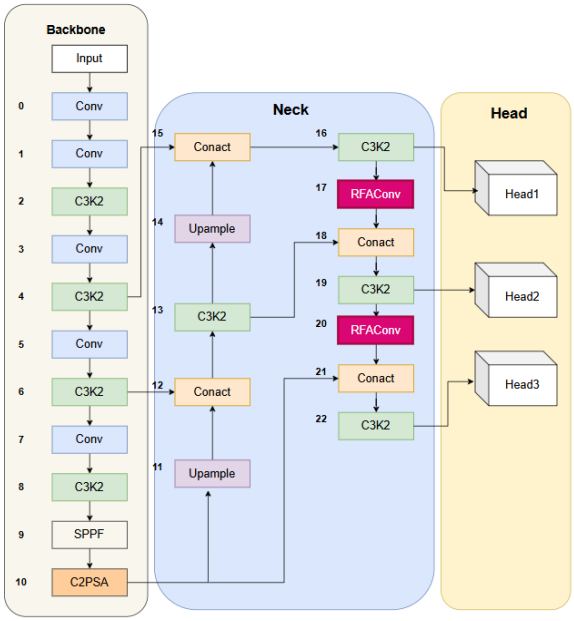

Fig. 1. YOLOv11-RFAConv Architecture Overview

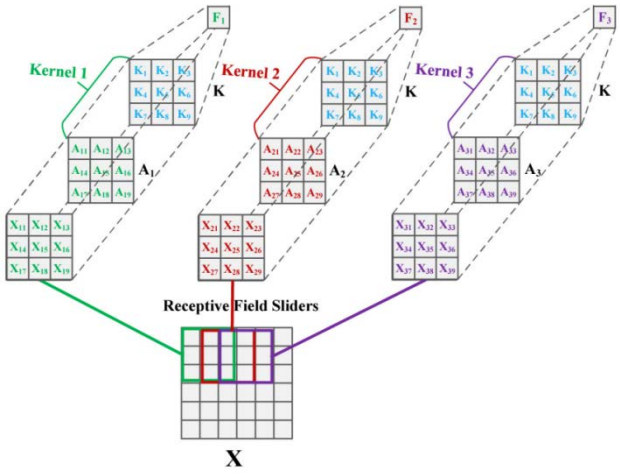

Fig. 2. Standard 3×3 convolution operation in RFAConv

Fig. 2 illustrates a standard 3×3 convolution operation in RFAConv, where features are computed by multiplying a 3×3 kernel K with corresponding receptive field patches of the input X and summing the products. Each element $X_{i,j}$ in the receptive field is multiplied by its corresponding kernel weight $K_{i,j}$, and the results are aggregated to produce a new feature value F. This process slides across the entire input, generating a feature map while maintaining local connectivity and weight sharing-meaning the same kernel weights are applied universally across the input.

This mechanism allows the convolutional kernels to dynamically adapt to the feature distribution of different receptive fields by decoupling the constraints of parameter sharing, significantly enhancing the representation capability of multi-scale targets and dense areas in ship detection.

IV. Experiment And Results Analysis

A. Dataset and Experimental Setup

To assess the effectiveness of the proposed method, we employed the publicly available SAR-Ship-Dataset. This benchmark dataset contains 43,819 high-resolution ship images (640×640 pixels) with expert-curated annotations specifically designed for multi-scale object detection in complex maritime environments.

In addition, two well-known neural networks are deployed for comparison with the proposed YOLOv11-RFAConv method, which are YOLOv11n and YOLOv11n-CBAM. It is noticed that all methods share the same training parameters. learning rate is set as 0.01, momentum is 0.937, weight decay is 3.0, optimizer is stochastic gradient descent (SGD), batch size are set as 4 and training epochs are set as 300.

Four established evaluation metrics were adopted for comparative analysis: Precision (P), Recall (R),

mean Average Precision at 50 % IoU threshold (mAP50), and mean Average Precision across 50–95 % IoU thresholds (mAP50-95). Their mathematical formulations are systematically presented in the following

$$P = \frac{TP}{TP+FP}, \tag{1}$$

where TP is true positive, FP is false positive,

$$R = \frac{TP}{TP + FN}, \tag{2}$$

where FN is false negative.

$$mAP_{50} = \frac{1}{C}\sum_{c=1}^{C} AP_c(IoU = 0.5), \tag{3}$$

where C is object categories, and AP_c is average precision for class c,

$$mAP_{50-95} = \frac{1}{10}\sum_{k=0}^{9} mAP_{0.5+0.05k}. \tag{4}$$

This formula computed as mean mAP over IoU thresholds from 0.5 to 0.95 with 0.05 increments.

To ensure reproducibility, experiment was performed on a single laptop computer equipped with an NVIDIA GeForce RTX 3060 GPU, under strictly controlled software environments: Python 3.9.21 and PyTorch 2.3.0.

B. Results Analysis

As quantitatively demonstrated in Table, the comparative analysis reveals distinct performance characteristics among the three detection frameworks. The baseline YOLOv11n achieves initial metrics of P = 0.876, R = 0.930, mAP50 = 0.950, and mAP50-95 = 0.606. YOLOv11n -CBAM module yields a 2.51 % precision improvement (0.898) accompanied by a marginal 1.05 % mAP50 increase (0.960), though at the cost of 1.08 % recall reduction (0.920) and 2.64 % mAP50-95 degradation (0.590). In comparison, the proposed YOLOv11-RFAConv demonstrates superior holistic performance with 2.74 % precision gain (0.900), 1.58 % mAP50 enhancement (0.965), and particularly notable 3.14 % mAP50-95 improvement (0.625), despite a tolerable 1.08 % recall decrease (0.920). This configuration establishes an optimal performance equilibrium, exhibiting 3.8 % greater mAP50-95 robustness than YOLOv11-CBAM method.

The Fig. 1 presents the training curves of mean Average Precision (mAP50) for three YOLO-series models (YOLOv11, YOLOv11-CBAM, and YOLOv11-RFAConv) in the ship detection task, illustrating their performance evolution across training epochs. The YOLOv11-RFAConv model demonstrates superior performance, consistently achieving higher mAP50 values throughout most training epochs compared to the other two models, which confirms the effectiveness of the RFAConv attention mechanism in enhancing detection accuracy for ships in complex backgrounds and multi-scale scenarios. In contrast, the YOLOv11-CBAM model exhibits relatively stable yet lower mAP50 values across all epochs, while the YOLOv11 model shows rapid initial improvement in early training stages but suffers from performance degradation in later phases. Overall, the integration of RFAConv into YOLOv11 delivers the best performance for ship detection, offering a robust and efficient solution for maritime vessel identification in challenging marine environments.

PERFORMANCE EVALUATION TABLE FOR OBJECT DETECTION EXPERIMENTS

Methods	P	R	mAP50	mAP50-95
YOLOv11n [6]	0.876	0.930	0.950	0.606
YOLOv11n-CBAM [2]	0.898	0.920	0.960	0.590
YOLOv11n-RFAConv	0.900	0.920	0.965	0.625

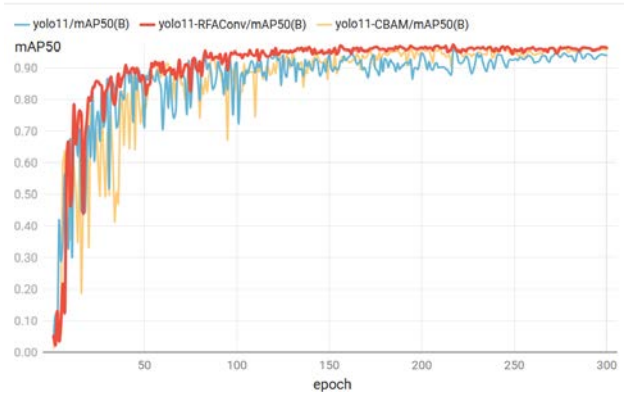

Fig. 1. The model's mAP50 curve over training epochs

The trend of the performance curves reveals show as Fig. 2 that the YOLOv11n-RFAC model consistently outperforms the other two variants throughout the training process, particularly during the early and middle stages, where its mAP50-95 values increased more rapidly and exhibited greater stability, ultimately maintaining the highest detection accuracy in the later phases. In contrast, while both the base YOLOv11n and YOLOv11n-CBAM models showed gradual performance improvements, they experienced more pronounced fluctuations at certain stages and achieved slightly lower final accuracy compared to YOLOv11n-RFAC. This demonstrates that the RFAC module significantly enhances the model's feature extraction capability and detection accuracy, enabling

superior and more stable performance in complex scenarios.

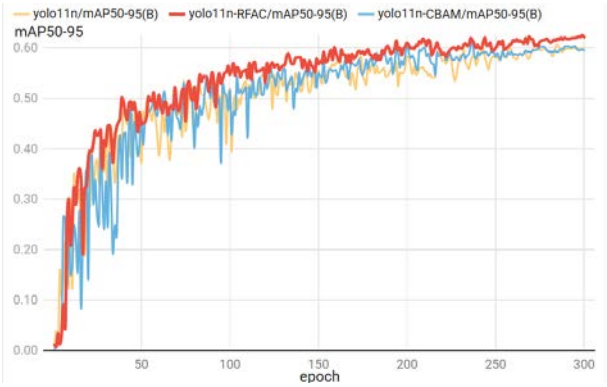

Fig. 2. The model's mAP50-95 curve over training epochs

The Fig. 3 highlights the limitations of the YOLOv11 model in ship detection, where false positives and duplicate detections frequently occur. For instance, in case (a), the YOLOv11 model incorrectly identifies background regions as ships, while the YOLOv11-RFAConv model successfully avoids such errors and accurately detects genuine ship targets. Moreover, in case (b), the YOLOv11 model generates redundant detections for the same object, whereas the YOLOv11-RFAConv model produces only a single high-confidence bounding box, demonstrating significantly improved stability and precision. These observations indicate that the integration of the RFAConv module substantially enhances the model's detection accuracy and robustness, effectively reducing both false alarms and redundant detections. This advancement offers a more reliable solution for ship detection in complex maritime scenarios.

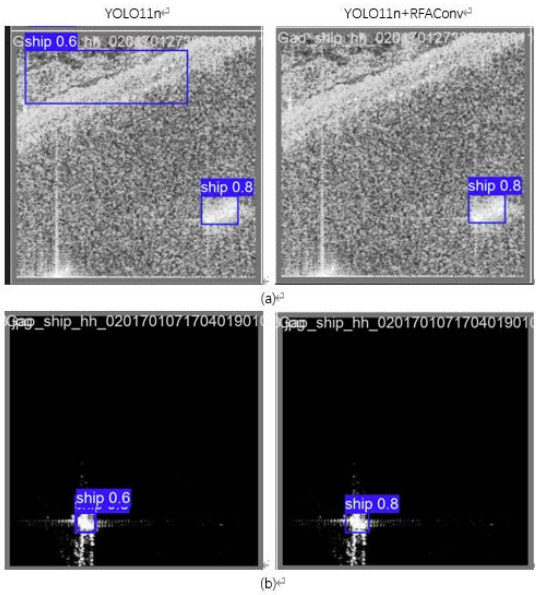

Fig. 3. YOLOv11 False Detections (a), YOLOv11 Duplicate Detections (b)

V. Conclusion

This paper proposes a SAR ship detection method based on a dynamic receptive field attention mechanism, aiming to address the challenges posed by densely distributed small targets and background interference in complex marine environments for detection algorithms. By introducing Receptive Field Attention Convolution into the YOLOv11 model, the method overcomes the limitations of traditional convolutional kernel parameter sharing and dynamically generates receptive field attention weights, thereby enhancing the model's perception capability for local feature significance. Experiments conducted on the SAR-Ship-Dataset demonstrate that, compared to the original YOLOv11n and the CBAM-integrated YOLOv11n-CBAM, the improved YOLOv11n-RFAConv model achieves outstanding performance in the mAP50-95 metric, with accuracy improved by 3.14 %, while maintaining low computational overhead. This approach provides an efficient and robust solution for ship detection in complex scenarios.

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Efficient Light Field Image Super-Resolution with Shared-Attention Transformers

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***Abstract*. Light-field (LF) image super-resolution (SR) aims to reconstruct high-resolution LF images from low-resolution LF images. Although current Transformer-based methods have achieved significant performance in LF image SR tasks, these methods usually face the problem of high computational cost, where most of the computational resources are consumed by the self-attention mechanism. In this paper, we propose a simple yet effective lightweight method that targets the computational efficiency bottleneck of Transformer-based LF image SR models. Our proposed method uses attention weight sharing as the core mechanism, and designs a dedicated compensation strategy to maintain the model performance. Experimental results on five public LF datasets demonstrate the effectiveness and efficiency of our method.**

***Keywords:* light field, image super-resolution, lightweight, attention, weight sharing**

I. INTRODUCTION

The Light Field (LF) camera is capable of recording both the intensity and direction of light rays, supporting the application of advanced computational photography applications, including post refocusing, depth perception, and foreground occlusion removal.

The advancement of deep learning has enabled convolutional neural networks (CNNs) to become widely used for LF image super-resolution (SR). Yoon et al. [1] introduced the first CNN-based method (i.e., LFCNN) for LF image SR. Zhang et al. [2] proposed ResLF, which combines the input view with neighboring view features through a residual network to enhance the resolution of the center view of the LF. Wang et al. [3] proposed DistgSSR which employs specialized convolutional modules to process the decomposed 2D subspace.

With the development of deep learning, Transformer is widely used in the field of LF image SR. Liang et al. [4] proposed the first Transformer-based LF image SR method called LFT, which alternates between spatial and angular self-attention modules. Wang et al. [5] proposed DPT, which considers each vertical or horizontal angular view of a sub-aperture image (SAI) as a sequence and models LF image SR as a sequence-to-sequence reconstruction process. Liang et al. [6] proposed EPIT, which learns non-local spatial-angular correlations of LF images to achieve improved SR performance.

However, the existing Transformer-based LF image SR methods generally face the problems of high consumption of computational resources and high training difficulties, and the multi-layer Transformer structure generally suffers from excessive inter-layer attentional similarity, which leads to a serious waste of computational resources. In this paper, we propose a lightweight Transformer-based model to achieve efficient LF image SR. In our method, we reduce the high computational consumption by sharing the attention maps among different Transformer layers. We conduct experiments to validate the effectiveness of our method.

Our contributions can be summarized as follows:

- We propose a simple yet effective lightweighting method for efficient LF image SR.
- We perform attention map sharing to effectively reduce the floating point operations (FLOPs).

- Extensive experiments on public LF datasets demonstrate that our method can achieve comparable SR performance with significantly reduced computational costs.

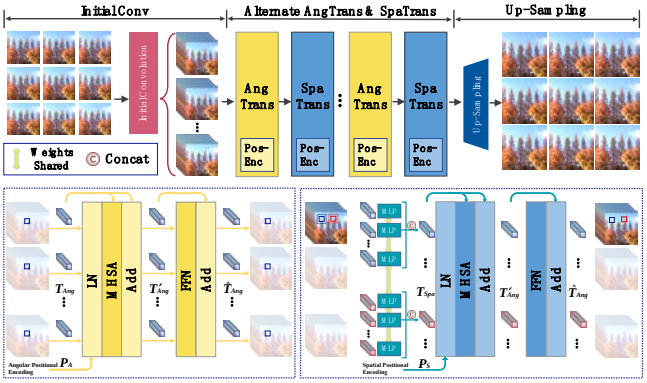


Fig. 1. Overview of the LFT Network Framework [4]

II. Proposed Method

A. Overview of the LFT Network Framework

To validate the effectiveness of our proposed method, we design and implement a shared attention weighting mechanism on LFT. Below we provide a brief overview of LFT's multi-layer Transformer architecture. Readers can refer to [4] for the detailed architecture of the LFT network.

The Alternate AngTrans & SpaTrans module (Fig. 1), as the core component of the LFT architecture, consists of multiple angle-transformers (AngTrans) alternating with spatial-transformers (SpaTrans). In the original implementation [4], the AltFilter unit consists of one AngTrans and one SpaTrans, and the LFT contains four cascaded AltFilter modules.

B. Attention-sharing lightweight method

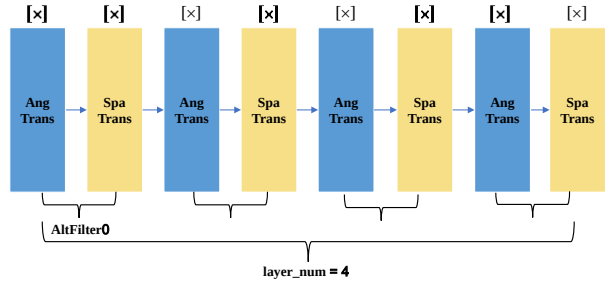
The above mechanism suggests that stacking multiple Transformer layers may lead to a significant increase in computational complexity. Although this architecture enables more comprehensive access to spatial contextual information and integration of complementary features from different viewpoints, its computational complexity may become a key obstacle in practical deployment scenarios.

In order to achieve lightweight design, this study proposes to reduce the process of attention weight calculation, a major component in the computational complexity of the Transformer model, through the attention weight sharing strategy. The distinctions between different versions of LFT with layer_num=4 in this chapter (namely LFT, LFTmulti8, and LFTmulti4) are as 0.

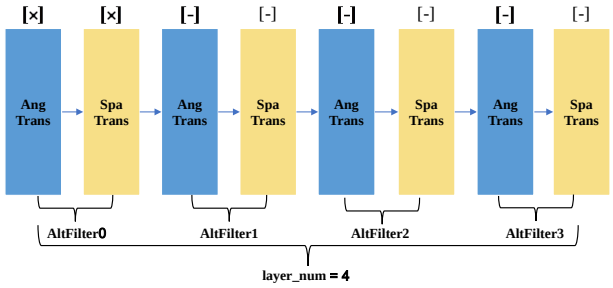
III. Experiments

A. Implementation Details

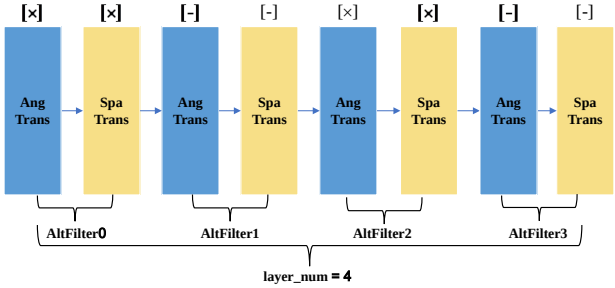
In terms of datasets, we follow the experimental setup of the literature [4] and use five public LF datasets [7–11] for method validation. we validate our method on five public LF datasets. All LF images used in training and testing maintain an angular resolution of 5×5. During training, we crop LF images into 64×64 patches, then generate 32×32 LF sub-blocks through bicubic downsampling.



(a)Baseline LFT Ang-Spa Transformer framework



(b)Ang-Spa Transformer framework with attention weights computed only in the first layer and shared across subsequent layers (LFTmulti8)



(c)Ang-Spa Transformer framework with alternating-layer attention sharing (odd layers compute weights, even layers reuse previous ones) (LFTmulti4)

Fig. 2. Different Ang-Spa Transformer frameworks compared and analyzed in this paper([×] denotes attention weight computation, while [−] indicates weight computation skipping with reuse of attention weights from the preceding layer's corresponding Transformer module.)

In terms of evaluation metrics, we use peak signal-to-noise ratio (PSNR) and structural similarity (SSIM) as quantitative measures for LF performance analysis.

The similarity between the interlayer attention weights was quantitatively measured by cosine similarity. The metric is subsequently benchmarked on a test set of five datasets, and the final evaluation results are averaged across the dataset scores. For the performance evaluation of $A \times A$ SAIs for M scenes in a single dataset, we first compute the metric values for $A \times A$ SAIs within each scene, and subsequently average the scores across all scenes. For computational complexity, we use inference time as a metric. Note that, time is computed with four input LF of size 5×5×32×32. The best results are in bold faces.

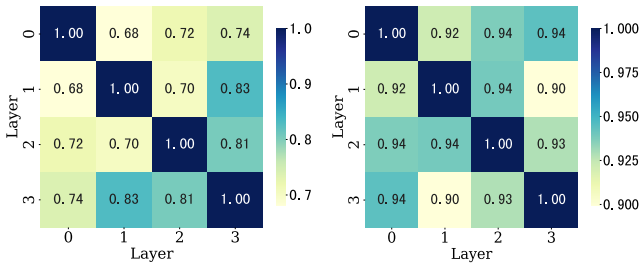
All experiments are conducted on the OpenBayes platform using an Nvidia RTX A6000 GPU, implemented via PyTorch framework. Network weights are initialized using Xavier method and optimized with Adam. For 2× super-resolution, the batch size is set to 4. The initial learning rate is set to 2×10^{-4}, employing a step decay strategy (decay factor γ=0.5) with learning rate reduction every 15 epochs.

The complete training process comprises 50 epochs. This paper compares the lightweight LFT models (LFTmulti4 and LFTmulti8) with state-of-the-art methods, including 3 single-image super-resolution algorithms [12–14] and 9 LF image super-resolution methods [2, 4, 5, 15–20]. Data is sourced from [4] and retraining experiments, with all models using training and testing datasets identical to those employed in our proposed framework.

B. Analysis of Weight Similarities for Shared Parameter Validation

TABLE I. demonstrates low variance values (all below 10^{-2} across test sets, verifying the validity of using the average cosine similarity to assess the correlation of the inter-layer attentional weights. 0'heatmap further reveals that: spatial attention weights show a high degree of consistency between the first and subsequent layers (mean cosine similarity > 0.9); angular attention weights maintain a relatively high cross-layer correlation, although their similarity is lower than that of spatial attention weights. These observations confirm the feasibility of reusing initial-layer attention weights. By multiplexing the attention weights in such a way, we propose LFTmulti8, where all other layers multiplex the weights of the first layer.

For this results, We can also use an alternating weight sharing strategy: the odd-numbered layers compute the weights and the even-numbered layers reuse the weights. Especially for the angular attention weights, the average cosine similarity of its layer 3 and layer 4 angular attention weights is 0.81, which is more similar and more feasible to reuse compared to the direct reuse of the first layer. We propose LFTmulti4, whose attentional weight reuse approach adopts the above strategy, which can be significantly verified in later experiments for its performance enhancement effectiveness.



(a)Average Angular Attention Weight Similarity (b)Average Spatial Attention Weight Similarity

Fig. 3. Heatmap of Inter-layer Attention Weight Similarity (layer_num=4)

TABLE I. VARIANCE OF ATTENTION WEIGHT SIMILARITIES ACROSS LAYERS ON TEST SETS OF MULTIPLE DATASETS

Datasets	**Layer Pair**					
	0-1	***0-2***	***0-3***	***1-2***	***1-3***	***2-3***
EPFL	33/87	28/11	9/400	15/45	**65**/45[a]	40/24
HClnew	25/207	38/152	3/333	14/105	41/20	46/37
HCIold	17/224	34/165	4/**567**	14/51	29/14	37/11
INRIA	14/53	13/38	6/212	9/54	38/40	23/24
STFgantry	16/150	25/102	9/195	9/162	22/14	23/41

[a.] Tabulated data entries are formatted as spatial attention variance/angular attention variance, delimited by slashes. Actual values are obtained by multiplying the tabulated data by 10^{-5}. Maximum variance values for both spatial and angular attention in the figures are highlighted in **boldface**.

TABLE II. MEAN SIMILARITY OF ANGULAR ATTENTION AEIGHTS ACROSS LAYERS ON TEST SETS OF MULTIPLE DATASETS

Datasets	**Layer Pair**					
	0-1	***0-2***	***0-3***	***1-2***	***1-3***	***2-3***
EPFL	0.65	0.68	0.67	0.70	0.82	0.80
HClnew	0.71	0.75	0.78	0.71	0.83	0.80
HCIold	0.68	0.72	0.75	0.72	0.84	0.81
INRIA	0.65	0.69	0.69	0.69	0.82	0.80
STFgantry	0.72	0.76	0.80	0.71	0.84	0.81

TABLE III. MEAN SIMILARITY OF SPATIAL ATTENTION WEIGHTS ACROSS LAYERS ON TEST SETS OF MULTIPLE DATASETS

Datasets	**Layer Pair**					
	0-1	***0-2***	***0-3***	***1-2***	***1-3***	***2-3***
EPFL	0.92	0.94	0.94	0.93	0.89	0.92
HClnew	0.92	0.94	0.94	0.94	0.90	0.93
HCIold	0.92	0.94	0.95	0.95	0.91	0.94
INRIA	0.93	0.94	0.94	0.94	0.90	0.93
STFgantry	0.92	0.93	0.94	0.94	0.89	0.92

C. Comparison on Benchmark Datasets

1) Quantitative Results: In terms of image quality enhancement, quantitative results under 2×SR are compared with state-of-the-art algorithms across five datasets in TABLE IV. Both lightweight LFT variants (LFTmulti8 and LFTmulti4) achieve competitive performance. As shown in TABLE IV. and TABLE V. the lightweight model LFTmulti8 shows an average PSNR degradation of about 0.27 dB compared to the original LFT model, while SSIM shows almost no degradation. For the performance-enhanced lightweight variant LFTmulti4, its PSNR improves by about 0.09 dB compared to LFTmulti8, and decreases by about 0.18 dB compared to the baseline LFT model. It should be noted that LFTmulti4 achieves superior results to the original LFT model on HCInew and HCIold datasets, while showing approximately 0.4dB performance degradation on other datasets. This discrepancy may stem from parameter sharing that improves the training efficiency of shallow feature processing, while the shared attention weights result in a degradation of deep feature extraction performance.

2) Qualitative Results: Qualitative results are shown in 0, where single-image super-resolution methods struggle to reliably recover missing details. For example, the blurred outputs generated by VDSR, EDSR and RCAN lack detail representation, while ESRGAN generates texture but is accompanied by obvious artifacts. In contrast, the light-field image super-resolution method achieves significant quality improvement over traditional single-image super-resolution algorithms by utilizing multi-view angle information. Experimental results also confirm that all the lightweight models implemented in our framework (LFTmulti8 and LFTmulti4) achieve significant super-resolution results.

3) Efficiency: In terms of computational efficiency, we measure the runtime versus the number of parameters (#Param.) for different algorithms. As shown in TABLE V. LFTmulti8 and LFTmulti4 achieve about 53.4 % and 47.0 % time reduction over the original LFT model, respectively. And under the same experimental setup, the lightweight models exhibit significant training speedups. The original LFT model takes about 3 hours per epoch, while the lightweight LFTmulti8 takes only about 1 hour to complete an epoch.

TABLE V. COMPUTATIONAL COMPLEXITY VERSUS RECONSTRUCTION PERFORMANCE

Methods	**2×SR**		
	Time	***#Param.***	***PSNR/SSIM***
LFT	0.2089s	1.11M	**38.85/0.986**
LFTmulti8	**0.0973s**	1.11M	38.58/**0.986**
LFTmulti4	0.1108s	1.11M	38.67/**0.986**

IV. CONCLUSION

In this paper, we present a simple but effective lightweight multilayer Transformer approach that is realized by attention weight sharing and applied to the LFT architecture (denoted as LFTmulti8). We also compensate the performance loss by varying the weight sharing method (LFTmulti4). Experiments show that our weight sharing method significantly reduces the computational cost of LFT with minimal quality loss. Follow-up studies should explore the generalizability of this weight-sharing paradigm across different multilayer Transformer architectures and empirically verify its potential effectiveness in accelerating model convergence.

TABLE IV. PSNR/SSIM VALUES ACHIEVED BY DIFFERENT METHODS FOR 2X SR.

Methods	**Datasets**				
	EPFL	***HCInew***	***HCIold***	***INRIA***	***STFgantry***
Bicubic	29.74/0.941	31.89/0.939	37.69/0.979	31.33/0.959	31.06/0.954
VDSR	32.50/0.960	34.3710.956	40.61/0.987	34.43/0.974	35.54/0.979
EDSR	33.09/0.963	34.83/0.959	41.01/0.988	34.97/0.977	36.29/0.982
RCAN	33.16/0.964	34.98/0.960	41.05/0.988	35.01/0.977	36.33/0.983
resLF	33.62/0.971	36.69/0.974	43.42/0.993	35.39/0.981	38.36/0.990
LFSSR	33.68/0.974	36.81/0.975	43.81/0.994	35.28/0.983	37.95/0.990
LF-ATO	34.27/0.976	37.24/0.977	44.20/0.994	36.15/0.984	39.64/0.993
LF-InterNet	34.14/0.972	37.28/0.977	44.45/0.995	35.80/0.985	38.72/0.992
LF-DFnet	34.44/0.977	37.44/0.979	44.23/0.994	36.36/0.984	39.61/0.993
MEG-Net	34.30/0.977	37.42/0.978	36.09/0.985	44.08/0.994	38.77/0.991
LF-IINet	34.68/0.977	37.74/0.979	**44.84/0.995**	36.57/0.985	39.86/**0.994**
DPT	34.48/0.976	37.35/0.977	44.31/0.994	36.40/0.984	39.52/0.993
LFT	**34.80/0.978**	37.84/**0.979**	44.52/**0.995**	**36.59/0.986**	**40.51/0.994**
LFTmulti8	34.57/**0.978**	37.72/**0.979**	44.35/0.994	36.26/0.985	40.00/**0.994**
LFTmulti4	34.44/**0.978**	**37.92/0.979**	44.73/**0.995**	36.11/0.985	40.15/**0.994**

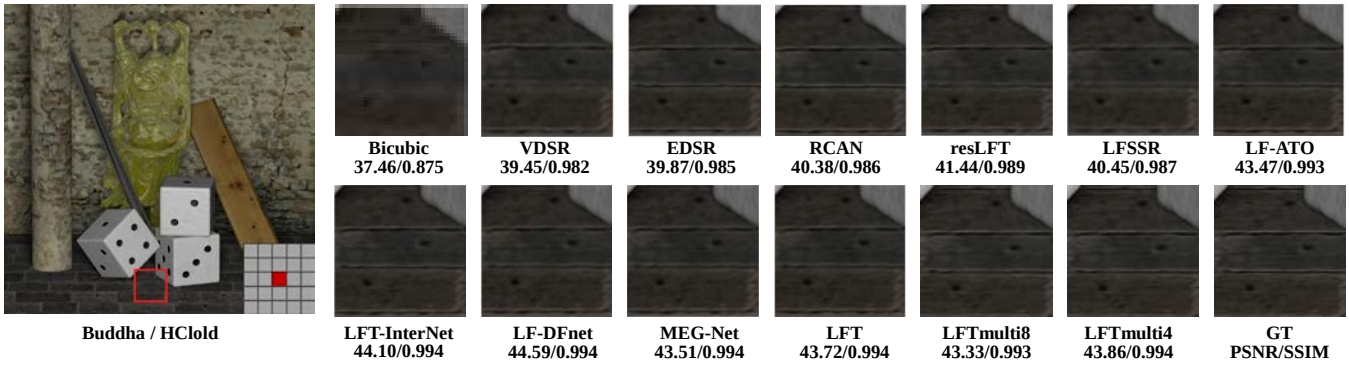


Fig. 4. Visual results achieved by different methods for 2xSR

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A PCA-Based Approach for Dynamic Yellow Chromatophore Detection in Cuttlefish Skin

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***Abstract*. This paper presents a program for detecting yellow chromatophores on the skin of a cuttlefish using computer vision and machine learning methods. The task is challenging due to the dynamic changes in the size of chromatophores, their potential disappearance, and the presence of non-uniform lighting and background. To address this, Principal Component Analysis (PCA) is employed to effectively isolate the color features of yellow chromatophores against a complex background. The algorithm includes data normalization, color space transformation, and image reconstruction using the first principal component associated with the yellow color. The proposed approach demonstrates robustness to lighting variations and allows for real-time detection of dynamic chromatophore structures, making it promising for analyzing cuttlefish behavior and camouflage.**

***Keywords:* cephalopod camouflage computer vision, dynamic skin patterns cephalopods, PCA image segmentation color, unsupervised learning image segmentation**

I. INTRODUCTION

The remarkable ability of cephalopods, such as cuttlefish, to rapidly change their skin coloration and patterning serves critical functions in camouflage, signaling, and communication within their complex marine environments [1, 2]. This dynamic coloration is primarily mediated by specialized organs called chromatophores, which can rapidly expand or contract under neural control [3, 4]. Accurately detecting and quantifying the activity of individual chromatophores, particularly those responsible for specific hues like yellow, presents a significant challenge in biological research and inspires advancements in bio-inspired robotics and adaptive materials [2, 5]. The transient nature of these patterns, coupled with varying sizes, irregular shapes, and often non-uniform illumination and complex backgrounds in aquatic environments, makes precise computational analysis difficult [1, 3]. Traditional image processing techniques often struggle with these complexities, leading to the need for robust algorithms that can effectively isolate and track these dynamic cellular structures. Recent advancements in computer vision, particularly those leveraging machine learning and dimensionality reduction, offer promising avenues for addressing these intricate biological segmentation problems [4, 6]. This paper introduces a novel approach for yellow chromatophore detection in cuttlefish skin based on Principal Component Analysis (PCA), designed to overcome the inherent complexities of these biological images.

II. IMAGE CHARACTERISTICS AND CHROMATOPHORE PROPERTIES

Cuttlefish skin is a complex biological canvas, featuring thousands of chromatophores – small, deformable sacs of pigment that expand and contract due to radial muscle action [1, 3]. Yellow chromatophores, specifically, contribute to a range of bright patterns. The primary challenge in their detection arises from their inherent dynamism; these chromatophores can change size, shape, and even seemingly disappear or emerge within fractions of a second [2, 5]. Furthermore, the visual data often exhibit non-uniform illumination, where lighting conditions vary across the image, casting shadows or creating highlights that can obscure the target chromatophores. The background itself is rarely uniform, often consisting of intricate skin textures, other types of chromatophores (e.g., brown, red), or environmental elements that complicate segmentation [3]. The non-rigid and highly adaptive nature of the cuttlefish skin means that chromatophores are not static entities, but rather dynamic textures that continually deform and shift, making traditional object detection methods based on fixed templates or strict color thresholds largely ineffective [3, 7]. This necessitates an algorithm capable of distinguishing subtle chromatic differences amidst high variance and effectively separating the target yellow pigments from ambient noise and other dermal components. The ability of cephalopods to achieve such high-fidelity camouflage, despite their colorblindness, further underscores the complexity of their skin patterns and the need for sophisticated analytical tools [2].

III. Chromatophore Detection Algorithm

The proposed algorithm leverages Principal Component Analysis (PCA) to effectively isolate yellow chromatophores by transforming the image's color information into a more separable feature space. This method capitalizes on PCA's ability to reduce the dimensionality of data while retaining the components that account for the most variance, thus making it suitable for distinguishing subtle color variations in biological imagery [8, 9].

The algorithmic process can be broadly divided into the following sequential steps, as illustrated in the conceptual diagram below on Fig. 1.

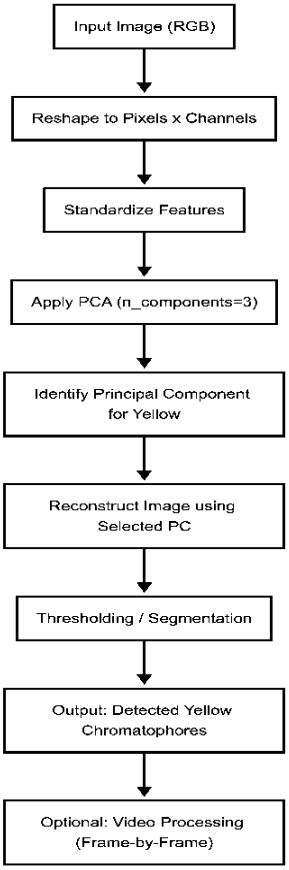

Fig. 1. Conceptual Diagram of the PCA-based Chromatophore Detection Algorithm

Each image is converted into a two-dimensional array where rows represent individual pixels and columns represent the three color channels (Red, Green, Blue). This transformation reshapes the H×W×3 image array into an (H×W)×3 feature matrix, where H and W are the height and width of the image. This initial step is critical for preparing the data for multivariate analysis.

Following reshaping, the pixel color values are standardized using StandardScaler. This crucial preprocessing step scales the data such that each color channel has a mean of 0 and a standard deviation of 1. Standardization ensures that channels with naturally larger value ranges do not disproportionately influence the PCA, allowing the algorithm to focus on the underlying chromatic variations rather than absolute intensity differences [7, 10]. This normalization is particularly important in images with uneven lighting, as it helps to mitigate the impact of global brightness variations.

Subsequently, Principal Component Analysis is applied to the standardized feature matrix with n_components=3. PCA identifies a new set of orthogonal basis vectors, called principal components, which capture the maximum variance in the data. The first principal component (PC1) accounts for the largest possible variance in the data, the second (PC2) for the next largest, and so on. In the context of RGB images, these principal components often correspond to meaningful visual properties. For instance, one component might capture overall brightness, while others might represent color contrasts or specific color axes. By analyzing the loadings of the original RGB channels onto these principal components, one can identify the component(s) that best represent the yellow chromatic information. The covariance matrix, as shown in the provided code, further reveals the statistical relationships between the scaled color features, indicating how closely related the variations in different color channels.

After PCA, the data is transformed into the principal component space, generating "scores" for each pixel along these new axes. To isolate the yellow chromatophores, the algorithm then reconstructs the image using only the principal component(s) identified as most relevant to the yellow color. For example, if PC1 is found to capture the most significant yellow-related variance, the image is reconstructed using only the scores corresponding to PC1 and the PC1 loading vector. This reconstruction effectively filters out information irrelevant to the desired color, enhancing the visibility of the target yellow regions while suppressing background noise and other colors [7]. This process is robust against varying illumination, as PCA inherently seeks out features that exhibit consistent variance across the dataset, rather than being solely dependent on absolute color values [8].

The final step in this algorithm, though not explicitly detailed in the provided code snippets but implicitly necessary for segmentation, involves applying a thresholding technique to the PCA-reconstructed image. Since the reconstruction highlights the target yellow regions, a simple intensity-based threshold can then be applied to create a binary mask, separating the yellow chromatophores from the remaining background. Morphological operations, such as erosion

and dilation, could further refine this mask by removing small noise particles and smoothing chromatophore boundaries [11]. For dynamic scenarios, such as video analysis, this entire process can be applied frame by frame, enabling the tracking and quantification of chromatophore activity over time, a crucial aspect for behavioral studies [4, 12].

IV. Results of Chromatophore Detection

The PCA-based algorithm demonstrates a robust capability for distinguishing yellow chromatophores amidst the complex and dynamic background of cuttlefish skin. The power of this approach lies in its ability to decorrelate color channels and isolate the most significant axes of variation, which often correspond to the desired chromatic features.

For illustration, let's consider the provided images as representing different stages of the algorithm's application. Assuming on Fig. 2 represents an original image of cuttlefish skin, it would typically show a complex scene with varied colors and textures, reflecting the natural patterns and potentially other chromatophore types. After the PCA transformation and reconstruction targeting the yellow component, an image similar to Fig. 3 could be obtained, where the yellow regions are significantly enhanced and separated from other colors and background noise, effectively reducing the dimensionality of the color space to emphasize the target features. Finally, applying a suitable threshold to this enhanced image would yield a segmented output, as might be represented by Fig. 4, clearly highlighting the yellow chromatophores as distinct objects against a clean background.

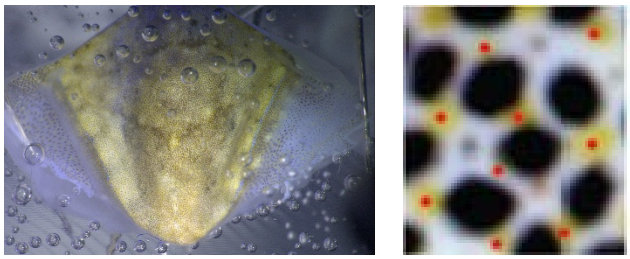

Fig. 2. Example of Original Cuttlefish Skin Image and scaled fragment

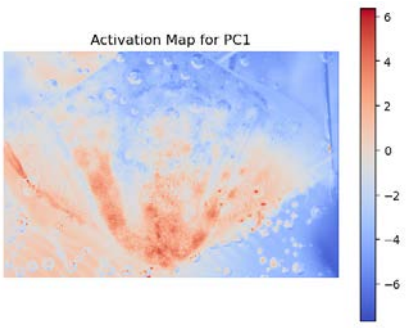

Fig. 3. Intermediate PCA Processed Image Highlighting Yellow

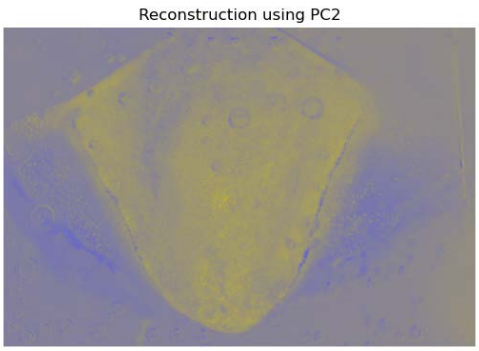

Fig. 4. Final Segmented Yellow Chromatophores

A significant advantage of this PCA-based approach is its inherent robustness to non-uniform illumination. By focusing on the principal components that capture chromatic differences rather than absolute pixel intensities, the algorithm is less susceptible to changes in lighting conditions across the image or over time [8]. This makes it particularly suitable for capturing biological phenomena in uncontrolled or semi-controlled environments. Furthermore, PCA efficiently reduces the dimensionality of the color data, effectively decorrelating the intricate relationships between color channels and allowing for a more straightforward separation of target colors. The algorithm's ability to isolate specific color information makes it adaptable for detecting other chromatophore colors (e.g., red or brown) by simply selecting different principal components for reconstruction. Its unsupervised nature also reduces the need for extensive labeled datasets, which are often scarce in specialized biological imaging [11].

V. Conclusion

The precise detection and analysis of dynamic chromatophores in cephalopod skin represent a vital area of research, contributing to our understanding of biological camouflage and inspiring novel adaptive technologies. This paper has presented a robust PCA-based algorithm for the detection of yellow chromatophores in cuttlefish, addressing the significant challenges posed by their dynamic nature, irregular shapes, and variable image conditions. By leveraging Principal Component Analysis for dimensionality reduction and feature extraction, the algorithm effectively isolates the specific chromatic information corresponding to yellow, even in the presence of non-uniform illumination and complex backgrounds. The method's ability to enhance and segment target colors demonstrates a promising approach for quantitative analysis of cephalopod skin patterning and behavior [14]. Future work could focus on integrating advanced machine learning techniques, such as deep learning models (e.g., U-Net or DeepLabV3), for more automated and potentially more robust segmentation

and tracking of chromatophores, particularly for long-term video analysis and real-time applications [15, 16]. Further optimization of the PCA components selection and the post-processing steps could also enhance accuracy and computational efficiency, ultimately providing a more comprehensive tool for researchers studying the fascinating world of cephalopod camouflage and for broader applications in computer vision for aquatic animal monitoring [17].

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An Automatic Bird Voice Recognition System Based on Artificial Intelligence Technologies

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Abstract. **The article introduces an advanced model for recognising bird sounds in real-world scenarios. Built upon the pre-trained EfficientNetB3 architecture, the model incorporates multiple stages of audio signal preprocessing and employs a specialised classification scheme designed for a multi-label task, enabling independent detection of the 116 bird species within an audio segment.**

Keywords: **artificial intelligence, bird voice recognition, automatic processing, annotation, Mel-spectrogram, convolutional neural network, deep learning**

I. Introduction

The convergence of artificial intelligence (AI) and bioacoustics in recent years has expanded the scope of wildlife monitoring and conservation. One particularly promising application is the development of automatic bird voice recognition systems, which utilise AI-driven technologies to accurately detect and classify avian vocalisations [1]. As birds play a crucial role in ecological balance – serving as pollinators, seed dispersers, and indicators of environmental health – the ability to monitor their populations with minimal human intervention has become increasingly important.

Traditional methods of bird monitoring, often reliant on manual observation and expert analysis, are time-consuming, labour-intensive, and subject to human error. In contrast, modern AI techniques, such as deep learning and neural networks, offer significant improvements in processing speed and accuracy [2]. These technologies enable systems to learn complex patterns in bird calls, adapt to diverse acoustic environments, and even differentiate between species with subtle variations in their voices.

By harnessing the power of artificial intelligence, this innovative approach not only streamlines the process of bird identification and tracking but also paves the way for real-time, scalable monitoring solutions in complex and rapidly changing natural habitats [3].

II. Description of the Model

The pre-trained neural network *EfficientNetB3*, modified by removing the final classification layer, is used as the base architecture for the classification model [4]. EfficientNetB3 is one of the models in the EfficientNet family – a group of convolutional neural networks (CNNs) that balance model depth, width, and resolution in a principled manner. Originally designed for image classification tasks, EfficientNetB3 (along with its siblings) has been shown to deliver high accuracy with fewer parameters and less computational cost. When applied to bird voice recognition, the typical approach is to convert audio signals (bird calls and songs) into time-frequency representations (e.g., spectrograms or Mel-spectrograms) and then treat these as "images" input into the CNN.

EfficientNetB3 is derived using neural architecture search to optimally scale network dimensions. It uses a compound scaling method to strike a balance between network depth (number of layers), width (number of channels), and image resolution. It contains mobile inverted bottlenecks, squeeze-and-excitation (SE) blocks, and swish (or mish) activations, which help improve the representational capacity of the network while keeping the number of parameters and flops relatively low.

A. EfficientNetB3 Application to Bird Voices

The choice of this architecture is based on its high efficiency in terms of accuracy and computational complexity. By balancing an increase in depth, width, and input image resolution, EfficientNetB3 achieves competitive performance with a moderate number of parameters. Moreover, models built on EfficientNet have consistently delivered top-notch results across

various tasks involving the acoustic classification of birds, including the BirdCLEF competitions. This proven track record confirms its practical suitability for such applications, making it the preferred choice for this study.

Bird voice recordings are preprocessed by converting raw waveforms into spectrograms (or Mel-spectrograms). This conversion transforms the temporal audio data into a two-dimensional representation with time on one axis and frequency on the other, essentially producing an "image" that captures the energy distribution over time and frequency.

The spectrogram images are then resised to the appropriate input resolution expected by EfficientNetB3. Since EfficientNetB3 was designed for images, these spectrograms can be fed directly into the model. It processes these spectrogram images through layers of convolutions, where early layers typically extract low-level features (edges, textures) and later layers capture higher-level patterns (frequency modulations, harmonics) that may correspond to specific bird vocalisation patterns.

Typically, either a version pretrained on large-scale image datasets is used or the network, is trained from scratch on a dedicated bird audio dataset. Fine-tuning a pretrained model often results in better performance, as the network has already learnt generic visual features that can be repurposed to capture the unique structures in spectrograms.

EfficientNetB3 has a number of advantages in the voice recognition process in comparison with other convolutional neural networks. They are:

- Efficiency: given its balanced architecture, CNN is computationally efficient while still achieving competitive accuracy. This is especially beneficial when deploying bird voice recognition systems on edge devices or in field studies where computational resources may be limited.

- Robustness to Variations: bird vocalisations often contain subtle variations in timing and frequency. The robustness and capability of EfficientNetB3 to hierarchically capture local and global patterns make it well-suited for distinguishing between different species or even detecting variations within the same species' calls.

- Scalability: depending on the dataset size and diversity, CNN can be scaled (or even combined with data augmentation techniques) to improve recognition accuracy for challenging bird species or noisy backgrounds.

B. Components of the EfficientNetB3

The main components of the EfficientNetB3 architecture are the mobile inverted *MBConv* block and the *Squeeze-and-Excitement* optimisation. The inverted residual block starts by expanding the input feature map into a more multidimensional space using a 1×1 convolution, then applies a depth-first convolution in this expanded space, and finally uses another 1×1 convolution that projects the feature map back into a space with a smaller dimension, the same as the input dimension (Fig. 1). The "inverted" aspect comes from this expansion of dimension at the beginning of the block and a reduction at the end, which is the opposite of the traditional approach, where the expansion occurs towards the end of the remaining block.

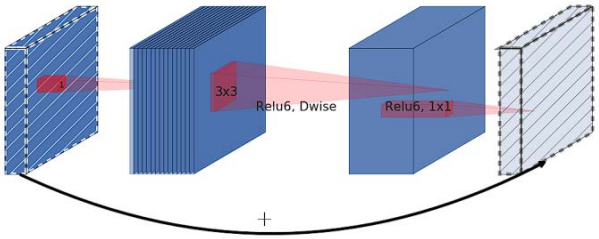

Fig. 1. Inverted residual block of EfficientNet

Squeeze-and-Excitement simply allows the model to emphasise useful features and suppress less useful ones [5]. This is done in two steps, such as:

- Squeeze (compression). This phase combines the spatial dimensions (width and height) of feature maps for each channel into a single value using global averaging. This results in a compact feature descriptor that summarises the global distribution for each channel, reducing each channel to a single scalar value.

- Excitement. At this stage, the model, using a fully connected layer applied after the compression stage, creates a collection of weights by channels (activations or estimates). The last step is to apply these learned importance estimates to the initial channel input feature map, effectively scaling each channel by its corresponding score.

SE is a building block for CNN to improve the interdependencies between channels by performing dynamic recalibration across all channels. This means that instead of giving all channels the same weight, the network will dynamically assign a high weight to the most important channels. The Fig. 2 shows the components of the block. This process allows the network to emphasise more important features and minimise the importance of less important ones by dynamically correcting feature maps based on the studied content of the input images.

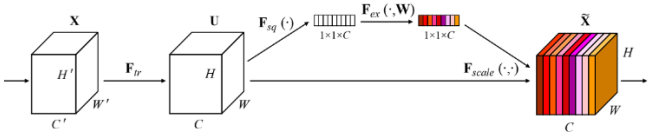

Fig. 2. The Squeeze-and-Excitation Block

Thus, EfficientNetB3 includes all of the above elements in its architecture which is shown of Fig. 3.

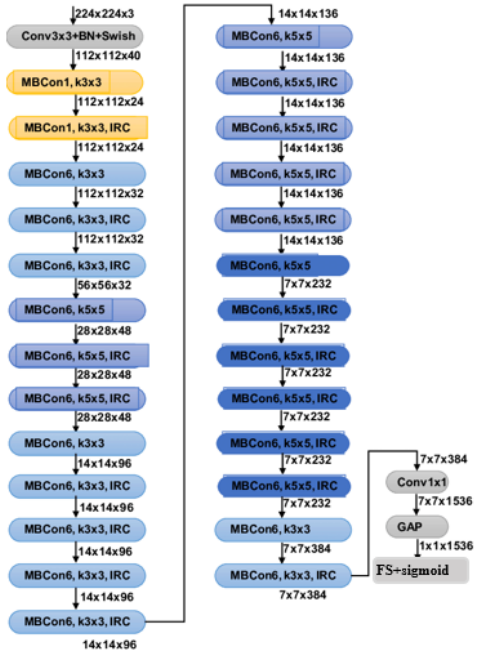

Fig. 3. EfficientNetB3 model architecture

III. Design and Implementation of a Deep Learning Model

A. Pre-processing of data for model training

Belarusian researchers have assembled a comprehensive database from various sources while collecting, annotating, and generating animal vocal signals. This database comprises over 3,000 audio recordings representing 116 bird species, yielding approximately 50,000 annotated vocalisations.

Before submitting audio recordings to the input of the model, they undergo preprocessing – a series of steps designed to enhance the quality of the extracted features and improve classification outcomes [6]. First, background noise is removed to minimise the impact of irrelevant acoustic interference that could distort the spectral characteristics of the target signal and reduce recognition accuracy. This noise reduction step improves the signal-to-noise ratio, which is particularly important for field recordings that often contain diverse background sounds, such as wind, water, or insects.

Next, the recordings are divided into fixed 2-second segments. This window size strikes a balance between containing sufficient informational content and preventing the model from being overwhelmed by too much data. In addition, to expand the training dataset and enhance the model's robustness to temporal variations in sound, an augmentation strategy is employed: each window's boundaries are randomly shifted by up to 0.5 seconds. This approach yields a more varied representation of the input data and bolsters the model's generalisation capabilities.

After segmentation, each audio window undergoes normalisation and dynamic compression. Normalisation eliminates amplitude discrepancies among different audio fragments, ensuring the model does not favour louder sounds. Compression amplifies low-intensity signals, preserving subtle yet critical acoustic features.

Finally, Mel-spectrograms with a lower frequency limit of 200 Hz are generated from the processed windows. This frequency threshold is selected based on the typical range of avian vocalisations, as frequencies below 200 Hz usually consist of low-frequency noise (such as footsteps or wind) that does not provide useful information for the recognition task. Consequently, Mel-spectrograms serve as an informative input representation for the neural network.

B. Deep learning model

To develop experimental software for automatically recognising animal vocalisations, we focused on designing a model and its corresponding algorithms. At the end of the network's convolutional part, a *GlobalAveragePooling2D* layer was added to collect spatial information from each feature channel. This layer reduces the feature space's dimensionality while preserving the most important features, thereby lowering the risk of retraining [7].

Next, a *dropout* layer with a dropout rate of 0.4 is applied. This regularisation method enhances the model's ability to generalize by randomly "disconnecting" certain neurones during training. This prevents overfitting to the training data and encourages the formation of more robust features.

The final fully connected layer comprises 116 output neurones equipped with a sigmoid activation function. The number of neurones corresponds to the number of target classes – different bird species. The sigmoid function is chosen because the problem is framed as a multi-label classification, meaning each species is predicted independently. This approach accommodates situations where multiple vocalisations may appear in a single audio clip [8].

Binary *cross-entropy* serves as the loss function, which aligns with the multi-label task where each output neuron represents an independent *binary*

decision (i.e., whether a bird species is present or not). The model parameters are optimised using the *Adam* algorithm, which combines the benefits of adaptive gradient correction and momentum-based updates, ensuring quick convergence and stability even on complex, noisy data.

C. Evaluating the quality of the model's work

Standard classification metrics – precision, recall, and f1-score – are used to assess the model's performance. For each bird species, a detailed report is generated, providing the values of these metrics. Additionally, a summary table is compiled to reflect the distribution of predicted probabilities for different species, enabling an analysis of the model's prediction confidence. A fixed probability threshold of 0.8 is used to interpret the model's output: a prediction is considered positive for a particular class if the corresponding output value exceeds this threshold. This threshold helps to minimise false positive classifications and enhance recognition accuracy.

The fragment of the trained model and its results for the 10 best recognised bird species out of 116 are presented below according to precision, recall, and f-1 score metrics. The last field represents the number of data examples in the test sample for which metrics were calculated. The metrics are presented for each bird species individually, as well as the average values for all species using different counting algorithms. Besides that, the last four lines show micro avg, macro avg, weighted avg, samples avg for averaging metrics of 116 bird species (Table I). *Micro Averaging* calculates the total true positives, false negatives, and false positives across all classes and then computes the metric. *Macro averaging* esteems the metric independently for each class and then takes a simple average (i.e., unweighted mean) of these per-class metrics. This treats all classes equally, regardless of their support (number of instances). *Weighted averaging* computes the metric for each class and then averages them, but with each class's contribution weighted by the number of instances (support) in that class. *Samples averaging* calculates the metric for each sample (i.e., instance) individually and then averages these scores across all samples.

We additionally formed the probability distribution table for bird species predictions to assess the confidence of the model in its predictions, whether they are false or true (Table II). A fragment of this table shows the values of the average, median, minimum, and maximum predicted probabilities for each bird species, as well as the support value, which shows the number of data instances in the test sample. Statistics for the table are calculated based on predicted labels, that is, for those probabilities that are higher than 0.8, since this was the confidence threshold previously set.

TABLE I. THE RESULTS OF TRAINING THR MODEL

Class of a bird	***precision***	***recall***	***f1-score***	***support***
caprimulguseuropaeus	1.00	0.99	0.99	158
bombycillagarrulus	1.00	0.94	0.97	63
laniusminor	1.00	0.92	0.96	90
aegithaloscaudatus	0.98	0.95	0.96	97
loxiapytyopsittacus	0.97	0.95	0.96	78
haliaeetusalbicilla	0.98	0.93	0.95	98
aegoliusfunereus	0.94	0.94	0.94	65
accipiternisus	0.92	0.95	0.93	91
clangaclanga	1.00	0.87	0.93	54
coloeusmonedula	1.00	0.85	0.92	61
micro avg	*0.92*	*0.73*	*0.81*	*10609*
macro avg	*0.92*	*0.74*	*0.82*	*10609*
weighted avg	*0.91*	*0.73*	*0.80*	*10609*
samples avg	*0.78*	*0.76*	*0.76*	*10609*

TABLE II. THE PROBABILITY DISTRIBUTION TABLE FOR BIRD SPECIES PREDICTIONS

Label	***mean***	***median***	***min***	***max***	***support***
caprimulguseuropaeus	1.00	1.00	0.85	1.0	156
bombycillagarrulus	0.99	1.00	0.82	1.0	59
laniusminor	0.99	1.00	0.84	1.0	83
aegithaloscaudatus	0.99	1.00	0.85	1.0	94
loxiapytyopsittacus	0.99	1.00	0.81	1.0	76
haliaeetusalbicilla	0.99	1.00	0.86	1.0	93
aegoliusfunereus	0.99	1.00	0.87	1.0	65
accipiternisus	0.90	1.00	0.86	1.0	93
clangaclanga	0.98	1.00	0.84	1.0	47
coloeusmonedula	0.99	1.00	0.84	1.0	52

D. Model modifications and their impact on classification quality

During the model refinement process, modifications were made to the previous version to boost recognition accuracy and overall generalisation. These changes led to improved key metrics (precision, recall, and F1-score), indicating better classification quality. First, an audio preprocessing stage that removes background noise was added. This significantly reduced the number of false-positive classifications by eliminating irrelevant acoustic components, while also increasing the proportion of true-positive predictions for the primary target classes – bird species commonly present in the training data [9].

Second, the order of operations in the preprocessing chain was revised. Previously, audio recordings were divided into time windows after generating spectrograms. In the updated version, windows are formed before the spectral transformation stage. This modification prevented distortions in the vocalisations that can occur during the compression of longer audio fragments, ultimately enhancing the reliability of the

extracted features. Finally, the probability threshold for a positive prediction was raised to 0.8. This adjustment was made to increase precision by filtering out low-confidence predictions, thereby reducing the number of false positives. As a result, the values of prediction quality metrics averaged over all bird species obtained for the final model are *precision* – 0.92, *recall* – 0.74, *f1-score* – 0.82.

IV. Conclusion

The study demonstrates the successful integration of advanced deep learning techniques and bioacoustic analysis to develop an automatic bird voice recognition system. By leveraging the EfficientNetB3 architecture, which has shown high efficiency in both accuracy and computational complexity, the model effectively converts bird vocalisations into informative spectrogram representations and achieves competitive performance even on real-world, noisy audio data.

Key enhancements – the introduction of preprocessing steps to mitigate background noise, the strategic segmentation of audio recordings with data augmentation, and the fine-tuning of model parameters such as dropout rates and probability thresholds – have all contributed to significant improvements in recognition accuracy. The refined model, using robust metrics such as precision, recall, and f1-score, exhibits an average precision of 0.92, recall of 0.74, and f1-score of 0.82 across 116 bird species [10].

These results underline the practical potential of AI-driven bird monitoring systems in supporting wildlife conservation and ecological research. The approach outlined here not only streamlines the process of bird identification but also establishes a scalable framework for real-time monitoring in complex natural habitats. Future work may involve further refinement of the model, expansion of the database, and adaptation to additional applications within bioacoustics to continue advancing the capabilities of automatic wildlife monitoring systems.

Acknowledgment

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Comparative Analysis of HRV Parameters Using Time Series and Absolute Increments in Normal and Arrhythmic ECG Signals

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***Abstract. Relevance*. The work is devoted to the study of the effectiveness of various methods for assessing heart rate variability (HRV), aimed at determining the differences in various HRV parameters using statistical methods based on ECG records with signs of arrhythmia and conditionally healthy subjects. *Purpose*. Using statistical indicators, assess the differences in HRV parameters obtained for different sets of ECG signals. *Tasks*. Implementation of algorithms for calculating HRV parameters using various methods. Calculation of HRV parameters using various methods. Assess the differences in HRV parameters using statistical indicators on similar data sets. Assess the differences in HRV parameters using different data sets, including ECG signals with signs of arrhythmia and conditionally healthy subjects. *Solutions*. Two methods for obtaining statistical parameters of HRV are considered: the classical method based on RR intervals and the method with absolute increments. The comparison allows us to evaluate the differences in the parameters obtained based on different types of signals. To identify the differences between the results obtained, the Fisher criterion was used. The results were presented in graphical form. *Analysis of the results*. The results showed that the parameters obtained by replacing the time series with a series of their differences allow us to more effectively detect the differences between the considered types of signals. The most pronounced differences were found in the method with the replacement of a series of cardiointervals: for RMSSD, the dispersion with arrhythmia exceeded the control by 10.86 times, for SDNN – by 9.90 times.**

***Keywords*: Electrocardiography, ECG, Heart Rate Variability, HRV, SDNN, RMSSD, Fisher criterion**

I. INTRODUCTION

In the modern world, one of the most important problems is the health of the population. The accuracy of the diagnosis and further treatment depend on the speed and correctness of obtaining results about the state of the body, so improving the methods of obtaining relevant information is still an urgent task. Heart rate variability (HRV) is one of such methods, demonstrating the unevenness of cardiac cycles [1].

Quantitative assessment of HRV is carried out by calculating indicators based on changes in cardiac intervals. Statistical methods are time domain analysis, considering a set of time intervals and any physiological process affecting the human cardiovascular system will change the values of the HRV parameters. Based on these changes, it is possible to predict a person's condition, so a low value of the standard deviation of the values of cardiointervals (SDNN) after myocardial infarction during Holter monitoring indicates a high chance of an unfavorable outcome for the patient and is one of the clear predictions of mortality risks in patients [2–4].

Therefore, special attention should be paid to improving the methods for obtaining these parameters. The purpose of this study is to implement algorithms for obtaining statistical parameters of HRV using various methods and comparing parameters on arrhythmic and control signals.

II. MATERIALS AND METHODS

The implementation of statistical parameters of HRV was performed using Matlab. For comparison, files [5] with cardiointervals of the control group and with arrhythmic signals were taken. Since the presented signals differ greatly in the duration of recording: from 2 to 24 hours, the first operation is to reduce them to the same length of the time interval by the minimum value, which is exactly two hours.

However, the use of time series as a basis for calculating target indicators has an alternative point of view [6]. Fedorov V.F., M. D. draws attention to the fact that the cardiac cycle begins with the “P” wave, and in the methods of HRV analysis, cardiointervals between the “R” waves are used, since they are easier to determine. But it turns out that the interval in question analyzes half of the previous cardiac cycle and half of the next one instead of the duration of the real cardiac cycle. Also, a critical assessment of the use of time series is confirmed by the fact that at different resting HR in two patients, SDNN will differ, but the values of the variation coefficient (CVr) will be the same, since

the variation coefficient is a relative indicator and reflects adaptability from the point of view of physiology. To exclude such inaccuracies, it is proposed to conduct the analysis not on RR intervals, but on their increments. For this, the time series is transformed into a series of their differences:

$$\tau_n = T_n - T_{n-1},$$

where T_n is the duration of the cardiocycle with the number n, and τ_n is its absolute increment compared to the previous one.

The following parameters were selected for comparison:

SDNN – the standard deviation of the values of cardiointervals for the entire period under consideration;

RMSSD – the square root of the sum of the squares of the difference in the values of successive pairs of cardiointervals (reflecting the activity of the autonomous regulation circuit, the higher the value, the more active the parasympathetic regulation link).

After analyzing the obtained results, the data from the control group raised doubts and upon closer examination it was decided to leave only 13 signals, since the rest contained RR intervals that exceeded the average signal values several times.

III. Results

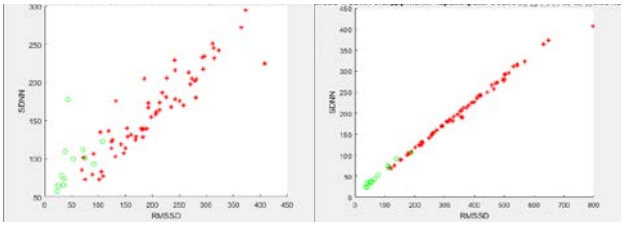
For the obtained calculations, a descriptive characteristic is derived both for the statistical indicators of HRV calculated in a standard way and for the parameters calculated with a number of absolute increments for both groups of signals: arrhythmic and control (Tabl. I). Median values for each group are taken as a comparison.

TABLE I. The obtained median values of statistical parameters

Statistical parameters	SDNN	RMSSD
Parameters based on cardiointervals		
Signals with arrhythmia	163.931	192.729
Signals of the control group	101.28	82.889
Signals of the reduced control group	92.614	37.748
Parameters with replacement of cardiointervals with absolute increments		
Signals with arrhythmia	192.717	353.425
Signals of the control group	82.885	138.903
Signals of the reduced control group	37.745	56.454

The results of the median values of statistical parameters of the reduced control group are close to normal, while the primarily taken signals stand out strongly in the values of the RMSSD parameter.

To illustrate the results obtained, a graphical representation of the relationship between the parameters obtained by both methods is provided below (Fig. 1).



a b

Fig. 1. Comparison of parameters: a - SDNN and RMSSD by the standard method; b - SDNN and RMSSD with replacement of cardiointervals by a series of absolute increments

The parameters of the control group are highlighted in green, the parameters of the arrhythmic group are highlighted in red. The comparison of the SDNN and RMSSD parameters by the standard method (Fig. 1a) and with the replacement of the cardiac cycle by a series of absolute increments (Fig. 1b) shows that the indicators with the replacement of the series provide a more visual separation between arrhythmic and non-arrhythmic signals.

To identify the differences between the obtained results, the Fisher criterion was used (Tabl. II). In the table, the parameter name includes the following information: the name of the parameter (SDNN, RMSSD), the relation to the arrhythmic group (ARRH) or to the control (CTRL) and whether the parameters were calculated with the replacement of the cardiac series by a series of absolute increments (Ab_In). The significance level was chosen as a = 0.05.

TABLE II. Calculations of Fisher's criterion

Ratio of parameters	Fcalc	Ftable
Statistical parameters		
SDNN_ARRH to SDNN_ARRH_Ab_In	2.49	1.53
SDNN_CTRL to SDNN_CTRL_Ab_In	1.51	2.69
SDNN_CTRL to SDNN_ARRH	2.64	2.38
SDNN_CTRL_Ab_In to SDNN_ARRH_Ab_In	9.90	2.38
RMSSD_ARRH to RMSSD_ARRH_Ab_In	3.38	1.53
RMSSD_CTRL to RMSSD_CTRL_Ab_In	3.08	2.69
RMSSD_CTRL to RMSSD_ARRH	9.90	2.38
RMSSD_CTRL_Ab_In to RMSSD_ARRH_Ab_In	10.85	2.38

IV. Discussion

When comparing the results of the HRV parameters on the replacement of cardiointervals by a series of absolute increments on the graphs, the data anomalies (outliers) parameters are most clearly visible than for the classical one; this method also makes the differentiation of indicators by source – control/arrhythmic – more visual, since the difference between the indicators has

increased significantly, which makes it easier to identify cases of arrhythmia.

V. Conclusion

The results obtained by replacing the cardiointervals with a series of absolute increments increase the differentiation of arrhythmic signals and signals of the control group. This clearly demonstrates the difference between these categories, which confirms the method of calculating the heart rate variability indicators proposed by Fedorov. The analysis showed that RMSSD is a more sensitive indicator for detecting differences in heart rate variability – all four comparisons demonstrated statistically significant differences, while for SDNN only 2 out of 4 comparisons were significant. The most pronounced differences were found between values with the replacement of the time series with absolute increments: for RMSSD, the dispersion in this group with arrhythmia exceeded the control by 10.86 times, for SDNN – by 9.90 times.

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Video Data Processing Algorithm for Optical Surveillance Systems to Detect and Determine Orbits of Unknown Space Objects

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***Abstract*. This paper presents a video data processing algorithm for optical surveillance systems designed to detect unknown space objects. The algorithm employs a set of matched filters constructed based on an experimentally established relationship between the difference frame Fourier spectrum and the space object velocity projection onto the frame plane. It is shown that the correlation peak magnitude and the symmetry of correlation patterns are directly dependent on the extent of match between velocity projections in the frame plane of the reference mask and the detected satellite. The proposed method utilizes a minimum distance criterion along with signal and noise function metrics of the mask and detection region to evaluate correlation patterns and select the optimal solution when an unknown space object is detected in the same region by multiple matched filters. By estimating the velocity projection in the frame plane and using angular measurements of the space object, an initial approximation of the slant range vector in the topocentric coordinate system can be obtained, enabling the determination of its orbital parameters.**

Keywords: **space object detection, optical surveillance, matched filtering, correlation analysis, orbit determination**

I. INTRODUCTION

The challenge of rapidly detecting unknown space objects (space debris, asteroids, small satellites on the first day after launch) and performing initial orbit determination has become critically important due to the growing number of satellite launches [1, 2]. Optical observation methods for detecting and measuring orbits of space objects have gained widespread adoption compared to radar systems due to their comparative accessibility in software and hardware solutions. These include: visual tracking, astrometric methods (precise positional measurements), photometric techniques (brightness analysis), spectral analysis, synchronous multi-station observations.

II. ALGORITHM OVERVIEW

The development of passive optical systems using small-aperture telescopes (<50 cm) to acquire supplementary data on space objects helps alleviate congestion in global near-Earth space monitoring networks [3–5]. Belarusian State University has developed a mobile optical observation system capable of performing angular measurements of low-orbit space objects [6], with its core components illustrated in Fig. 1. The methodology for detecting small moving objects of unknown brightness against quasi-periodic noise in optoelectronic video surveillance systems involved analyzing diffraction patterns of difference frames from video sequences in spatial and frequency domains.

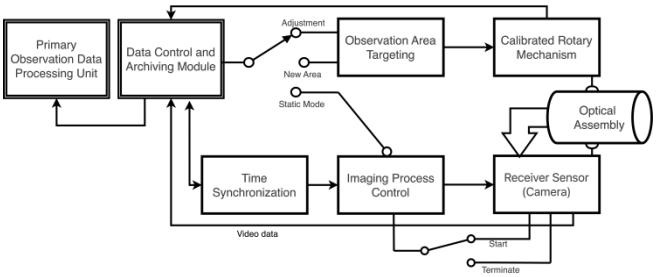

Fig. 1. Key components of a mobile optical observation system for monitoring low-Earth orbit space objects

The construction of a set matched filters is based on an experimentally established relationship between the Fourier spectrum shape of a difference frame and the projection magnitude of the space object velocity projection onto the frame plane [2]. According to the algorithm, the input video stream sequence with N frames is divided into subsequences. For each subsequence, a difference frame is generated as a sign-alternating series of sums:

$$D_j = \sum_{i=0}^{j} (-1)^{j-i} S_i,$$

where $S_i = \sum_{k=ni}^{n(i+1)-1} F_k$ is the sum of a group of n frames from the video sequence, F_k is the j-th frame of the video sequence.

The difference frame for N frames of the video sequence is given by:

$$D_N = \sum_{i=0}^{N-1} (-1)^{N-1-i} S_i.$$

The difference frames of the subsequences D_N are divided into blocks of size $m \times m$. For each individual block of the difference frame, the amplitude spectrum is calculated. The amplitude spectra of the blocks and sets of matched filters (masks) are used to compute spatial correlation values. The Decision-Making Function (DMF), based on the maximum correlation value and evaluation metrics of the signal/noise functions of the mask and detection region determines the presence/absence of a signal. The Minimal Distance (MD) criterion assesses correlation patterns and selects the optimal decision when an unknown space object is detected in the same region by multiple matched filters (masks). In other words, this false-positive exclusion and correlation pattern evaluation metric identifies the optimal choice when $n > 1$ matched filters detect an unknown space object in a given region.

It has been established that in detection regions, the velocity projection in the frame plane of an unknown space object V_{pd} and that of a reference satellite with known orbital parameters V_{pm} exhibit similar values, satisfying the relation $V_{pd} \approx V_{pm}$. Detecting an unknown space object within the optoelectronic system's pointing region and estimating its the velocity projection in the frame plane V_{pd} enables the initial approximation of the slant range vector in the topocentric coordinate system [7, 8] as:

$$\boldsymbol{\rho}_{X_1Y_1Z_1}(t) = \frac{V_{pd}(t) \cdot \Delta t}{\beta} \mathbf{L}(t),$$

where $\mathbf{L}(t)$ is the unit vector directed along the slant range vector $\boldsymbol{\rho}_{X_1Y_1Z_1}$, β is the angle between the slant range vectors at times t and $t+\Delta t$, Δt is the time interval between measurements of the angular coordinates (right ascension α and declination δ) of the space object within the detection region.

The initial approximation of the slant range vector enables the calculation of the space object position vector in the detection region. To determine the object's orbit, two position radius vectors (measured in the geocentric inertial coordinate system at times t_{1d} and t_{2d} ($\mathbf{r}_{1d}(x_{1d}, y_{1d}, z_{1d})$, $\mathbf{r}_{2d}(x_{2d}, y_{2d}, z_{2d})$) are used. The orbital parameters (semi-major axis a, inclination i, eccentricity e, longitude of the ascending node Ω, argument of latitude u) of the detected satellite are computed from the two known position vectors $\mathbf{r}_{1d}$ and $\mathbf{r}_{2d}$ by solving Lambert's problem via the Gauss method [9, 10].

III. Results and Discussion

Experimental results are presented for the detection algorithm implementation in the initial orbit determination method, applied to the rocket stage SL-12/RB (NORAD 15772) using a matched filter parameterized with the reference satellite/mask Seasat 1 (NORAD 10967). The errors in determining the velocity magnitude $(V_P)_d$ in the frame plane for the detected satellite SL-12/RB were: 0.0115 km/s for the first region and 0.0635 km/s for the second region. All errors calculated against SGP model predictions [8]. Fig. 2a–e shows the blocks of difference frames of the reference satellite (Seasat 1) and the detected object (SL-12/RB), as well as their cross-correlation patterns between the two objects across both detection regions.

Based on detection and slant-range calculations in Regions 1 and 2, the absolute errors in the components of the position radius vector were: $(\Delta x_{1d}, \Delta y_{1d}, \Delta z_{1d})^{err}_{abs}$ = (1.63; 0.47; 2.37) km for Region 1; $(\Delta x_{4d}, \Delta y_{4d}, \Delta z_{4d})^{err}_{abs}$ = (–0.81; –3.17; –8.05) km for Region 2. This corresponds to a position vector magnitude error of: 2.91 km for Region 1; 8.69 km for Region 2. For angular measurements with a 0.6-second interval, the absolute velocity vector error of the detected SL-12/RB rocket stage was: $(\Delta V_{1X}, \Delta V_{1Y}, \Delta V_{1Z})^{err}_{abs}$ = (–0.035; –0.051; –0.138) km/s (equivalent to a velocity magnitude error of 0.220 km/s).

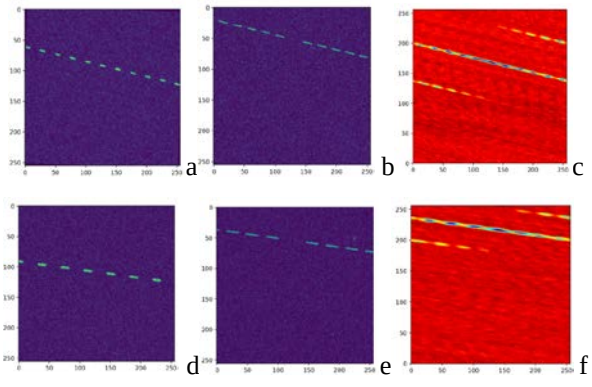

Fig. 2. First (a, b, c) and second (d, e, f) detection regions of the rocket stage SL-12/RB (NORAD: 15772)

The results demonstrate that the proposed method successfully determined the angular orbital parameters

of the SL-12/RB stage for a 0.6-second measurement interval between detection regions with the following absolute errors: 0.271° for inclination *i*, –0.632° for longitude of ascending node Ω, 0.208° for argument of latitude *u*. Additionally, absolute errors for semi-major axis *a* and eccentricity *e* were: 19.71 km and 0.0144. The obtained results demonstrate accuracy comparable to that of initial orbit determination by expensive wide-aperture optical systems, where the errors in the initial determination of the semi-major axis and angular orbital parameters of the detected space object are on average less than 50 km and no worse than 0.5 deg, respective.

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GPU-Only Neural Network Inference Using Fragment Shaders in OpenGL

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***Abstract*. This paper addresses the efficient use of neural networks on graphics processing units (GPUs). A GPU-only inference pipeline was designed and implemented using fragment shaders in OpenGL. The proposed solution avoids reliance on CPU interaction, allowing for real-time neural network execution on a wide range of devices, including mobile and embedded platforms. Performance was benchmarked against industry-standard frameworks such as TensorFlow Lite and MediaPipe. The results demonstrate that GPU shader-based inference can achieve competitive latency, with significantly reduced energy consumption and memory usage. This approach is applicable to fields such as augmented reality, automotive systems, and biomedical imaging.**

***Keywords*: neural networks, GPU, fragment shaders, OpenGL, real-time inference, TensorFlow Lite, MediaPipe, ESPCN**

I. Introduction

In recent years, there has been a marked increase in de- mand for high-performance and low-latency neural network execution on edge devices. Conventional CPU-based solutions frequently prove incapable of meeting real-time constraints or necessitate excessive power. Graphics processing units (GPUs) were originally developed for the purpose of rendering graphics. However, they have evolved into a potent substitute due to their massively parallel architecture.

This paper explores the potential of fragment shaders [5], which are commonly employed in rendering pipelines, for the purpose of neural network inference. In contrast to general-purpose compute APIs such as CUDA or Vulkan Compute, fragment shaders demonstrate a high level of platform support, encompassing mobile and embedded systems.

II. Related Work

Existing libraries such as TensorFlow Lite [1] and PyTorch Mobile [2] support GPU acceleration, yet still rely on CPU – GPU communication and intermediate memory copies. While the efficacy of this architecture is evident, it must be noted that it introduces latency and overhead.

A number of studies have been conducted on the utilization of WebGL and OpenGL shaders for the purpose of inference. However, a significant proportion of these implementations are confined to fundamental operations, or alternatively, demonstrate inadequate scalability. The present work is an expansion of these concepts, with the objective of constructing a comprehensive, scalable inference pipeline on GPU that utilizes solely fragment shaders.

III. System Design

The proposed pipeline is implemented in OpenGL [5] and comprises the following stages:

1) Model Preprocessing: Conversion of trained models into shader-executable instructions. This involves quantization, layer merging, and texture mapping for weights and biases.

2) Shader Execution: Each neural network layer is translated into a GLSL fragment shader, compiled at runtime, and executed via full screen rendering.

3) Output Handling: Results are extracted from render targets and can be displayed or used as input for further GPU computations.

This approach eliminates CPU involvement during inference, minimizing context switching and memory copy overhead.

IV. Fragment shader

Fragment shaders [5] are able to access texture data stored in a specialized memory facility known as the texture cache. This approach frequently yields faster results than accessing data stored in global memory, particularly in cases where texture data is accessed multiple times.

In convolutional neural networks (CNNs), the most common operation, and consequently one of the most complex, is convolution. Convolution in two dimensions or images is a context-dependent algorithm in which the output value is computed as the sum of the products of the kernel and sampled input pixels. This renders the fragment shader a suitable use case when developing an output mechanism for CNN deployment.

In the process of translating the operations performed by the CNN into a realizable pipeline, it is imperative to recognise that the input layer data will be in the texture and processed by the vertex and fragment shaders. Subsequently, the data is written to the render target. Depending on the number of input and output channels, the data can be stored either as a 2D texture storing 4 channels or as a 2D texture array storing another 4 channels. In the context of the convolution operation within the fragment shader, the weights are to be transmitted through the uniform buffer object or as input uniforms.

ESPCN [4] MODEL LAYER RATIO AND NUMBER OF RENDER PASSES

	ESPCN model	**Number of passes**
Layer 1	Conv2D output $n \times n \times 16$	4 render passes
Layer 2	Conv2D output $n \times n \times 16$	4 render passes
Layer 3	Conv2D output $n \times n \times 4$	1 render pass
Layer 4	Subpixel output $2n \times 2n \times 1$	1 render pass

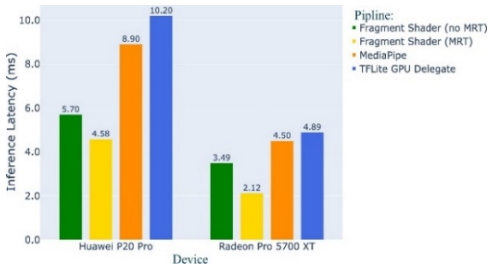
In general terms, the necessary .glsl files are created directly after the data is extracted from the model file, using templates that are unique to each layer and which are written in advance. For the model that has been selected, three templates are required: one for the convolutional layer, one for the activation layer, and one for the subpixel convolutional layer.

It is also noteworthy that each shader is responsible for generating the 4-channel output in the render pass. The calculation of a layer that possesses more than four outputs necessitates the implementation of multiple .glsl files and render passes. This implementation was required for the selected model. As illustrated in Table, the layers are accompanied by their respective quantities of render passes.

V. EVALUATION OF LATENCY

The testing encompassed two devices characterised by markedly divergent architectures and computing capabilities: a Huawei P20 Pro mobile smartphone, which is based on an ARM Mali-G72 MP12 GPU, and a laptop equipped with discrete AMD Radeon Pro 5700 XT graphics. The utilisation of these devices facilitates a comparative analysis of the performance of mobile and desktop GPUs in the domain of high-performance real-time inference.

As demonstrated in Figure, the shader implementation (in both modes) exhibits a substantial advantage in terms of execution time in comparison to MediaPipe [3] and TFLite [1]. It is evident that on the Huawei P20 Pro, the pipelining on fragment shaders yielded an average latency of 5.3 milliseconds, whereas MediaPipe [3] and TFLite [1] exhibited respective averages of 8.9 and 10.2 milliseconds. The discrepancy is particularly evident in the desktop system, wherein the shader implementation exhibits latency ranging from 2.1 to 3.5 milliseconds, whereas MediaPipe [3] and TFLite [1] demonstrate latency exceeding 4 milliseconds.



Comparison of ESPCN [4] model inference latency on different GPUs and pipelines

The results obtained demonstrate that, with effective organization of the computational graph of the model and the judicious selection of GPU-oriented primitives, the implemented pipelines can exhibit significantly superior performance in comparison to existing solutions without the necessity for third-party libraries or platform dependencies. The advantage is especially apparent in mobile inferencing, where response time is critical to ensure the quality of user experience in augmented reality and real-time computer vision tasks.

VI. CONCLUSION

This paper presents a GPU-only pipeline to run the ESPCN [4] model on OpenGL [5] shaders without $CPU \Rightarrow GPU$ overhead. The developed pipeline demonstrates that fragment shaders can be effectively utilized for neural network infer- ence. Due to the limited number of operations within the ESPCN network, the overheads associated with data transformation and transfer within the universal framework, and the subsequent return of results to the GPU pipeline are of considerable significance. The mean processing time for a frame in the implemented pipeline is more than twofold shorter than when using universal libraries, thus demonstrating the efficacy of the selected approach.

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Evaluation of Effectiveness of the Method of Multilevel Amplitude Discrimination of ECG Signal in Arrhythmia Detection

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***Abstract*. Relevance: The work is devoted to the study of the effectiveness of the method of multilevel amplitude discrimination, which allows to obtain the distribution of amplitudes of the ECG signal, aimed at determining the differences between ECG recordings of patients with arrhythmia and normal heart rate using statistical criteria. Objectives: Using statistical criteria, to evaluate the differences in the distributions obtained for arrhythmic and normal ECG signals. Tasks: Construction of actual distributions of ECG signal values for patients with arrhythmia and normal heart rhythm. The formation of averaged distributions for each type of signal. Evaluation of the statistical significance of differences between the distributions of arrhythmic and normal type signals. Solutions: The application of the method of multilevel amplitude discrimination in relation to ECG signals of various types is considered. The Pearson and Kolmogorov-Smirnov criteria were used to identify differences between the distributions obtained. The results of the study were presented graphically. Analysis of the results: The calculated value of the Pearson criterion was 17847.745, which exceeds the critical value of the criterion (44.985) at a significance level of 0.05 for a given number of degrees of freedom 31. The calculated value of the Kolmogorov-Smirnov criterion is 26.849, which exceeds the critical value of the criterion (1.385) at a significance level of 0.05. Thus, the multilevel amplitude discrimination method effectively detects differences between normal and arrhythmic ECG signals.**

***Keywords*: multilevel amplitude discrimination, amplitude distribution, ECG signals, Pearson criterion, Kolmogorov-Smirnov criterion**

I. Introduction

The ECG signal is one of the main indicators of the state of the cardiovascular system. The functioning of the heart is a rhythmic process, so any deviation from the norm should be interpreted as a disease or anomaly. There are many statistical analysis methods for processing ECG signals that are used in the classification of conditions and diseases [1]. One of the methods of statistical study of ECG signals is the method of multilevel amplitude discrimination, which allows to obtain the distribution of the amplitudes of the ECG signal [2].

II. Main Part

A. Theoretical Research

The multilevel amplitude discrimination method is used for the digital ECG signal, represented by a set of u_i values measured at certain time points (samples), where $i = 1, ..., n$, n is the number of samples in the lead.

When analyzing ECG signals, it is necessary to ensure their comparability, therefore, the signals must have the same frequency and time duration.

Differences in the amplitude of the signals are eliminated by normalizing the signal values using the formula:

$$u0_i = [u_i - \min(u_i)]/[\max(u_i) - \min(u_i)], \quad (1)$$

where $u0_i$ is the normalized value of the signal, u_i is the actual value of the signal, $\min(u_i)$ is the minimum value of the signal, $\max(u_i)$ is the maximum value of the signal.

The range of signal values is divided into a pre-selected number of intervals m and the number of signal values falling into each of these intervals is determined.

The Pearson criterion [3] belongs to a group of nonparametric criteria (independent of the shape of the sample distribution) and allows you to check the significance of differences between absolute (or relative) frequencies for two given samples. The application of the criterion involves the formulation of a null hypothesis about the absence of differences between two given samples. In this study, the null hypothesis is assumed that there are no differences between the averaged histograms of ECG signal distributions of many healthy people and many patients with arrhythmia.

Next, the criterion statistics are calculated:

$$\chi^2 = \Sigma[(f_{ar} - f_{norm})^2/f_{norm}], \quad (1)$$

where f_{norm} are the frequencies of the averaged histogram of healthy people, f_{ar} are the frequencies of the averaged histogram of patients with arrhythmia.

A critical value $(\chi^2)_{cv}$ is selected for the accepted significance level of the criterion α and the number of degrees of freedom $df = m - 1$, where m is the number of histogram intervals. Next, the calculated value of the criterion is compared with the critical one. If the calculated value exceeds the critical value, the null hypothesis must be rejected. Otherwise, the hypothesis that there are no differences between the histograms of sets of healthy people and people with arrhythmia is accepted.

The Kolmogorov-Smirnov criterion can also be used to determine the differences between two sample distributions. To apply it, it is necessary to calculate the accumulated relative frequencies for each distribution, and then calculate the calculated value of the criterion using the formula:

$$D = (n_{ar} \cdot n_{norm}/(n_{ar} + n_{norm}))^{0.5} \cdot \max |c_{ar}(i) - c_{norm}(i)|, \quad (3)$$

where $c_{ar}(i)$ is the accumulated relative frequencies of the arrhythmic signal, $c_{norm}(i)$ is the accumulated relative frequencies for the normal signal, n_{ar} is the sample size of the arrhythmic signal, and n_{norm} is the sample size of the normal signal.

Next, the calculated value of the criterion is compared with the critical value D_{cv} for the selected significance level. If the calculated value does not exceed the critical value, then at the selected significance level, the null hypothesis about the absence of differences between the ECG signal distributions of healthy people and patients with arrhythmia is accepted. If the calculated value exceeds the critical value, the null hypothesis must be rejected.

B. Experimental Research

For comparison, ECG signals were selected from the databases of the Physionet Internet resource: Mit-bih-normal-sinus-rhythm-database-1.0.0 (ECG of healthy people, 18 signals from different people, each of the signals is represented in two leads, the frequency of measurement of the signal is 128 Hz) [4, 5] and Mit-bih-supraventricular-arrhythmia-database-1.0.0 (ECG of patients with supraventricular arrhythmia, 78 signals from different people, each of the signals is represented in two leads, the measurement frequency of the signal is 128 Hz) [4, 6]. To ensure comparability of the data, the same number of values was selected for each signal (38400 samples).

During signal processing, histograms of the amplitude distribution over m=32 intervals of normalized values were obtained. An average histogram of the distribution was formed for each type of signal (the average values of the actual histogram frequencies from the corresponding sample were taken as frequencies for each group). Results are shown in Fig. 1.

When using statistical criteria, the significance level $\alpha = 0.05$ was selected. This means that statistically significant differences can be detected with a probability of 0.95.

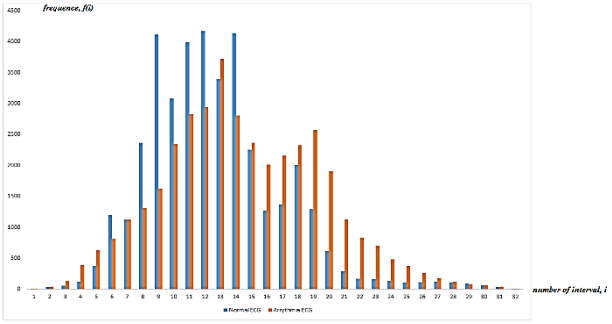

Fig. 1. Histograms of the average distributions of normal and arrhythmic signals (orange – arrhythmia, blue – norm)

The calculated value of the Pearson criterion by (2) is $\chi^2 = 17847.745$, which exceeds the critical value of the criterion $(\chi^2)_{cv} = 44{,}985$ at a significance level $\alpha = 0.05$ for a given number of degrees of freedom $df = 31$.

A graphical interpretation of the Kolmogorov-Smirnov criterion is shown in Fig. 2.

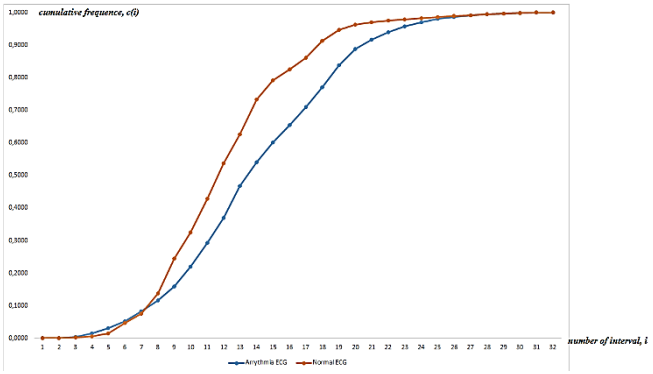

Fig. 2. Graphs of the functions of the averaged distributions of normal and arrhythmic signals (orange – arrhythmia, blue – norm)

The calculated value of the Kolmogorov-Smirnov criterion by (3) is $D = 26.849$, which exceeds the critical value of the criterion $D_{cv} = 1.385$ at the significance level $\alpha = 0.05$.

III. Conclision

Thus, the method of multilevel amplitude discrimination can be used to establish differences between ECG signals of normal and arrhythmic type. The results of applying the statistical criteria of Pearson and Kolmogorov-Smirnov confirm the statistical significance of the distribution differences.

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Distributed Analytical Energy Monitoring System

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Abstract. **This paper presents a comprehensive energy consumption monitoring system designed to meet modern requirements for efficiency and environmental safety of energy system. The developed system consists on the following main components: measuring modules embedded into the devices under monitoring, client, online distributed analytical monitoring system with database and means for data processing and visualization. The platform implements advanced data visualization using Apache Superset and employs finite difference methods for anomaly detection in power consumption patterns. A linear predictive model incorporating anomaly count parameters enables equipment lifetime estimation and predictive maintenance scheduling. The system demonstrates high applicability for monitoring electrical energy sources, including hydrogen fuel cell systems.**

Keywords: **energy monitoring, Hall effect sensor, anomaly detection, predictive maintenance, IoT, data visualization**

I. Introduction

Modern requirements for energy efficiency and environmental safety necessitate the development of electrical energy control systems. Such systems can monitor both consumers [1] and electrical energy sources in local or remote modes [2]. These systems are especially important when organizing management and control systems for electrical energy sources based on hydrogen fuel cells [3–6] since they provide data sets for development dedicated systems for their diagnostics and state of health prognosis.

To organize the corresponding distributed monitoring system, the special modern solution is required with the possibility of data accumulation, analysis, decision making and visualization. The development of such system is the main task of present paper.

II. System Architecture and Implementation

The developed system consists on the following main components: measuring modules embedded into the devices under monitoring, client, online distributed analytical monitoring system with database and means for data processing and visualization. The diagram presented in Fig. 1 illustrates a system architecture comprising several interconnected components. A Device serves as the primary data source, transmitting raw sensor or operational data via telecommunication networks to a central Server (Backend on Kotlin). This server, implemented using Kotlin, acts as the core processing unit, handling incoming data and managing system logic.

The visualization platform is implemented using the Superset BI tool, as confirmed by the interface image presented in Fig. 2. The interface demonstrates key energy indicators – maximum and minimum voltage, maximum current value, and total energy consumption, presented as separate cards. Additionally, the screen displays a graph illustrating the dynamics of energy consumption changes over time, where sharp spikes and general power change trends are clearly distinguishable.

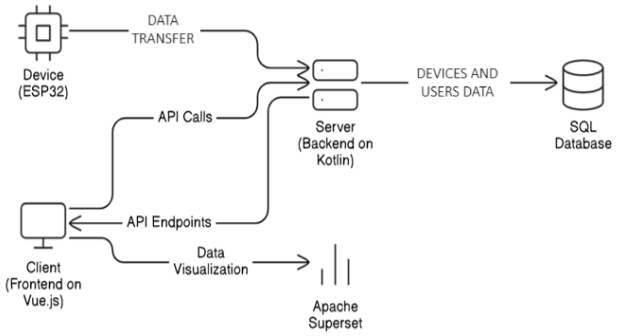

Fig. 1. Architecture of the platform

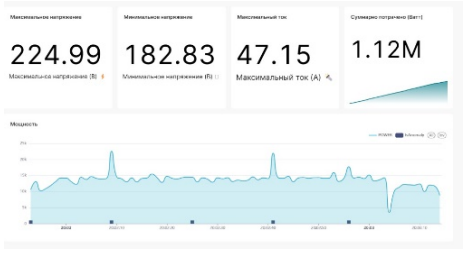

Fig. 2. Measured data display in Superset interface

A Client (Frontend on Vue.js), developed with Vue.js, interacts with the server through API Calls and receives API Endpoints for various functionalities. This

client is responsible for user interaction and presenting information.

The Server stores persistent information, including Device and User Data, in a SQL Database. This database ensures data integrity and provides structured storage for all critical system information.

For analytical purposes and visual representation of data, the Client sends Data Visualization requests to Apache Superset. Apache Superset is utilized for creating interactive dashboards and reports, enabling comprehensive analysis of the collected data.

The Superset platform interface provides operators with the ability to view current parameter values and their historical trends. The graphical module allows configuring data update time intervals, applying additional filtering and smoothing methods.

III. Anomaly Detection Algorithm

A. Finite Difference Method

One of the central aspects of the analysis is the finite difference method used to evaluate changes in measured current $I(t)$. According to the developed algorithm, the difference $\Delta I = I(t+\Delta t) - I(t)$ is calculated for each time interval. When the established threshold is exceeded, the system registers anomalous changes, which may indicate deviations from normal operating mode and the need for diagnostic measures. The modulus $|I'(t)| = \Delta I/\Delta t$ is registered, and when it exceeds threshold T, anomalous changes are recorded (in practice, spikes of approximately +600 and -600 W/min are observed).

Fig. 3 presents the dependence of the smoothed power derivative on time, calculated from measurement data obtained during system monitoring. This dependence was obtained by applying the finite difference method to the original time series of energy indicators, previously cleaned of high-frequency noise using moving average filtering.

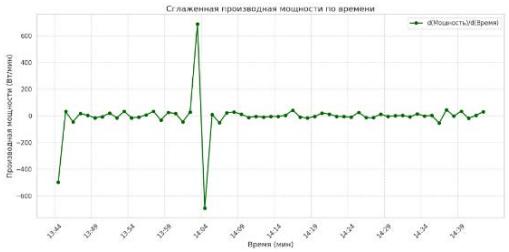

Fig. 3. Differentiation results of original energy consumption data

Differentiation in this case allows evaluating the rate of power change, which is an important diagnostic parameter for detecting transient processes and anomalous modes in system operation. The obtained graph shows a sharp spike in power derivative values near the 13:40 time mark, where the amplitude of changes approximately reaches +600 and -600 units (W/min or equivalent measurement unit used in the study). Such an extreme transition indicates rapid changes in the system's energy regime and points to the occurrence of critical impact or transition to a non-standard state requiring immediate response.

IV. Predictive Maintenance Model

A. Linear Regression Model

The differentiated data allows conclusions about equipment operation and its service life. An important component of the proposed system is the integration of the "Number of anomalies" parameter (A) into a linear model:

$$Y = \beta_0 + \beta_1 A, \quad (1)$$

where Y represents the conditional value of the system's remaining resource. This indicator allows forecasting the remaining equipment service life and serves as a basis for preventive maintenance planning. Including parameter A in the model provides quantitative assessment of identified anomalies' impact on degradation processes, which increases the reliability of diagnostic forecasts and allows timely correction of operating modes to prevent critical failures.

The application of smoothing algorithms reduced the influence of random fluctuations, ensuring reliable representation of the true nature of power change dynamics. The differentiation result provides information about instantaneous changes in the system. The obtained data can be used to build adaptive control algorithms ensuring operational regulation of processes in technical condition control systems.

V. Results and Discussion

The comprehensive approach combining precise parameter measurement, effective data processing, and competent application of analytical models demonstrates high applicability of the system for monitoring the technical condition of electrical energy sources. The developed methodology not only improves diagnostic efficiency but also provides a foundation for implementing adaptive control algorithms in distributed control systems, contributing to increased reliability and efficiency of power system operation.

Key achievements include: high-precision measurement, real-time visualization, automated anomaly detection, predictive maintenance capability, scalable architecture.

VI. Conclusion

The developed energy consumption monitoring system demonstrates significant potential for improving the reliability and efficiency of electrical energy source management. The integration of precise measurement

techniques, advanced data processing algorithms, and predictive analytics provides a comprehensive solution for modern energy management challenges.

Future work will focus on expanding the system's capabilities to include machine learning algorithms for pattern recognition and enhanced predictive accuracy. Additionally, integration with renewable energy sources and energy storage systems will be explored to support the transition toward sustainable energy infrastructure.

ACKNOWLEDGMENT

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A-LightNet: A Lightweight YOLOv8n-Based Model for Aerial Small Object Detection

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Abstract. **Aerial imagery often presents unique challenges for object detection tasks, especially when detecting small-scale objects such as pedestrians, vehicles, and equipment from high altitudes. This paper proposes A-LightNet, an enhanced and lightweight object detection model based on YOLOv8n, tailored specifically for aerial small object detection. We introduce a multi-scale attention fusion module and high-resolution context enhancement, along with an optimized head structure for precise localization. Evaluated on the VisDrone dataset, our model outperforms baseline YOLOv8n in both accuracy and efficiency while maintaining compactness for deployment on UAV platforms.**

Keywords: **Aerial object detection, small target, YOLOv8n, lightweight model, UAV, VisDrone**

I. Introduction

In the field of aerial surveillance and UAV-based imaging, detecting small-scale objects poses a significant challenge due to limited pixel coverage, dense scenes, and complex backgrounds. Traditional object detectors often suffer from missed detections or low precision in such scenarios. Although YOLOv8n provides a lightweight and fast detection framework, its performance degrades when dealing with tiny aerial targets. This motivates our work: developing an enhanced YOLOv8n-based architecture for small object detection from UAV imagery.

II. Related work

Many recent studies aim to address small object detection challenges using improved feature fusion, attention modules, and dataset-driven anchor tuning. VisDrone, as a benchmark dataset, highlights the difficulty of UAV-based detection tasks, where most annotated targets fall under the "small" category. While YOLOv5s and SSD variants are commonly used, recent works like OD-YOLO and TinyDet explore structure-aware optimization for UAV scenes. However, they either sacrifice speed or increase model complexity significantly.

III. Methodology

A-LightNet builds upon the YOLOv8n architecture with three key enhancements:

1. Multi-Scale Attention Fusion (MAF): We insert an attention module across the neck layers to enhance relevant features at each scale while suppressing background noise. 2. High-Resolution Pathway (HRP): A shallow feature path (P2 layer) is reintroduced into the neck to retain fine-grained spatial information crucial for small target representation. 3. Decoupled Head with UAV Optimization (DH-UAV): Separate classification and regression heads are introduced with tailored anchor design specific to VisDrone target sizes.

The object detection task is formulated as a joint classification and localization problem. The loss function L is composed of three components:

$$L = \lambda_{cls} \cdot L_{cls} + \lambda_{obj} \cdot L_{obj} + \lambda_{box} \cdot L_{box} . \quad (1)$$

We adopt the CIoU loss for bounding box regression:

$$L_{box} = 1 - IoU + \frac{\rho^2(b, b^{gt})}{c^2} + \alpha v , \quad (2)$$

where:

– ρ is the Euclidean distance between the center points of the predicted box b and the ground truth box b^{gt}.

– c is the diagonal length of the smallest enclosing box.

– v measures the similarity of aspect ratios.

– α is a positive weighting factor.

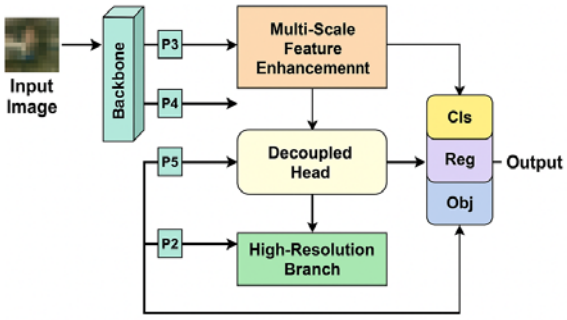

Fig. 1. Model Structure of A-LightNet

IV. Experiments

We evaluate A-LightNet on the VisDrone2019 dataset using mAP@0.5, Precision, Recall, and FPS as metrics. Training uses standard augmentation, SGD optimizer, and batch size 16 for 100 epochs.

Performance Comparison of YOLOv8n and A-LightNet on the VisDrone Dataset

Model	mAP@0.5	Precision	Recall	FPS
YOLOv8n	67.2 %	71.4 %	68.1 %	123
A-LightNet	74.1 %	78.8 %	76.2 %	117

PR curves show consistent gain across all categories, especially for small pedestrian and vehicle detection.

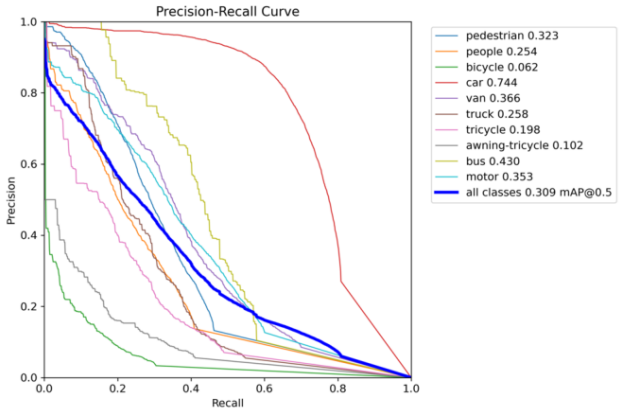

Fig. 2. Precision-Recall Curve Comparison on VisDrone

V. Conclusion

A-LightNet demonstrates that with careful architectural tuning, YOLOv8n can be significantly improved for aerial small object detection. The model achieves higher accuracy while maintaining real-time capability. Future work will explore transformer-based backbone replacement and real UAV deployment.

Acknowledgment

This work is supported by Belarusian State University. The author thanks the UAV research group and VisDrone challenge organizers.

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Structural and Circuit Design Aspects of Implementing a Two-Level Computational Control Unit for an Unmanned Vehicle

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Abstract. **This paper presents a two-level computational control unit designed for unmanned vehicles, addressing the challenge of achieving autonomy, reliability, and scalability in dynamic environments. The system integrates a low-level block with STM32H7 and STM32F4 microcontrollers for real-time sensor processing and actuator control, and a high-level ARM-based PC for advanced computations, including machine vision and route planning. Implemented on an MTZ-112N-01 mini-tractor, the system demonstrates effective autonomous navigation, obstacle avoidance, and robust communication. The proposed architecture optimizes resource distribution, enhances fault tolerance, and offers significant advantages over traditional single-level systems in terms of flexibility and energy efficiency.**

Keywords: **unmanned vehicle, two-level architecture, microcontroller, sensor integration, real-time control**

I. INTRODUCTION

The rapid growth of unmanned vehicle applications in agriculture, logistics, and defense underscores the need for robust control systems capable of ensuring autonomy, reliability, and adaptability [1, 2]. Existing solutions often face challenges in integrating diverse sensors, processing large data volumes in real time, and maintaining energy efficiency due to the limited resources of microcontrollers [3, 4]. This research addresses these issues by developing a twolevel computational control unit that combines low-level microcontrollers for real-time operations with a high-level ARM-based processor for complex tasks, implemented on an MTZ-112N-01 mini-tractor.

II. PROBLEM STATEMENT

Unmanned vehicles require control systems that balance real-time responsiveness with the ability to process complex algorithms, such as machine vision and route planning, while maintaining low power consumption and scalability [5]. Single-level architectures often struggle with resource constraints, leading to performance bottlenecks or high energy demands [6]. Additionally, integrating heterogeneous sensors (e.g., LiDAR, cameras, sonars) poses challenges in data synchronization and compatibility [7]. This work aims to addresses these limitations and supports autonomous operations in dynamic environments.

III. PROPOSED SOLUTION

A. Two-Level Architecture

The proposed system employs a two-level architecture comprising a low-level computational block (LLB) and a high-level computational block (HLB). The LLB, based on STM32H7 and STM32F4 microcontrollers, handles real-time tasks, including sensor data acquisition (from sonars, laser rangefinders, and analog cameras) and actuator control (e.g., servomotors, hydraulic valves). It supports up to 14 digital inputs and 14 digital outputs, six 60W PWM channels, and interfaces like RS232, UART, and CAN, with galvanic isolation for noise immunity [8]. The HLB, an ARM-based PC (e.g., Khadas VIM4), performs complex computations, such as machine vision using optimized algorithms and route planning, and manages external communications via Ethernet and 3G/4G modems.

B. Sensor and Actuator Integration

The system integrates eight automotive sonars, two laser rangefinders, and two analog cameras, supported by custom metal mounts for flexible positioning. A GNSS module with RTK and inertial navigation units (accelerometers, gyroscopes, magnetometers) ensure precise positioning. A separate power board manages tractor electronics, including linear actuators for brake and clutch control, ensuring electromagnetic compatibility [9].

C. Communication and Interfaces

Ethernet provides high-speed, reliable data exchange between LLB and HLB, supporting real-time machine vision and remote monitoring. A 121-pin TE1241434-1 connector enables flexible peripheral integration, while radio modems (e.g., Nevod-5) and a ELRS controller ensure robust remote control over 1 km [10].

IV. Implementation and Results

A. Implementation on MTZ-112N-01

The control unit was implemented on an MTZ-112N-01 mini-tractor. Sensors were calibrated to ensure accurate data collection, with sonars connected via CAN, rangefinders via UART, and cameras via an ADV7180 decoder processed by the STM32F4's DCMI interface. A custom odometer, using an inductive sensor and a perforated disc, was developed to measure speed and distance, addressing the tractor's lack of native odometry [11]. The system was housed in durable, lightweight enclosures to protect against environmental factors.

B. Field Testing

Field tests on an asphalt road validated the system's performance. The tractor followed predefined routes (e.g., circular and figure-eight patterns) at speeds up to 8 km/h, using GNSS RTK and inertial navigation for precise tracking. The system detected obstacles via sonars and cameras, executing avoidance maneuvers or stopping to prevent collisions. Machine vision algorithms, optimized for microcontrollers using STM32Cube.AI, enabled reliable object detection [12].

C. Performance Outcomes

The two-level architecture ensured real-time responsiveness (LLB) and intelligent decision-making (HLB). The system demonstrated low power consumption, high reliability, and scalability, with the LLB maintaining critical functions during HLB failures. Data logging facilitated performance analysis, confirming effective sensor integration and robust communication.

V. Significance and Comparison

Compared to single-level systems [3, 6], the two-level architecture offers superior resource distribution, isolating critical tasks to ensure fault tolerance. Unlike high-level-only solutions [13], it achieves energy efficiency suitable for compact platforms. The use of STM32 microcontrollers for machine vision, as opposed to GPU-based systems [14], reduces costs and power demands, aligning with findings in [12, 15]. The system's modular design and standardized interfaces (e.g., Ethernet, CAN) enhance scalability over modular architectures lacking standardization [7].

VI. Conclusions

The two-level control unit advances unmanned vehicle technology by combining real-time control with advanced computation, as demonstrated on the MTZ-112N-01. Its scalability, reliability, and energy efficiency make it suitable for diverse applications. Future work includes developing a configurator to simplify system setup, enhancing accessibility for developers.

Acknowledgment

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Methods for Reconstructing Parts Training Images from a Pre-trained Neural Network

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Abstract. **Neural networks have had a major impact on the field of computer vision and are now integral to many modern systems. However, their widespread use raises new security concerns, especially regarding the protection of proprietary and potentially sensitive training data. Since trained neural networks may encode information about the data they were trained on, it becomes possible to reconstruct parts of that data from the model's weights.**

This work investigates methods for reconstructing training data from pre-trained neural networks. We explore existing approaches and propose two new methods – one tailored for homogeneous networks, and another applicable to arbitrary architectures given partial training history. These methods are experimentally evaluated, and we demonstrate that, under certain conditions, it is possible to reconstruct full or partial training samples, revealing significant privacy risks in neural network deployment.

Keywords: **neural networks, dataset reconstruction, attacks on neural networks, neural network security**

I. Introduction

Let $D = \{x_i, y_i\}_{i=1}^{N}$ be a training dataset, where $x_i \in R^{H\times W\times 3}, y_i \in \{0,1\}$ – a dataset for a binary classification task. Let $f(\cdot, \theta)$ be a neural network trained on D. The task is to extract some samples from D, using only weights of the trained model.

Neural network $f(\cdot, \theta)$ is called homogeneous if $\exists L > 0 \forall \alpha > 0: f(x, \alpha\theta) = \alpha^L f(x, \theta)$. Note, that linear operators, including convolution, ReLU activation function, batch normalization are homogeneous.

Neural network converges in direction $\hat{\theta}$ if $\lim_{t\to\infty} \frac{\theta_t}{||\theta_t||} = \hat{\theta}$.

The work [1] studies directional convergence of homogeneous neural network, trained using gradient descent algorithm.

The work [2] proposes a KKT method for reconstructing data from a training dataset based on results of [1] from pre-trained homogeneous models. The method is evaluated on MLP models.

II. Methods for reconstructing training data

Let $L(y_{\text{true}}, y_{\text{pred}})$ be a differentiable over $y_{\text{pred}} = f(x, \theta)$ function. Neural networks are trained by the gradient descent algorithm:

$$\theta_{t+1} = \theta_t - \mu \nabla_\theta L(y_{\text{true}}, f(x, \theta_t)). \quad (1)$$

Where μ is learning rate. The gradient descent process (1) can be rewritten in terms of ODE:

$$\begin{cases} \theta(t) = -\nabla_\theta L\left(y_{\text{true}}, f(x, \theta(t))\right), \\ \theta(t) = \theta_0. \end{cases} \quad (2)$$

Neural networks are usually trained till convergence. By making assumptions about convergence, we can develop methods for reconstructing training data.

A. Stationary method

Suppose, that model has converged to a stationary point. We can describe it with the equation:

$$\nabla_\theta L(y_{\text{true}}, f(x, \theta)) = 0. \quad (3)$$

Training data satisfies equation (3). Reconstructions can be found by solving optimization problem:

$$||\nabla_\theta L(y, f(x, \theta))|| \to \min_{x,y}. \quad (4)$$

In practice, we weren't able to reconstruct any training samples using this method. This method is called stationary method.

B. KKT method

This method was proposed in paper [2] and is based on theorem, proved in [1].

Theorem [1]. Let $\Phi(\cdot, \theta)$ be a homogeneous neural network with ReLU activation functions. If the log-loss is minimized and there exists a timestep t, such that

$L\big(x_i, f(x_i, \theta_t)\big) < 1, \forall i,$ then gradient descent converges to a point (5):

$$\min_{\theta} \frac{1}{2}||\theta||^2, \forall 1 \le i \le n: \frac{y_i - 0.5}{0.5} \Phi(x_i, \theta) \ge 1. \quad (5)$$

The KKT method [2] is formulated as solution of the following optimization problem:

$$||\theta - \sum_{i=1}^{N} \lambda_i y_i \nabla_\theta \Phi(x_i, \theta)|| + \gamma \sum_{i=1}^{N} \max(0, -\lambda_i) \to \min_{x,y,\lambda}. \quad (6)$$

Note, that this method works only for homogeneous neural networks, which correctly classify all the training data and have loss values constraint.

C. Directional method

We propose a new method for reconstructing training data from homogeneous neural networks. As KKT method, this method also requires correct classification of all training samples and directional convergence of the model, but doesn't make any assumptions about loss values.

Let $\epsilon_t = \nabla_\theta L\big(y_{\text{true}}, f(x, \theta_t)\big)$. If ϵ_t has opposite to θ_t direction, then we have (7) and (8):

$$\frac{\epsilon_t}{||\epsilon_t||} + \frac{\theta_t}{||\theta_t||} = 0. \quad (7)$$

Using (1) and (7) we get that:

$$\theta_{t+1} = \theta_t - \mu\epsilon_t = \theta_t \left(1 + \mu \frac{||\epsilon_t||}{||\theta_t||}\right). \quad (8)$$

Due to homogeneity of $f(\cdot, \theta)$, the logits absolute value will increase after update and, as all training data is already correctly classified, the loss will decrease.

The idea of the algorithm is to find such x, y that the loss gradient has the opposite direction to the weights. It can be formulated as optimization problem:

$$\left|\left| \frac{\nabla_\theta L(y, f(x,\theta))}{||\nabla_\theta L(y, f(x,\theta))||} + \frac{\theta}{||\theta||} \right|\right| \to \min_{x,y} \quad (9)$$

D. Training simulation

Suppose we know not only last model's weights θ_1, we also know some previous weights θ_0. The idea of the algorithm to find such x, y that would move weights from θ_0 to θ_1. As we don't know number of iterations and learning rate the model was trained with, we can only make assumptions about the direction of antigradient.

Let $d = \theta_1 - \theta_0$. The idea of the algorithm is to find reconstructions x, y as the solution of optimization problem:

$$\left|\left| \frac{\nabla_\theta L(y, f(x,\theta))}{||\nabla_\theta L(y, f(x,\theta))||} + \frac{d}{||d||} \right|\right| \to \min_{x,y}. \quad (10)$$

Note that this method is not bounded to architecture and can be used for arbitrary neural networks.

III. Experiments

For experiments MNIST [3] and a dataset of generated histology images were used. We took 200 images from MNIST dataset, the target classes were odd and even.

For KKT and directional algorithms VGG-like [4] and FC models were used. These models didn't have biases in linear layers (except the first one) to ensure homogeneity. For training simulation, ViT [5] and ResNet-18 [6] were used.

The reconstructions using KKT method for FC models and reconstructions using directional method for VGG-like model are presented in the Fig. 1. KKT method didn't yield any reconstructions for VGG-like model and directional method didn't yield any reconstructions for FC model. Fig. 2 contains results for training simulation for ViT, Fig. 3 – for ResNet-18.

In the figures you can see, that KKT method yielded more reconstructions than directional methods, but the quality of directional method samples are higher.

Training simulation yielded reconstructions for both ResNet-18 and ViT. Reconstructions are not pixel-wise, as from KKT and directional methods, but that contain parts of training images. Reconstructions from ViT contain patches, because of its architecture, which splits the image into patches. ResNet reconstructions are smooth, but contain more noise.

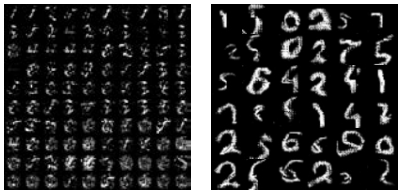

Fig. 1. Left: samples, reconstructed from FC model using KKT method. Right: samples, reconstructed from VGG-like model using directional method

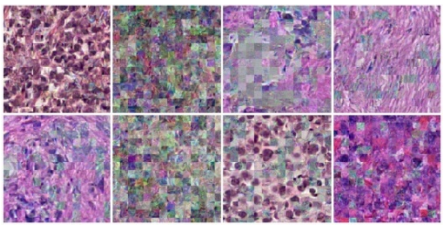

Fig. 2. Samples, reconstructed from ViT using training simulation

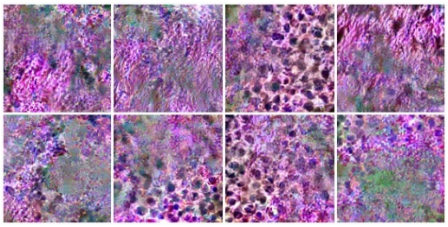

Fig. 3. Samples, reconstructed from ResNet-18 using training simulation

IV. Conclusion

In this work, the methods for reconstructing training samples from neural networks were studied. Two new methods were proposed, one is appliable only for homogeneous networks, the other one is appliable for arbitrary networks, but requires information about initial training weights. The proposed methods show ability to make pixel reconstructions of training samples. Directional method yields less samples compared to KKT method, but reconstructed samples have better quality. Training simulation method is able to reconstruct parts from training samples and it doesn't make any assumptions about network architecture.

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Segmentation-Based Attention Mask for Enhancing Fundus Image Diagnosing

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Abstract. **Approach to improve the classification of ocular diseases from fundus images by leveraging semantic segmentation as an attention mechanism. Key anatomical structures – optic disc, optic cup, and retinal vessels – are segmented using deep learning models and combined into weighted attention masks. These masks guide a classifier based on EfficientNetB6 to focus on clinically relevant regions, resulting in significant improvements in diagnostic accuracy. The method enhances detection sensitivity for subtle disease features and increases model interpretability.**

Keywords: **deep learning, medical image analysis, computer vision, semantic segmentation, attention mechanism, medical image classification, retina pathology detection, computer-aided diagnosis**

I. Introduction

Fundus imaging is essential for non-invasive, high-resolution visualization of the retina, aiding diagnosis of many ocular diseases. Interpretation requires expert knowledge and can be time-consuming, especially where ophthalmologists are scarce [1]. Deep learning, particularly convolutional neural networks (CNNs), have made advances in medical image classification, including retinal disease detection. However, typical end-to-end models use global image features, potentially diluting important localized clinical information. This limits early disease detection when signs are subtle [2].

To address this, attention mechanisms focusing on clinically relevant areas are increasingly used [3]. This study applies semantic segmentation as attention masks highlighting key anatomical zones (optic disc, cup, vessels) to enhance classifier focus and accuracy.

A. Symptoms of Ocular Diseases in Fundus Imaging

Fundus photography visualizes retinal structures critical in diagnosing:

- Myopia: Axial elongation causes retinal thinning, peripapillary atrophy, tilted discs.
- Hypertension: Microvascular changes like arteriolar narrowing, AV nicking, hemorrhages, cotton wool spots.
- Diabetic Retinopathy: Microaneurysms, hemorrhages, exudates, neovascularization, macular edema.
- Glaucoma: Increased cup-to-disc ratio, neuroretinal rim thinning, disc hemorrhages.
- Cataract: Lens opacity reduces image contrast, causing blur.
- Age-Related Macular Degeneration: Drusen, pigment changes, subretinal hemorrhages, fluid accumulation.

Accurate segmentation of these features enables precise diagnostic algorithms [4].

II. Multiclass Semantic Segmentation Methods

A. Optic Disc and Optic Cup Segmentation

A modified U-Net in PyTorch segments optic disc and cup from RGB images (256×256). The network outputs dual-channel masks indicating disc and cup regions. The architecture uses symmetric encoder-decoder blocks with skip connections, two convolutional layers per block, and ReLU activations.

Training used Binary Cross-Entropy loss with early stopping over 30 epochs. Performance metrics included:

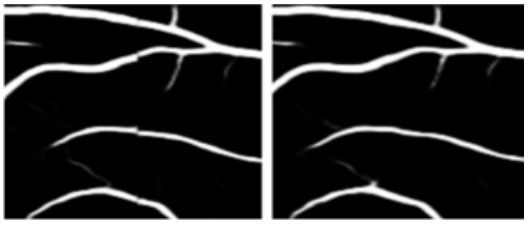
- Dice coefficient ~0.95 (disc), ~0.88 (cup).
- Binary IoU 0.92 (disc), 0.83 (cup).

The optic cup showed lower accuracy due to smaller size and class imbalance. Loss fluctuations indicate sensitivity to anatomical variability.

B. Blood Vessel Segmentation

The vessel segmentation model used a U-Net with ResNet18 backbone pretrained on ImageNet, trained in two stages: pretraining on public datasets (DRIVE [6], CHASE DB1 [7], HRF [8]), then fine-tuning on target images.

Images resized to 996×996, split into overlapping tiles (352×352) to reduce border artifacts, then merged with alpha blending for smooth transitions. Loss combined binary cross-entropy and Jaccard index [9], achieving high-quality vessel segmentation. This process is shown in Figure.



Left – result of segmentation model on neighboring tiles, right – tiles merged with alpha blending

III. EfficientNetB6 Classifier (Baseline)

We trained a classifier on a curated ODIR-5K dataset with seven classes:

- Pathological Myopia
- Hypertensive Retinopathy
- Diabetic Retinopathy
- Glaucoma
- Cataract
- Age-related Macular Degeneration (AMD)
- Normal (Healthy).

Images were resized to 224×224 and augmented with rotation (±30°), shifts (10 %), zoom (20 %), and flips.

Model used EfficientNetB6 backbone (no top), with global average pooling, dense layer (224 units, ReLU), dropout (0.3), and softmax output (7 classes) [10].

Training parameters:

- Loss: sparse categorical crossentropy
- Optimizer: Adam, lr=1e-4
- Epochs: 30
- Batch size: 8
- Early stopping with patience 5.

Results: Overall test accuracy 78.3 %; best accuracy for Myopia (94 %) and AMD (90 %); poorest for Diabetic Retinopathy (29 %) and Healthy (69 %).

IV. EfficientNetB6 Classifier Using Semantic Attention Mask

To enhance performance, we generated semantic attention masks per image using pretrained segmentation models for optic disc, cup, and vessels. Each mask was weighted based on clinical relevance:

- Disc: 0.9
- Cup: 1.0
- Vessels: 0.8
- Background: 0.2

A composite attention mask M is computed as a weighted sum of the individual segmentation maps:

$$M = w_{\text{disc}} \cdot \text{mask}_{\text{disc}} + w_{\text{cup}} \cdot \text{mask}_{\text{cup}} + w_{\text{vessels}} \times$$

$$\times \text{mask}_{\text{vessels}} + w_{\text{background}} \cdot (1 - \text{combined\_mask}),$$

where combined_mask denotes the union of all binary object masks. The attention-enhanced image I_{attn} is then obtained via element-wise multiplication:

$$I_{attn}(x, y) = I(x, y) \cdot M(x, y)$$

This operation suppresses less informative background regions while amplifying features in diagnostically critical areas.

The modified images I_{attn} are fed into the same EfficientNetB6 classifier described earlier. The training configuration – loss function, optimizer, learning rate, and number of epochs – remains unchanged to ensure a consistent comparison with the baseline model.

This strategy allows the network to concentrate on regions most likely to contain pathological changes, and leads to measurable improvements in classification accuracy, especially in complex or borderline cases.

Results: Overall accuracy improved to 92.2 %, with highest accuracies for Cataract (96.6 %) and Myopia (96.0 %), and the lowest still above 84 % for Diabetic Retinopathy and Healthy classes.

V. Conclusion

This study demonstrates that using attention masks generated through semantic segmentation significantly enhances the classification of retinal diseases from fundus images. By highlighting key anatomical structures – the optic disc, optic cup, and retinal vessels – these masks effectively guide the classifier to focus on clinically relevant regions, which leads to substantial improvements in diagnostic accuracy.

In addition to improving accuracy, the use of attention masks increases the interpretability of the model by revealing which image regions contribute most to its decisions. Such transparency is essential in medical settings, providing clinicians with justifiable diagnostic results. Moreover, the system's ability to adapt by adjusting mask weights based on classification errors enhances its robustness and effectiveness in real-world applications.

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Deep Learning Methods for Miltiple Sclerosis Lesions Segmentation on MRI Data

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Abstract. **Multiple sclerosis is a dangerous human disease that has no etiological cure. Diagnosis of the disease in its early stages involves MRI and analyzing the resulting images for the presence of lesion foci to identify the stage of the disease. The aim of the work described in the paper is to train a model using modern deep learning and data preprocessing methods for automatic segmentation of multiple sclerosis lesions on MRI data.**

Keywords: **multiple sclerosis, MRI, image segmentation, CNN**

I. INTRODUCTION

Multiple sclerosis is a human autoimmune disease, often seen in young adults, in which the immune system attacks neurons, contributing to the destruction of the cells myelin sheaths. The destruction of myelin sheaths leads to vision problems, impaired walking or balance, impaired mental clarity, numbness or weakness, especially in the legs and arms, and depression [1].

Diagnosis of this disease necessarily includes a stage of examination with MRI. The images obtained using this method must localize the foci of multiple sclerosis lesions in the brain in order to make a diagnosis and determine the severity of the disease [2]. This process is difficult and time-consuming, as the foci are often small areas that are difficult to distinguish from normal tissue.

II. TRAINING

A. Convilution Neural Netwroks with 3D convolution

To automate the segmentation of multiple sclerosis (MS) foci, we employ deep learning-based convolutional neural networks (CNNs), which have become the standard for medical image analysis due to their ability to learn hierarchical features directly from data [3]. Among CNN architectures, U-Net has emerged as a leading solution for segmentation tasks, particularly in medical imaging, owing to its symmetric encoder-decoder structure and skip connections that preserve spatial context while recovering fine-grained details [4].

In this work, we utilize a 3D U-Net architecture, which extends the original 2D U-Net by replacing 2D convolutions with volumetric (3D) convolutions. This modification allows the model to process 3D MRI scans as holistic volumetric structures, capturing spatial relationships along all three axes (height, width, depth). For MS segmentation, this is critical: 3D convolutions explicitly model the spatial distribution of lesions across adjacent slices, improving detection of small or irregularly shaped foci that might be overlooked in slice-by-slice 2D analysis [5]. Additionally, 3D context helps reduce false positives by leveraging anatomical consistency across planes.

However, 3D CNNs introduce significant computational challenges. The number of trainable parameters increases dramatically compared to 2D counterparts [6].

B. Dataset and pre-processing methods

The training data were MRI images that contained multiple sclerosis foci as well as masks for the corresponding lesion areas. The dataset incorporated images acquired through three distinct MRI sequences, each providing unique contrast mechanisms to highlight different tissue properties:

- T1-weighted imaging: optimal for visualizing anatomical structures and detecting gray matter lesions;
- T2-weighted imaging: highly sensitive to fluid-filled lesions, making it indispensable for MS diagnosis;
- FLAIR (Fluid-Attenuated Inversion Recovery): Particularly effective in suppressing cerebrospinal fluid (CSF) signals, thereby improving the visibility of periventricular and cortical lesions.

All images were initially categorized into groups, where each group was a series of images of a single patient taken at intervals. 256 images were used for dataset creation:

- training dataset is composed of 204 images;
- 32 were used for validation;
- remaining images were used for 20.

The images for one patient were exclusively found in one of the datasets.

To mitigate slow model training and standardize data, we implement the following optimizations all MRI volumes were resampled and cropped to a uniform size of 160×160×96 voxels. The transverse (axial) plane consisted of 96 slices, ensuring sufficient coverage of the brain along the inferior-superior axis. The sagittal and coronal planes were standardized to 160 slices each, preserving anatomical alignment and resolution.

To avoid overfitting additional data augmentations was used. It includes vertical and horizontal flipping of the image, random changes in brightness and contrast and adding gaussian noise.

Prior to training, the data underwent normalization to translate pixel values into the range $[0; 1]$. After normalization gaussian blur and contrast enhancing were applied for denoising and better distinction between the lesion and normal brain nerve tissue respectively. Contrast enhancing was performed with specific 3D kernel for each image in our dataset.

C. Training and evalutation

The model was trained on an NVIDIA GPU 5070 Ti (with CUDA 12.9). Training required ~48 hours for 50,000 iterations (batch size=2), with inference time of ~1 second per 3D scan (160×160×96 voxels) on the same hardware.

Training was performed on 120 epochs using the Adam optimizer [6]. A combined loss function was used:

$$L_{comb} = \lambda L_{BCE} + (1 - \lambda) L_{Dice}, \quad (1)$$

where L_{comb} is the combined loss function, λ is the coefficient that determines the contribution of binary cross entropy to the combined loss function, L_{BCE} is the binary cross entropy, and L_{Dice} is the Dice loss function.

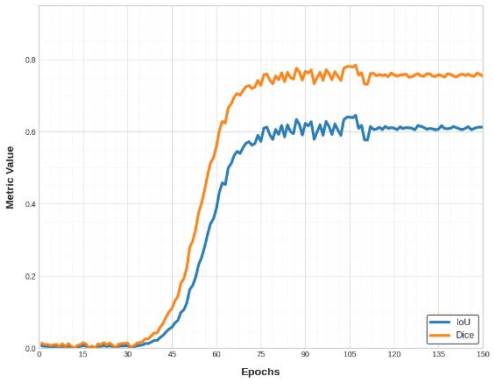

Fig. 1. IoU and Dice metrics progression during training

To train the model, a search for suitable hyperparameters using the grid search method. The most appropriate value for the learning coefficient was 0.0001, followed by a 10-fold decrease in this value with no growth of the model metrics over 5 epochs.

Fig. 1 shows the charts of changes in model's learning metrics, where maximum score was gained. Due to data size, it's complexity and difference between MRI scan types in first epochs model struggles to learn patterns from data. Only after 30-40 epochs metrics are starting to grow significantly.

III. Results and Discussion

After training, the model was evaluated on the validation and test samples where it performed at 0.78 and 0.72 on the Dice metric respectively. Fig. 2 represents, that the lowest score model commonly gets on FLAIR images, which are the smallest type of images in size in dataset.

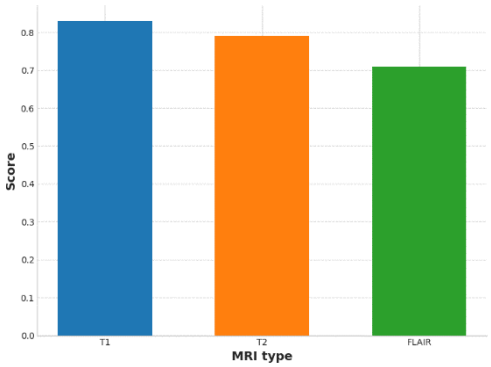

Fig. 2. Dice metrics across main types of MRI images

Thus, the paper presents a method to automate the recognition of multiple sclerosis on MRI images. With the current results, the model can already be applied in medical institutions to assist physicians in making a diagnosis.

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Comparison of Alternative Methods to Laplacian Pyramidal Decomposition in Image Fusion Problem

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***Abstract*. This paper presents a comparative analysis of image fusion methods, including classical Laplacian pyramidal decomposition, wavelet transform with different wavelet types and discrete cosine transform (DCT). The study evaluates these methods using the structural similarity index (SSIM), peak signal-to-noise ratio (PSNR) and execution time.**

***Keywords:* classical Laplacian pyramidal decomposition, wavelet transform, discrete cosine transform (DCT), SSIM, PSNR, computational efficiency**

I. Introduction

Image fusion is the process of combining multiple images of the same scene – captured with different exposure levels, focus settings or sensors – into a single composite image that provides more comprehensive information. This technology is widely used in computer vision, video surveillance and high dynamic range (HDR) imaging.

One of the classic approaches to image fusion is the Exposure Fusion method, which utilizes pyramidal image decomposition [1]. This technique employs Laplacian pyramidal decomposition, where the image is represented as a hierarchy of multi-scale frequency components. The fusion process occurs at each pyramid level, followed by reconstruction to generate the final composite image.

While numerous alternatives to classical Laplacian pyramidal decomposition exist, our preliminary study [5] indicates that the most promising approaches include wavelet transform (with various wavelet types) and discrete transform (DCT).

II. Classical Laplacian pyramidal decomposition

The method based on classical Laplacian pyramidal decomposition involves first decomposing the input image into multiple resolution levels, each representing different frequency bands. This decomposition is performed through an iterative process of Gaussian smoothing (achieved by convolving the image with a Gaussian filter) followed by subsampling. Subsequently, the Laplacian pyramid is constructed by calculating the difference between each level of the Gaussian pyramid and the interpolated version of the next level [2].

Following this decomposition, level-wise fusion is performed. For each pyramid level, a weight map is computed and applied to perform weighted summation of all input images. In our experiments, we employed information-aware weighting schemes. After fusing all pyramid levels, the final image is reconstructed through inverse convolution operations.

This method effectively preserves both the low-frequency image components and high-frequency details.

III. Wavelet transform

The wavelet transform enables simultaneous processing of images in both spatial and frequency domains. The method can be summarized as follows. First, a two-dimensional discrete wavelet transform (2D DWT) is applied to each input image using various wavelet bases [3]. Specifically, our implementation employed: Daubechies wavelets (orders 1, 4 and 6), the fourth-order symmetric wavelet and the first-order Coiflet wavelet.

The wavelet transform produces a decomposition tuple:

$$(LL, (LH, HL, HH)), \quad (1)$$

where LL represents the approximation coefficients (low-frequency components), LH contains vertical detail coefficients, HL contains horizontal detail coefficients, HH contains diagonal detail coefficients.

For each corresponding coefficient across all images, an element-wise maximum operation is performed. This selects the optimal detail value at each pixel position from the available input images. After combining all components, the inverse wavelet transform is applied to reconstruct the final fused image.

Wavelet-based image fusion demonstrates computational efficiency, noise robustness and effective preservation of both global and local image features. However, the method's performance is

inherently dependent on wavelet selection, as the chosen wavelet type directly influence both the decomposition structure and the resulting fusion quality.

IV. Discrete cosine transform

The discrete cosine transform (DCT) converts an image from the spatial domain to the frequency domain. This transformation enables efficient analysis and fusion of energy-significant frequency components while preserving a compact information representation.

This method operates as follows. First, each input image is decomposed into its three color channels (R, G, B). A discrete cosine transform is then applied independently to each channel of every image [4]. For each frequency coefficient position, the maximum magnitude across all images is selected. The resulting matrix of combined coefficients undergoes inverse DCT transformation, producing a fused channel image. This process is repeated for all three channels, which are then recombined to generate the final fused image.

The DCT-based image fusion method enables rapid and computationally efficient merging while effectively preserving the most significant frequency components.

V. Metrics

The following metrics were employed for objective evaluation:

- SSIM (Structural Similarity Index) – quantifies structural similarity between images by comparing luminance, contrast and structural patterns. Value range from 0 to 1, with 1 indicating perfect structural correspondence.
- PSNR (Peak Signal-to Noise Ratio) – measures the ratio between maximum signal power and noise power. Higher values indicate superior detail preservation in the fused image.
- Execution time. Measured in seconds using precision timing. This metric serves as an indicator of the method's computational efficiency.

VI. Computational experiment

For experimental evaluation, we utilized 60 distinct image sets from Google's HDR+ Burst Photography Dataset [6]. This dataset comprises burst sequences captured with a single camera, along with corresponding reference images generated through HDR processing. These reference images served as ground truth for SSIM and PSNR metric calculations. In this context, while the PSNR and SSIM metrics do not fully reflect the perceptual quality of the resulting images (as HDR processing produces brighter and more balances outputs from identical exposure shots), they remain valuable for comparative analysis between different fusion methods.

VII. Results

The results are reported as mean values for each metric across all test images, aggregated by fusion method and presented in Tabl.

Comparative performance metrics across fusion methos

Method	The meaning of metrics		
	SSIM	***PSNR,dB***	***Execution time, s***
Laplacian pyramidal decomposition	0.433	14.190	8.139
Wavelet transform (Daubechies 1)	0.414	15.277	5.515
Wavelet transform (Daubechies 4)	0.423	15.316	6.237
Wavelet transform (Daubechies 6)	0.424	15.321	7.082
Wavelet transform (symmetric wavelet 4)	0.423	15.317	6.232
Wavelet transform (Coiflet 1)	0.421	15.309	6.249
Discrete cosine transform	0.428	14.978	6.174

The highest SSIM score was achieved by the Laplacian pyramidal decomposition method, while the lowest performance was observed with the first-order Daubechies wavelet transform. The highest PSNR value was achieved using the six-order Daubechies wavelet transform, whereas the Laplacian pyramidal decomposition method yielded the lowest PSNR measurement. The fastest execution time was achieved by the first-order Daubechies wavelet transform, while the Laplacian pyramidal decomposition method showed the slowest performance.

VIII. Conclusion

This study investigates three distinct approaches to image fusion: classical Laplacian pyramidal decomposition, wavelet transform employing various wavelet types and discrete cosine transform. A comprehensive comparative analysis was performed using three key evaluation metrics: SSIM, PSNR and execution time.

The experimental results demonstrated that the Laplacian pyramidal decomposition achieved the highest structural similarity with reference image, the sixth-order Daubechies wavelet transform yielded the optimal image restoration quality, while the first-order Daubechies wavelet transform exhibited the most computationally efficient performance. Although the classical Laplacian pyramidal decomposition method demonstrated superior SSIM, it underperformed in

other critical metrics, particularly PSNR and computational efficiency. In contrast, the wavelet transform approach achieved more balanced performance across all evaluation criteria. This was especially evident when employing fourth- and six-order Daubechies wavelets, as well as the fourth-order symmetric wavelet.

Based on the comprehensive evaluation, the six-order Daubechies wavelet transform emerges as the optimal approach, delivering the highest overall image quality. However, when computational efficiency takes priority, either the fourth-order Daubechies wavelet or fourth-order symmetric wavelet offers a favorable compromise, maintaining comparable image quality while significantly reducing processing time.

Future research directions should include more comprehensive investigation of wavelet-based approaches for image fusion, exploration of neural network methods to potentially achieve superior quality metrics and development of a specialized dataset containing varied exposure images. Additionally, rigorous analysis of methods performance when processing numerous images with extreme exposure conditions (both overexposed and underexposed regions) warrants further examination.

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Learning to Synthesize: GAN Optimization with Imitation and Distribution Feedback

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***Abstract*. Training of generative adversarial networks (GANs) for high-fidelity image synthesis faces persistent challenges: distribution shift, collapse of diversity, and synthetic data degradation in multilevel architectures. This paper presents an analysis of the causes of intermediate distribution distortion in multilevel GAN systems, proposes architectural solutions for preserving distributional fidelity, and introduces imitation learning based on distributional feedback for training stabilization. We further show how integrating distribution feedback enables direct assessment of output distribution fidelity. Experimental results indicate that the GAI (Generative Adversarial Imitation) training approach yields outputs more consistent with real data distributions than traditional GAN methods.**

***Keywords:* neural networks, multilevel generative adversarial networks, imitation learning, data distribution**

I. Introduction

Generative adversarial networks (GANs) are widely used in image synthesis tasks due to their capacity to approximate complex data distributions. However, in multilevel or hierarchical architectures, where generation is performed progressively, errors can accumulate. Each layer refines an approximation of the previous one, leading to distortions if not properly regularized [1, 2].

These issues are especially evident in domains requiring high distributional precision, such as medical imaging or satellite data. Optimizing GAN training in multi-level contexts demands attention to how data distributions evolve across layers, how intermediate outputs influence subsequent stages, and how architecture choices such as U-Net generators can mitigate or amplify distortions.

However, U-Net structures may lead to over-conditioning, a condition where the model becomes excessively dependent on low-level input features, potentially limiting its ability to generalize and capture the full diversity of the data distribution. As the network becomes reliant on low-level input features, it tends to generate outputs closer to conditional distributions P(x|x_in) than the full marginal P_data(x), resulting in lower diversity [3, 4].

To address both collapse [5] and generalization simultaneously, we introduce imitation learning into the training loop following the GAI method. The idea is to treat each intermediate GAN as a policy that mimics expert-like distributions from real data.

In this formulation, the GAN is rewarded not merely for fooling a discriminator, but for aligning its latent policy output with the expert's behavior – i.e., real data patterns in a feature space. This allows:

- Distribution-aware refinement at each stage.
- Integration of feedback loops measuring divergence in real-time.
- Adaptive fine-tuning of each stage to preserve global coherence.
- This approach is implemented through adversarial imitation learning augmented with policy-gradient optimization techniques applied within both the latent and perceptual feature spaces.

II. GAN imitation learning

A common issue in GAN-based image synthesis is the mismatch between the distribution of latent samples and the manifold of natural images. Imitation learning offers a solution by shaping the generator's sampling strategy through expert-guided behavior, effectively bridging the distributional gap. This alignment is particularly evident when combined with adaptive importance sampling (AIS), where IL serves to correct sampling biases and reduce the discrepancy between model-generated and real data distributions.

In multi-level GANs, such as MSGAN (Multi-Scale GAN) [6], the dependence of output parameters on the form and completeness of the initial sample is critical. The problem is exacerbated by the fact that each generation depends on previous levels. Errors and distortions originated at lower levels are propagated throughout the hierarchy or resolution levels, reducing the overall expressiveness and fidelity of the images.

In scenarios involving excessive synthetic sampling, the model may lose critical features of the original data distribution, which can lead to forgetting key aspects of that distribution [5]. Without appropriate distortion compensation mechanisms, the generation quality may deteriorate at each subsequent level. Distribution control at intermediate stages is necessary to prevent model degradation and sustainable learning [7, 8].

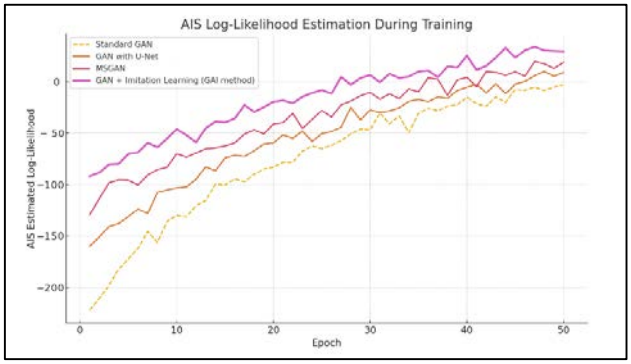

Fig. 1. AIS log-likelihood estimates with and without GAI

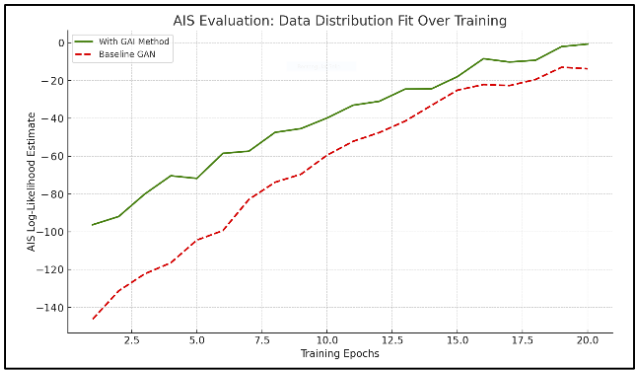

Fig. 2. AIS-based log-likelihood estimates for different GAN architectures during training

To mitigate the accumulation of distortions across levels, we use several training interventions: real-sample injection, auxiliary losses, reprojection modules and collaborative training.

III. Distribution Fit

Standard evaluation metrics like FID are limited to perceptual similarity. To assess how well GANs approximate the underlying data distribution, we employ Annealed Importance Sampling (AIS) to estimate the log-likelihood of the output data under a modeled posterior.

In the context of image synthesis, the generator in GAI models is treated as a policy function that learns to mimic expert trajectories – i.e., sequences of feature transitions that occur in real images – within a high-dimensional latent space. By integrating imitation learning, GAN models benefit from the following properties:

- Enhanced mode coverage.
- Reduced divergence from the real distribution: Behavioral cloning or inverse reinforcement objectives ensure that generated samples follow similar structural and semantic trajectories as real data, improving distributional overlap.
- Stabilized training dynamics: The additional learning signal mitigates oscillations and divergence in adversarial training by regularizing the generator's behavior toward expert-like outputs.

Fig. 1 compares the performance of a baseline GAN with that of an identical architecture enhanced by imitation learning techniques. It shows that GAI helps minimize the divergence between the generator's policy and expert behavior derived from real data samples.

Analysis of data distribution patterns in hierarchical GANs has demonstrated that incorporating U-Net architectures into the generator yields output distributions more closely aligned with those of real data, as measured by Inception Score [9]. However, this improved fidelity is accompanied by a narrowing of the distributional support, wherein the generator increasingly reproduces prototypical samples and fails to adequately capture infrequent data modes.

Fig. 2 illustrates the comparison between several GAN approaches. A higher estimated likelihood for GAI-enhanced GANs indicates a better fit to the target distribution.

IV. Conclusion

Generative Adversarial Networks have revolutionized the landscape of image synthesis, yet they remain sensitive to training instability and mode collapse. Numerous architectural and algorithmic advancements – such as U-Net-based generators [9], multi-scale discriminators and conditional networks [10] – have been proposed to mitigate these limitations. However, a core challenge persists: the consistent alignment between model-generated output and the statistical properties of the real data distribution across multiple training stages.

To evaluate the efficacy of our method, we utilize AIS to estimate the log-likelihood of the generator's distribution at each training epoch. AIS has proven to be a reliable metric for tracking distributional alignment over time [11]. As shown in Figure 1, the GAN augmented with imitation learning achieves significantly higher AIS estimates, indicating improved fidelity to the data distribution. Standard GANs, as well as those enhanced with U-Net or multi-scale modules, demonstrate more modest gains, often plateauing early in training.

In summary, empirical and theoretical studies consistently demonstrate that GAI and its variants outperform standard GAN-based approaches in training stability [12]. This underscores GAI's advantage over GANs in tasks requiring behavioral fidelity and efficient policy learning – an asset notably useful in multi-level GAN configurations.

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Reconstruction of the Spectral Image from RGB Images

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Abstract. **In this paper, the problem of spectral information recovery based on RGB images is considered. The color of vegetation can serve as an indicator of its condition, as it reflects changes in the pigment composition. Hyperspectral imaging allows you to obtain such data, but requires the use of expensive equipment. The paper analyzes modern approaches to spectrum reconstruction from conventional RGB images, which opens up prospects for more accessible environmental monitoring and analysis.**

Keywords: **spectrum, rgb, deconvolution, color, hyperspectral images, neural networks, reconstruction**

I. INTRODUCTION

Plant phenomics as a scientific discipline actively uses color information to study phenotypic traits. The color of vegetation is one of the most visual and informative indicators formed under the influence of various pigments and chemical compounds [1].

With the development of digital technologies, the need for automation of plant health monitoring processes is increasing. In this paper, it is proposed to use standard RGB images with subsequent reconstruction of spectral characteristics, which makes it possible to implement an affordable and scalable approach to phenotyping.

However, this approach must take into account the phenomenon of metamerism, a situation in which different spectral distributions can be perceived as the same color. This limitation makes it impossible to unambiguously restore the full spectrum for arbitrary objects [2]. Nevertheless, vegetation is a special case because its reflection spectra are characterized by high structural predictability. The biophysical properties of plants, such as the content of chlorophyll, carotenoids, and other pigments – determine the characteristic absorption and reflection zones of light, which significantly narrows down the many possible spectra [3].

Thus, despite the presence of metamerism, the reconstruction of spectral data from RGB images of vegetation becomes feasible with a high degree of reliability.

II. METHODS FOR OBTAINING SPECTRAL CHARACTERISTICS FROM STANDARD IMAGES

A. Deconvolution of color

To perform a quantitative analysis of the intensity distribution over wavelengths, it is necessary to determine the individual contribution of each pixel to image formation. Such a task in the theory of signal and image processing is known as the task of reverse convolution, or deconvolution.

One of the practical examples of this approach is the separation of color components in histological images. In the work of Ruifrock and Johnston, a technique of color deconvolution was proposed that allows decomposing the observed color value of a pixel into components corresponding to individual dyes [4]. This task is especially relevant in the case of multicolored staining of biological tissues, in which each dye specifically marks certain cellular structures. Since the camera registers only the final RGB image with superimposed signals from different dyes, a technique is required to restore individual components - that is, to determine the proportion of each dye in the formation of the color of a particular pixel.

The approach proposed in the study can be considered as a special case of the task of restoring spectral information from RGB data. By analogy, it is supposed to use a priori information about the spectral characteristics of the studied objects, which allows using a simplified and computationally efficient linear deconvolution model.

B. Hyperspectral images

Hyperspectral images are a type of images in which each pixel contains detailed spectral information. Unlike RGB images obtained with conventional cameras, hyperspectral images can include dozens, hundreds, or even thousands of narrow spectral channels [5]. The structure of hyperspectral images has a three – dimensional structure in the form of "cubes", where two dimensions correspond to spatial resolution, and the third to spectral resolution.

One of the approaches to obtaining hyperspectral images is to recover data from standard images. However, this process is accompanied by a significant

loss of information at the spectral integration stage, which makes the recovery task incorrect and its solution ambiguous.

The development of deep convolutional neural networks (CNN) has opened up new possibilities for reconstructing spectral information from images and signals, even in the absence of accurate information about the mechanisms of their formation. Due to their architecture focused on processing spatially structured data, such networks are able to efficiently extract significant features – including textures, borders, and shapes – through convolutional operations. This allows models to identify hidden dependencies in the data and perform reconstruction tasks with high accuracy, even in the presence of noise, distortion, or a limited amount of input information.

III. HRNET ARCHITECTURE AND METHODS FOR IMPROVING THE QUALITY OF FEATURES

Classical CNNs have a number of limitations. As the depth of the model increases, problems arise related to the attenuation or explosion of gradients, which complicates the learning process and reduces the stability of the model. In this regard, sparse encoding methods have traditionally been used in hyperspectral data recovery tasks. However, significant progress in the quality of reconstruction has become possible due to the emergence of new architectures with an improved system of connections between neurons.

In this study, it is proposed to use the residual neural network HRNet to solve the problem of spectral information recovery. This architecture combines the principles of ResNet and DenseNet. HRNet is organized as a system of parallel computing streams with a constant exchange of information between levels. Unlike traditional sequential architectures, here each layer transmits its output data not only to the next, but also to all subsequent layers, which ensures efficient feature extraction at various scales and contributes to a more accurate restoration of spectral characteristics.

In each dense block, the outputs of one layer are connected to the inputs of all subsequent layers. If layer l generates output x_l, the input of the next layer $l+1$ includes all previous outputs. In (1), $[x_0, x_1, x_2, \dots, x_l]$ is the union of the outputs of all previous layers, and H is a function that includes the operations of convolution, normalization, and activation [6]

$$x_{l+1} = H([x_0, x_1, x_2, \dots, x_l]). \quad (1)$$

Mechanisms such as PixelShuffle, PixelUnshuffle for saving information, residual dense blocks, global connections and the LeakyReLU activation function are integrated into the architecture. The initialization of weights using the Xavier method is also used.

IV. COMPARATIVE ANALYSIS OF SPECTRAL DATA EXTRACTION ALGORITHMS

In order to determine the most effective and easily integrated approach, the software was developed. The main functionality of the application is to interactively obtain graphs displaying the distribution of signal intensity over wavelengths based on a user-defined area of interest.

The developed program supports two input data formats: standard RGB images and hyperspectral images saved in RAW format. In the process of testing the selected spectral data generation methods, images obtained using the Muses9-HS full-frame hyperspectral camera were used, which made it possible to evaluate the effectiveness of the implemented algorithms.

The comparison of the two methods was carried out on the basis of a standard RGB image of the grass cover. To obtain a reference spectrum, each image was analyzed using a spectrometer. Fig. 1 shows photographs of the object under study taken at different times of the day – morning, afternoon and evening, as well as the reference spectrum obtained under control conditions.

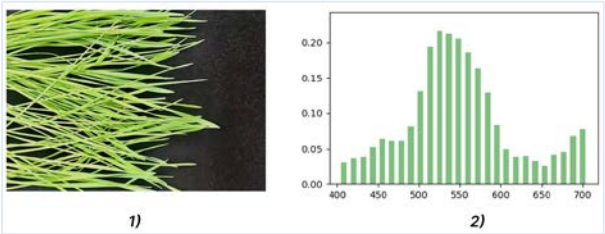

Fig. 1. The data set: *1* – original image, *2* – reference spectral characteristic recorded using a spectrometer under controlled conditions

The extracted intensity values from reconstructed hyperspectral images using HRNet demonstrated high accuracy of spectral information recovery. The model has successfully preserved the shape of the spectra for almost the entire wavelength range under consideration. The coincidence of the spectral peak positions with the reference data confirms the reliability of the results obtained.

As a result of experiments, it was revealed that color deconvolution does not take into account the spectrum of the light source, that is, it perceives variations in illumination as a change in the object itself. This can lead to a shift in the reconstructed spectra, especially if the lighting differs dramatically in color temperature or intensity. The results of spectral reflection reconstruction using the deconvolution method and the result obtained using a neural network that restores color characteristics without taking into account lighting are shown in Fig. 2.

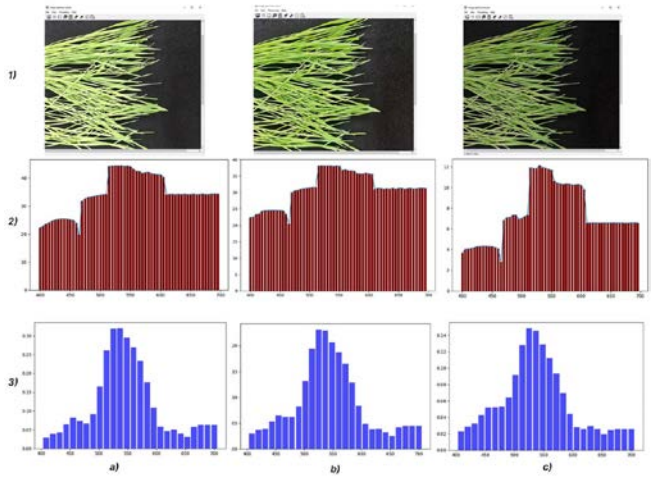

Fig. 2. The results of the restoration of the spectral characteristics of the plant using various methods: *1a–c* – original images, *2a–c* – spectral graphs obtained by deconvolution, *3a–c* – spectral graphs obtained using a neural network

A comparative analysis of spectral data obtained using a hyperspectral camera and reconstructed from RGB images confirmed that the neural network approach provides a more stable and adaptive solution. Thus, the use of hyperspectral images to restore spectral information is the most promising method in plant health monitoring tasks, providing the necessary accuracy at lower cost and higher flexibility in real conditions.

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Development of a ROS-Based Mobile Robot for High-Precision Indoor Mapping

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Abstract. **This paper presents a sensor data integration algorithm for solving the indoor mapping problem in mobile robotics. The mobile robot, developed using ROS Noetic for autonomous indoor mapping. The mobile platform was integrated into ROS through a specifically developed control driver, enabling interaction with sensor perception and data processing systems. This solution ensures precise motion control and effective fusion of data from odometry and a laser rangefinder. Additionally, noise filtering and data fusion algorithms were developed to enhance mapping accuracy. The obtained results demonstrate that the proposed approach enables the construction of highly detailed maps while adapting to environmental changes. Future work plans include the integration of additional sensors and further improvement of information processing algorithms.**

Keywords: **Simultaneous Localization and Mapping (SLAM), mobile robot, sensor fusion, indoor mapping, LiDAR, odometry, ROS Noetic, autonomous navigation, multi-sensor integration, real-time localization**

I. Introduction

Indoor mapping is a key task in robotics, enabling the creation of maps for autonomous navigation and spatial analysis. This is especially critical for mobile robots operating in dynamically changing environments such as warehouses, hospitals, and research laboratories [1].

One of the most effective approaches to mapping is the SLAM (Simultaneous Localization and Mapping) method, which allows a robot to navigate without prior knowledge of the environment [2]. This technology utilizes sensor data to determine the robot's position while simultaneously constructing a map of the surrounding environment, ensuring accurate navigation even in the presence of moving objects [3]. This study proposes a solution based on a mobile robotic platform equipped with a differential drive system, integrated into ROS Noetic. The platform demonstrates high maneuverability, energy efficiency, and adaptability to dynamic environmental changes. A specialized driver was developed to ensure bidirectional data exchange between hardware and software components, achieving positioning accuracy within ±2.5 cm over a 10-meter distance.

II. Autonomous Indoor Mapping Using a Mobile Robot

During the development of the mobile robot, key aspects of sensor data integration and information processing algorithms were addressed. Control is implemented through a custom-developed driver integrated into ROS Noetic, enabling precise positioning and efficient interaction with the sensor system, including the Hokuyo UST-10LX laser rangefinder and odometric data.

To improve mapping accuracy, noise filtering and data fusion algorithms have been applied. These methods significantly reduce errors arising during navigation and ensure the creation of highly detailed maps.

The PID (Proportional-Integral-Derivative) controller corrects control signals, minimizing deviations from the desired trajectory [4]. Interaction between the PID controller and ROS is organized through control topics in terms of ROS where velocity commands are published and mobile platform data is analyzed. Data processing from the mobile platform and transmission of control signals via ROS have been implemented, enabling dynamic adaptation of PID controller parameters based on movement conditions.

The motion control system leverages ROS Noetic's topic-driven architecture to process velocity commands (cmd_vel) from SLAM modules, encoder-derived odometry data (odometry, 20 Hz), and LiDAR point clouds (scan, 10 m range, 0.25° angular resolution). A hybrid feedback loop integrates these data streams to drive an adaptive PID controller, which dynamically corrects trajectory deviations. Sensor fusion from "odometry" and "scan" provides real-time positional estimates, while the PID module computes corrective actions to minimize tracking errors.

A software-hardware interface was implemented via UART serial communication to interact with ROS Noetic. This interface supports odometry data transmission (based on motor encoders) and command reception through the "cmd_vel" topic. To minimize positioning errors, hybrid filtering algorithms combining Kalman filter and particle filter were applied,

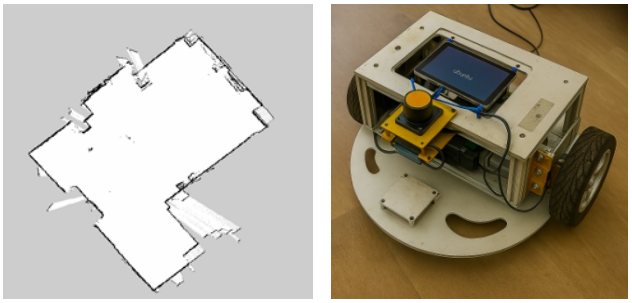
reducing measurement noise by 37% under low-light conditions and in the presence of moving objects. Key development stages included testing communication parameters: data transmission latency remained below 50 ms at a 20 Hz update rate, ensuring stable real-time operation. An autonomous navigation system was deployed, enabling dynamic trajectory reconfiguration in response to environmental changes.

To optimize performance, the controller employs a fuzzy logic subsystem that adjusts of the PID-controller K_p , K_i , and K_d gains based on contextual parameters such as platform speed and turning angles [6]. These adjustments are propagated via the "pid_params" topic, enabling real-time recalibration of control coefficients during operation. Genetic algorithm-based optimization further refines the PID parameters during system initialization, reducing root-mean-square trajectory deviation by 28 % compared to classical tuning methods. This dual-strategy approach-combining heuristic self-tuning with evolutionary optimization-ensures robustness across dynamic environments and varying operational conditions.

Experiments demonstrated that this combination improved mapping accuracy by 19 % compared to standalone SLAM.

III. Results

During testing, the robot demonstrated the ability to perform reliable and detailed indoor mapping. The integration of sensor data from the rangefinder, combined with noise filtering and data fusion algorithms, significantly enhanced process accuracy. As a result, high map detail, stable SLAM algorithm performance, and minimized navigation errors during localization were achieved (Figure).



a b

Indoor Mapping and Mobile Robot:
Map of the environment generated using SLAM technology (a);
The actual mobile robot used for mapping (b)

The presented robotic system demonstrates a promising solution for autonomous mapping and spatial analysis in mobile robotics. Planned enhancements include integrating IMU (Inertial Measurement Unit) and RGB-D cameras to enable semantic 3D mapping through OctoMap, while advancing SLAM algorithms to handle non-static obstacles and varying terrain complexities [7]. The adoption of these technologies will significantly enhance the robot's reliability and adaptability to changing operational conditions.

IV. Conclusion

The development of a system for autonomous indoor mapping based on SLAM technology and laser rangefinders has been carried out. In the creation of the mobile robot, particular attention was paid to integrating the mobile platform into ROS Noetic, developing the control driver, and calibrating sensors, which enabled achieving high positioning accuracy.

Additionally, noise filtering and data processing algorithms were implemented, ensuring reliable mapping even in low-light conditions and in the presence of moving objects. During testing, the system's reliability in complex dynamic environments was confirmed, along with its ability to adapt to environmental changes.

An efficiency analysis of various sensor data processing approaches and their impact on mapping accuracy was also conducted. During trials, optimal filtering and data fusion parameters were identified, minimizing localization errors and enhancing the detail of final maps. The implemented sensor fusion method demonstrated robustness against external factors such as laser signal reflections and dynamic environmental changes.

Future work includes integrating additional sensors, such as IMU and depth cameras, to ensure more reliable navigation and operation in complex multi-level environments. Moreover, advanced processing algoritms [8, 9] and integration with remote server will be considered [10]. Additionally, the implementation of imitation learning methods is planned, enabling the mobile robot to efficiently learn to solve complex tasks, such as navigating mazes, by analyzing behavioral patterns [11].

Acknowledgment

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Time-Frequency Characteristics of Ships in Range-Compressed SAR Data

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***Abstract*. Ship detection and recognition in range-compressed synthetic aperture radar (SAR) data is promising since it needs no time-consuming focusing steps. However, it is not easy because of the problems of low signal-to-clutter ratio, dispersed target energy, and limited detectability. Thus, the extraction and characterization of target information in low signal-to-clutter ratio range-compressed SAR data is urgently needed. This paper mainly characterizes ships using time-frequency techniques. The results of the short-time Fourier transform (STFT) of ships and sea clutter are presented and compared. Experimental results show that ships present a typical single-component linear frequency modulated (LFM) signal in the time-frequency domain while sea clutter does not, though the range-compressed SAR data is usually considered to be an approximate LFM signal along the azimuth direction. This is mainly because there is a lack of dominant scattering in the sea clutter, and thus it exhibits complex and random time-frequency characteristics.**

***Keywords:* Synthetic aperture radar (SAR), range-compressed data, ship, time-frequency characteristics**

I. INTRODUCTION

Synthetic aperture radar (SAR) is widely used for maritime target surveillance because of its all-weather, all-day high-resolution imaging capability [1]. Ship detection and recognition in range-compressed SAR data present a promising approach for maritime surveillance since they eliminate the need for time-consuming image focusing steps, thereby enabling faster data processing [2], [3]. However, this task remains highly challenging due to several inherent difficulties, including the low signal-to-clutter ratio (SCR), the dispersed nature of target energy across multiple range cells, and the limited detectability of ships against complex sea clutter [4]–[6]. These factors significantly degrade the performance of traditional detection methods, making it difficult to distinguish ship targets from background. Thus, the development of advanced techniques for the extraction and characterization of target information in low-SCR range-compressed SAR data is urgently needed to improve detection accuracy and reliability.

This paper primarily investigates the time-frequency characteristics of ships in range-compressed SAR data to enhance detection performance. The widely used time-frequency analysis method – the short-time Fourier transform (STFT) is applied to both ships and sea clutter, and their respective results are compared. Conventionally, range-compressed SAR data is often approximated as a linear frequency-modulated (LFM) signal along the azimuth direction due to the relative motion between the radar and the target. However, experimental results demonstrate that ships exhibit a typical single-component LFM signature in the time-frequency domain, whereas sea clutter does not. This discrepancy arises because sea clutter lacks a dominant scattering center and instead consists of numerous randomly distributed scatterers, leading to complex and stochastic time-frequency characteristics. In contrast, ships, with their rigid and structured geometry, produce coherent scattering responses that manifest as well-defined LFM patterns in the time-frequency domain. The study reveals distinct differences in the time-frequency representations of ships and sea clutter, which can be leveraged for improved target discrimination.

II. LFM Characteristics of Range-Comressed SAR Data

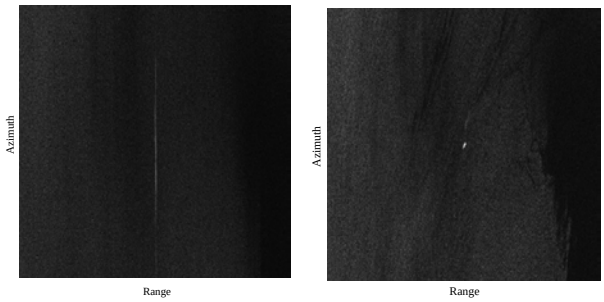
Based on the imaging principle, the range-compressed time domain after range compression can be approximated as [5],[7]

$$S_{rc}(\tau,\eta) \approx A_0 p_r[\tau - 2R(\eta)/c]\omega_a(\eta-\eta_c)\times \\ \times\exp\left\{-j\frac{4\pi f_0 R_0}{c}\right\}\exp\left\{-j\pi\frac{2V_r^2}{\lambda R_0}\eta^2\right\}, \quad (4)$$

where A_0 is a complex-valued quantity representing the backscattering coefficient of the target, τ is the fast time, η is the slow time, η_c is the time difference of the beam center, $p_r[\tau]$ is the range envelope after range compression, $\omega_a(\eta)$ is the azimuth envelope, f_0 is the radar center frequency, $R(\eta)$ is the instant range, R_0 is the shortest range, c is the light speed, λ is the wavelength, V_r is the velocity of the platform. As shown, the first phase term is constant, whereas the second phase term follows a quadratic phase variation. Consequently, the azimuth-direction signal maintains LFM properties.

III. Preliminary Eeperimental Results

The experimental data comes from ERS-2 [8]. Fig. 1 shows the range-compressed data and the two-dimension focused image. There is a ship in the center.



a) b)

Fig. 1. Amlitude images of an ERS-2 subset: Range-compressed data (a); Two-dimension focused image (b)

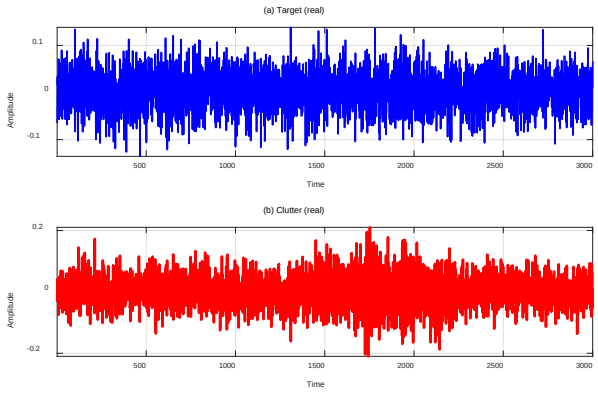


Fig. 2. Real parts of the profiles of the two azimuth lines: Ship target (a); Sea clutter (b)

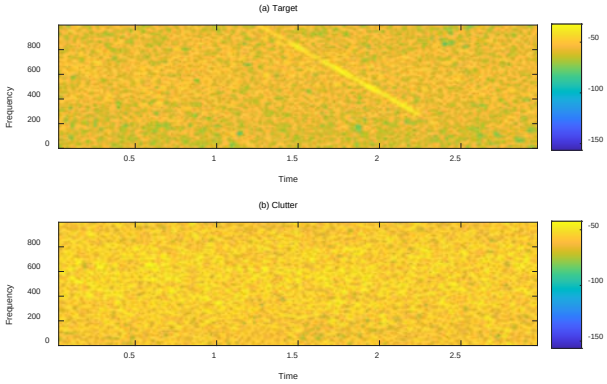


Fig. 3. STFT time-frequency results of of the two azimuth lines: Ship target (a); Sea clutter (b)

We select an azimuth line containing ship data at the same range gate as the experimental data and another azimuth line containing only sea clutter as an experimental comparator. The real parts of the profiles of the two azimuth lines are presented in Fig. 2. The STFT results are shown in Fig. 3. The STFT parameters are presented in Table.

STFT Parameters

Parameter	Value	Unit
Window	64-point Hamming	-
Number of overlapped samples	60	
Number of DFT points	1024	
Sample rate	1000	s^{-1}

From Fig. 2, it can be seen that the ship target has larger energy than the clutter. There are no obvious LFM patterns in the real parts of the target since of the mixture of clutter. From Fig. 3, it is observed there is a clear line in the STFT result of the target, indicating that there is a LFM signal. The slope of the line presents the LFM rate. The ends of the line are also very clear. However, there are no LFM patterns in the STFT result of the clutter. This is mainly because there is no dominant scattering in the echoes of sea clutter. Thus, the scattering of each point of the sea clutter forms a random signal, though the scattering of each single point follows an LFM signal. This difference can be leveraged for improved target discrimination.

IV. Conclusions

This paper analyzed the STFT time-frequency characteristics of the ship. It shows that the ship manifests as well-defined LFM pattern in the time-frequency domain while sea clutter does not. The time-frequency difference can help the identification of ships in range-compressed SAR data. This conclusion also

benefits other time-frequency techniques, e.g., fractional Fourier transforms, and wavelet transform.

ACKNOWLEDGMENT

The authors would like to thank the Alaska Satellite Facility (ASF) for providing ERS-2 data.

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Efficient Sensor Selection Framework for Non-linear System Optimization

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Abstract. **Sensor selection identifies an optimal sensor subset to minimize parameter estimation uncertainty, measured by mean squared error (MSE). We use frame potential (FP) as an efficient MSE proxy and propose the Fast Frank-Wolfe Algorithm for Nonlinear Models (FFWNLM), which exploits the multilinear extension of weighted FP for unprecedented speed in low-dimensional settings. We provide performance guarantees under specific conditions and validate FFWNLM's advantages numerically.**

Keywords: **Non-linear models, Multilinear extension, Sensor selection, Frame potential**

I. INTRODUCTION

In fields like remote sensing and environmental monitoring, deploying a large number of sensors for observations is costly, so selecting a subset of sensors (sensor selection) to minimize uncertainty in estimating unknown parameters is crucial. Exhaustive search for the optimal sensor subset is computationally expensive and often addressed suboptimally via greedy heuristics or convex optimization; greedy algorithms, with linear complexity, use submodular proxies for mean-squared error (MSE) and are near-optimal for monotone, normalized submodular functions, but existing methods for nonlinear models have high complexity. This paper transforms the sensor selection problem for nonlinear models into a continuous optimization problem via multilinear relaxation of weighted frame potential, proposes the Fast Frank-Wolfe Algorithm for non-linear models (FFWNLM), which is the fastest known when the unknown parameter dimension is low, bounds its performance theoretically, and verifies its advantages numerically. The main contribution is a fast, low-complexity algorithm for nonlinear model sensor selection with theoretical quality assurance.

II. PROBLEM STATEMENT

We consider a general nonlinear model with additive Gaussian noise:

$$y_t = g_t(\boldsymbol{\theta}) + n_t, t = 1, \dots, N,$$

where y_t is the t-th sensor measurement, $\boldsymbol{\theta} \in \mathbb{R}^K$ is the unknown parameter, $g_t(\cdot)$ is a nonlinear function, and $n_t \sim \mathcal{N}(0, \sigma^2)$. Let $\widehat{\boldsymbol{\theta}}$ denote the estimate of $\boldsymbol{\theta}$. The goal is to select L sensors from N candidates to achieve a desired estimation accuracy. This combinatorial optimization problem is formulated as:

$$\min_{\mathcal{L}} G(\mathcal{L}) \quad \text{s.t. } \mathcal{L} \subseteq \{1, \dots, N\},\ |\mathcal{L}| = L,$$

where $G(\mathcal{L})$ is a cost function reflecting estimation quality.

Since estimation quality depends on $\boldsymbol{\theta}$ due to nonlinearity, Rao et al. [5] discretize the parameter space into a grid $\mathcal{U} = \{\boldsymbol{\theta}_1, \dots, \boldsymbol{\theta}_D\}$. Around each grid point $\boldsymbol{\theta}_d$, $g_t(\boldsymbol{\theta})$ is linearized via first-order Taylor expansion:

$$y_t \approx g_t(\boldsymbol{\theta}_d) + \mathbf{h}_{t,d}^T(\boldsymbol{\theta} - \boldsymbol{\theta}_d) + n_t,$$

where $\mathbf{h}_{t,d}^T = \frac{\partial g_t(\boldsymbol{\theta})}{\partial \boldsymbol{\theta}^T}\Big|_{\boldsymbol{\theta}=\boldsymbol{\theta}_d}$. Stacking measurements yields:

$$\mathbf{y} = \mathbf{g}_d + \mathbf{H}_d(\boldsymbol{\theta} - \boldsymbol{\theta}_d) + \mathbf{n},$$

with $\mathbf{H}_d \in \mathbb{R}^{N \times K}$ containing $\mathbf{h}_{t,d}$ as rows.

For sensor subset $\mathcal{L}$, the least-squares MSE under $\boldsymbol{\theta}_d$ is:

$$\mathrm{MSE}_d(\mathcal{L}) = \sigma^2 \mathrm{tr}\{\mathbf{T}_d^{-1}(\mathcal{L})\},$$

where $\mathbf{T}_d(\mathcal{L}) = \sum_{i \in \mathcal{L}} \mathbf{h}_{i,d}\mathbf{h}_{i,d}^T$. The weighted MSE across all grid points is:

$$\mathrm{MSE}_{\mathrm{W}}(\mathcal{L}) = \sigma^2 \sum_{d=1}^{D} w_d \mathrm{tr}\{\mathbf{T}_d^{-1}(\mathcal{L})\},$$

with weights $w_d > 0$. Let $w_d = \| \mathbf{H}_d \|$, which reflects the rate of change of the function at the point $\boldsymbol{\theta}_d$. A larger gradient indicates that the function exhibits more rapid variations near $\boldsymbol{\theta}_d$, suggesting that this point may contain richer information about the function's behavior.

To avoid grid mismatch issues, the frame potential (FP) [2] is used as a surrogate for MSE. FP relates to MSE via:

$$c_1 \frac{\mathrm{FP}(\mathcal{L})}{\lambda_{\max}^2} \leq \mathrm{MSE}(\mathcal{L}) \leq c_2 \frac{\mathrm{FP}(\mathcal{L})}{\lambda_{\min}^2},$$

where c_1, c_2 are model-dependent constants. The weighted FP is defined as:

$$\mathrm{FP}_{\mathrm{W}}(\mathcal{L}) = \sum_{d=1}^{D} w_d \mathrm{tr}\{\mathbf{T}_d^T(\mathcal{L})\mathbf{T}_d(\mathcal{L})\}.$$

To handle the discrete nature of $\mathcal{L}$, we relax $\mathrm{FP_W}$ using a multilinear extension [3]. Let $F_d(\mathcal{S}) = = \mathrm{tr}\{\mathbf{T}_d^T(\mathcal{N} \setminus \mathcal{S})\mathbf{T}_d(\mathcal{N} \setminus \mathcal{S})\}$, and define:

$$F(\mathcal{S}) = \sum_{d=1}^{D} w_d F_d(\mathcal{S}).$$

The multilinear extension $\tilde{F}(\boldsymbol{x})$ for $\boldsymbol{x} \in [0,1]^N$ is:

$$\tilde{F}(\boldsymbol{x}) = \sum_{d=1}^{D} w_d \sum_{i,j=1}^{K} \left(\sum_{t=1}^{N} x_t h_{ti,d} h_{tj,d}\right)^2.$$

The sensor selection problem becomes:

$$\min_{\boldsymbol{x}} \tilde{F}(\boldsymbol{x}) \quad \text{s.t.}\, \boldsymbol{x} \in \{0,1\}^N, \| \boldsymbol{x} \|_1 = L. \tag{1}$$

III. Using the Template

The algorithm seeks to solve Problem 1, given that the matrices $\{\mathbf{H}_d, d = 1,2,\cdots,D\}$ are known. In Algorithm 1, p_t represents the partial derivative of $\tilde{F}(\boldsymbol{x})$ with respect to x_t evaluated at $\boldsymbol{x} = 0$, i.e., $p_t = = \frac{\partial \tilde{F}(\boldsymbol{x})}{\partial x_t}\Big|_{\boldsymbol{x}=0}$. Thus, Algorithm 1 returns an index set $\mathcal{S}$ with the smallest partial derivatives at $\boldsymbol{x} = 0$. The complexity of Algorithm 1 is $O(DNK^2)$. In contrast, the greedy algorithm has a complexity of $O(DNLK^3)$ for the weighted log-det cost and $O(DN^2LK)$ for the weighted FP cost [5]. Convex optimization-based sensor selection methods like SeDuMi [6] have a complexity of $O(N^3)$. Therefore, when $K \ll L$, our proposed algorithm exhibits the lowest complexity among these classical methods. Furthermore, we provide a theorem to demonstrate its near-optimality.

Algorithm 1: Fast Frank-Wolfe Algorithm for non-linear models (FFWNLM).

Input: $\mathbf{H}_d \in \mathbb{R}^{N\times K}, d = 1,2,\cdots,D; L;$

Compute $m_{ij,d} = \sum_{t=1}^{N} h_{ti,d} h_{tj,d}, i,j = 1,\cdots,K,$ $d = 1,2\cdots,D;$

Compute $p_t = \sum_{d=1}^{D} w_d \{\sum_{i=1}^{K}\sum_{j=1}^{K} m_{ij,d} h_{ti,d} h_{tj,d}\},$ $t = 1,2\cdots,N;$

Select the L elements with the smallest values from $\{p_1, p_2, \cdots, p_N\}$, denoted as $\{p_{l_1}, p_{l_2}, \cdots, p_{l_L}\}$;

Return: $\mathcal{L} = \{l_1, l_2, \cdots, l_L\}$.

Theorem 1: *Let $\mathcal{L}^*$ denote an optimal solution of Problem 1. Assume that for $t = 1,\cdots,N$, $i,j = 1,\cdots,K$, and $d = 1,\cdots,D$, we have $\sum_{t=1}^{N} h_{ti,d} h_{tj,d} > 0$ and $h_{ti,d} h_{tj,d} \geq 0$. Then, Algorithm 1 yields a set $\mathcal{L}$ satisfying*

$$\tilde{F}(0) - \tilde{F}(1_{\mathcal{N}\setminus\mathcal{L}}) \geq \frac{N}{N+L}\left[\tilde{F}(0) - \tilde{F}(1_{\mathcal{N}\setminus\mathcal{L}^*})\right].$$

Drawing on a proof approach similar to that of Theorem 2 in [4], and leveraging Theorem 1, we derive a bound for $\tilde{F}(\boldsymbol{x})$, as presented in Theorem 2.

Theorem 2: *Assume that $\{\boldsymbol{H}_d\}_{d=1}^{D}$ meet the conditions of Theorem 1. Let $\mathcal{L}^*$ be an optimal solution of Problem 1. The set $\mathcal{L}$ generated by Algorithm 1 is near-optimal with respect to FP, satisfying $\tilde{F}(1_{\mathcal{L}}) \leq \gamma \tilde{F}(1_{\mathcal{L}^*})$, where $\gamma = \frac{1}{N+L}\left(\tilde{F}(0)\frac{KL}{L_{min}^2} + N\right)$, and $L_{min} = \min_{|\mathcal{L}|=L} \sum_{i\in\mathcal{L}} \sum_{d=1}^{D} w_d \left\|\boldsymbol{h}_{i,d}\right\|_2^2$, with $\boldsymbol{h}_{i,d}$ denoting the i-th row of $\boldsymbol{H}_d$.*

Theorem 2 provides the approximation factor of FFWNLM relative to FP, ensuring the sub-optimality of its solution.

IV. Numerical Experiment

In this section, we showcase the advantages of our proposed algorithm, FFWNLM, through experimental evaluations. We compare FFWNLM with the Greedy algorithm (which minimizes the weighted FP cost), a widely-used approach for such problems that offers solution quality guarantees [5].

We set $\sigma^2 = 1$. The target domain $\mathcal{U}$ is discretized into a grid of $D = 30$ points, and we assume equal combining weights, i.e., $w_d = 1$ for $d = 1,2,\ldots,D$.

First, we generate 100 different problem instances. For each instance, we randomly create 30 matrices $\{\mathbf{H}_\mathrm{d} \in \mathbb{R}^{100\times 20}\}_{d=1}^{30}$. We then compute the average Mean Squared Error (MSE) of FFWNLM, the Greedy algorithm, and Random Sampling as a function of L. The results are depicted in Fig. 1, where the shaded area represents the range of Random Sampling. Clearly, FFWNLM outperforms the Greedy algorithm.

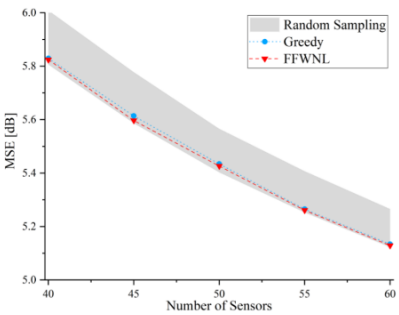

Fig. 1. Comparison in terms of MSE of FFWNL, Greedy Algorithm and Random sampling.

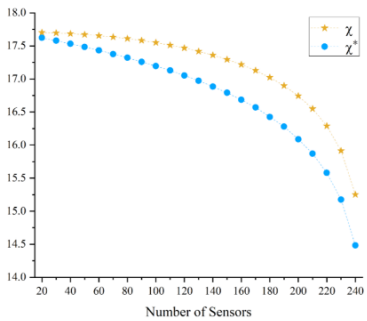

Fig. 2. Experimental verification of Theorem 3.1

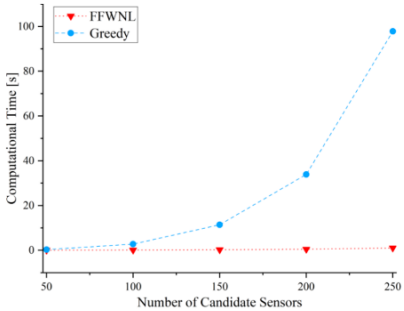

Fig. 3. Comparison of Computational time between FFWNL and Greedy Algorithm.

Next, we use these data to validate Theorem 1. We define $\chi = \log\{\tilde{F}(0) - \tilde{F}(1_S)\}$ and $\chi^* = = \log\left\{\frac{N}{N+L}[\tilde{F}(0) - \tilde{F}(1_{S^*})]\right\}$. Since the optimal value $\tilde{F}(1_{S^*})$ is unknown, we approximate it by taking the best result from 2000 random samplings. The values of χ and χ^* for different L are shown in Fig. 2. It is evident that χ is consistently greater than χ^*, and the gap between them is small when L is very small.

Finally, we compare the computational times of FFWNLM and the Greedy algorithm. We express computational time as a function of the number of candidate sensors N (noting that the optimization techniques are not applicable when N varies significantly). We set $K = N/5$, $L = 2K$, and $D = 30$. The results are shown in Fig. 3. Clearly, as N increases, the computational time of FFWNLM increases only slightly. In contrast, the Greedy algorithm's computational time grows significantly, and the gap between the two algorithms widens as N increases.

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Development of a Multitasking Control System for Small Underwater Robotic Vehicles Based on STM32 and FreeRtos

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Abstract. **This paper presents the design and implementation of a multitasking control system for a compact underwater robotic vehicle using the STM32F7 microcontroller and the FreeRTOS real-time operating system. The study discusses architectural solutions aimed at ensuring reliable motion control, remote command processing, and integration with external sensors. The developed system demonstrates the effectiveness of a multitasking approach in managing underwater robots.**

Keywords: **underwater robotics, STM32, FreeRTOS, digital transformation**

I. Introduction

Remotely operated micro-class underwater vehicles (ROVs) are increasingly demanded across a variety of fields – from the inspection of hydraulic structures to scientific research and educational applications. Current trends in the digital transformation of maritime transport and industry emphasize the need for affordable, reliable, and functional underwater robots with expandable capabilities. These robots must combine a high degree of autonomy, robustness in harsh underwater environments, and intuitive control interfaces [1, 2].

The goal of this study is to develop a hardware-software control system for a compact underwater robot.

II. System Requirements and Design Principles

Research objectives include:

1. Analyzing the requirements for the control system and designing an appropriate software architecture.

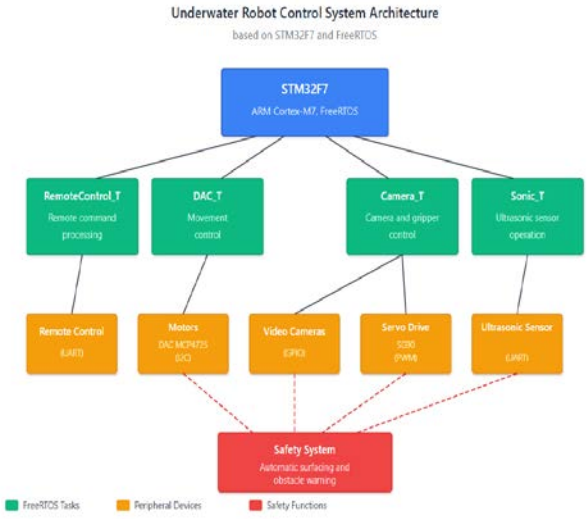
2. Developing a multitasking software framework based on STM32 microcontrollers.

3. Implementing software modules for motion control, remote command handling, manipulator control, and safety management.

4. Integrating various peripheral devices (digital-to-analog converter (DAC), ultrasonic sensors, servos, cameras) into a unified control system.

The following requirements were defined during the research process: multitasking capabilities, fault tolerance, modularity and scalability, and support for remote control.

The control system architecture (Figure) is based on principles of modularity and task distribution. At its core lies the STM32F7 microcontroller, built on the ARM Cortex-M7 core, which provides high processing performance, substantial memory resources, and a wide array of peripheral interfaces [3].



Architecture of the ROV control system

The system includes the following key components:

- A DAC for controlling two horizontal and one vertical thrusters.
- A servo motor for operating the gripper mechanism.
- Cameras for visual feedback.
- An ultrasonic distance sensor.
- A remote control interface based on UART.

III. Software implementation using FreeRTOS

The software architecture follows a multitasking model implemented via FreeRTOS, with clearly separated functional modules [4]:

1. RemoteControl_T – processes commands from the control unit.
2. DAC_T – controls the propulsion system.
3. Camera_T – manages the cameras and gripper servo.
4. Sonic_T – handles the ultrasonic sensor.

The remote control system is based on the UART interface, utilizing interrupts and data buffering. Commands are transmitted in the following format: button1/button2/rightX/rightY/leftX/leftY/connection.

To ensure communication reliability, the following mechanisms were implemented: input data validation, loss-of-connection handling, timeouts, and buffer resets upon prolonged data absence.

IV. Fault tolerance and safety mechanisms

Several fault-tolerant features have been incorporated to enhance the safety and reliability of the robot's operation: automatic surfacing upon signal loss, isolation of critical errors, and system state monitoring.

The developed architecture supports the straightforward integration of additional functionality, such as:

- Automation of routine operations.
- Integration of new sensors.
- Expansion of the manipulator's capabilities.

V. Conclusion

All research objectives have been successfully met. A detailed requirements analysis was conducted, resulting in the development of an optimized software architecture. A multitasking system based on STM32F7 and FreeRTOS was created to enable concurrent execution of robotic functions. Software modules for motion control, command processing, manipulator management, and safety systems were implemented. Peripheral devices (DAC, ultrasonic sensor, servo, cameras) were integrated into a unified, functionally segmented system. The resulting hardware-software complex demonstrates the viability of modern microcontrollers and real-time operating systems in underwater robotics.

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Model of Deep Belief Network Based on Ensemble of Restricted Boltzmann Machines

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***Abstract*. The paper deals with a problem related to efficient processing of large-scale images. The problem solving process using deep belief and convolutional neural networks is considered and an ensemble model of a deep belief network based on restricted Boltzmann machines is proposed. The analysis of the computational complexity of these networks is carried out and the ensemble model advantage in terms of the number of adjustable parameters and the required amount of computing resources is shown.**

***Keywords:* deep belief networks, restricted Boltzmann machine, convolutional neural networks, architecture**

I. INTRODUCTION

Today, deep convolutional neural networks [1] are typically used to process high-resolution images. However, when solving highly specialized problems, the presence of a large number of convolution layers leads to redundancy of the architecture [2]. Architectures redundancy requires a large amount of computations and slows down the operation of application systems built on their basis [3]. Deep belief networks contain a small number of compression layers. They provide higher compression quality than convolutional networks [4], but they are fully connected and require even more computations. To solve the redundancy problem, an ensemble model of a deep belief network based on restricted Boltzmann machines is proposed, which combines the positive properties of belief and convolutional networks.

II. ENSEMBLE MODEL

Let's consider in detail the essence of the proposed approach. The original raster image is divided into rectangular fragments-blocks of the same size. The resolution of the input images must be a multiple of the block sizes in width and height. When choosing the block size, a certain balance must be maintained. To maintain the semantic coherence of the input data and the network generalization ability, the block sizes should not be too small. And to reduce the number of parameters and the volume of calculations, they should not be too large. The number of *ensemble* blocks is determined experimentally based on the input images resolution and the requirements for the compression ratio.

It is proposed to design the compression layers architecture as an ensemble of r identical small-dimensional RBMs. That is, for each block-fragment of the image corresponds to a separate machine. In this case, the sizes and parameter sets of all machines are the same. And since the blocks are processed independently of each other, this leads to the absence of inter-core interaction and assembly of the result at the level of image blocks. That is, the proposed network architecture has natural parallelism. This architecture allows the construction of an ensemble of machines for any number of compression layers, not just the first one. Therefore, when designing a network architecture, it is necessary to determine the compression ratios in all compression layers.

Given the dimensionality of the input data, the ensembles of layers must satisfy the following two conditions:

1) the number of neurons in each layer must be a multiple of the number of RBM ensembles of the current and previous layers;

2) it is necessary to maintain the compression ratio of the RBMs that form the ensemble of layer machines.

To train the ensemble architecture, it is shown that it is sufficient to train one restricted Boltzmann machine on all blocks of images of the training dataset. The parameters of the trained machine are transferred to all other machines of the ensemble.

III. ARCHITECTURES EFFICIENCY EVALUATION

We will conduct a theoretical evaluation of the architectures efficiency using the example of processing one square color raster image with a resolution of one million pixels. We will compare the architectures efficiency by the number of tunable parameters, which determines the computational complexity of training, and by the volume of calculations per processed image.

When constructing the estimates, the size of the classifier – a multilayer perceptron – is not taken into account, since it is the same in all three architectures. When calculating the estimates, only calculations related to the neural networks weights are taken into account, since the number of other calculations is negligible for large architectures.

As a result of the calculations, the following estimates were obtained (Tabl. I).

TABLE I. COMPARATIVE ESTIMATES OF NEURAL NETWORKS COMPLEXITY

Neural network type	**Comparison parameter**	
	Amount of tunable parameters	***Amount of computations per one image***
Deep belief network	$1{,}5*10^{13}$	$1{,}5*10^{13}$
Deep convolutional network	$5{,}6*10^{4}$	$1{,}9*10^{10}$
Ensemble model	$9*10^{3}$	$2{,}4*10^{8}$

From the table it can be seen that the number of tunable parameters of a deep convolutional network is eight orders of magnitude less than the belief one. And the architecture of the ensemble of machines has similar parameters that are approximately six times smaller than deep convolutional networks. At the same time, this gap increases with increasing image resolution. The table also shows that the amount of computation for deep convolutional networks is three orders of magnitude lower than the belief ones. And the amount of calculations for the network architecture from an ensemble of machines is more than an order of magnitude less than convolutional ones. Moreover, as the image resolution increases, this difference increases.

Thus, training a network using an ensemble architecture does not require much time and computational resources. This allows it to be effectively trained for a specific applied task, so to speak, “from scratch.” That is, it allows building a highly specialized network. The above factors, taken together, contribute to reducing the overall response time of an application system built using an ensemble architecture. The above factors, taken together, contribute to reducing the overall response time of an application system built using an ensemble architecture. It is also worth noting that the proposed architecture allows you to adjust the input data compression degree based on the requirements of the application task, which is sometimes problematic when using convolutional networks.

IV. EXPERIMENTS

When describing the ensemble architecture, it was noted that the block size at the stage of image partitioning largely determines not only the speed of training and operation of the final network, but also the compression quality. The issues of choosing the block size were considered experimentally using the example of solving a practical problem (detection of non-natural changes) associated with the high-resolution images processing.

Let us describe the conditions for organizing and conducting the experiment. The initial data were images with a resolution of 4000×4000, describing the same area at different time moments. The images covered an area of the earth's surface measuring 800x800 meters. Various types of buildings were considered as objects for detection. To solve this problem, it is necessary to compress the input data with minimal losses for subsequent processing.

The compression process was carried out using an ensemble of restricted Boltzmann machines of the Gauss-Bernoulli type. The standard 8-fold compression ratio for this type of machine was set.

The equipment used was a computer with an Intel i7-4770k processor, an NVIDIA RTX 3070 graphics card, and 16 GB DDR3 1600 MHz RAM. The operating system was Lubuntu 20.04. Training was performed using an algorithm based on the Boltzmann annealing optimization scheme [5] (Tabl. II).

TABLE II. COMPRESSION RESULTS

Block size	**Quality function**				
	MSE	***PSNR***	***PSNR_HVS***	***SSIM***	***Training time, h***
2×2	167	26,2	25,8	0,860	0,075
2×4	124	27,4	27,0	0,887	0,25
4×4	116	27,7	27,3	0,895	1,5
5×5	114	27,7	27,3	0,896	2,5

From the experimental results, it can be concluded that the architecture based on the RBM ensemble demonstrates high compression quality. It is also quite obvious that using blocks larger than 4×4 does not make much sense: a small increase in compression quality is completely offset by the quadratic increase in training time. That is, using blocks of 4×4 size is optimal for building an ensemble.

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Data Processing in the Design of Pyramidal Horn Communication Terminal

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***Abstract*. Pyramidal horn communication terminal plays an important role in strong directional long-distance communication. There are two main difficulties in data processing during the design of the terminal. The first is to process the structural dimension data of the terminal itself, and the second is to process the internal and external dimension data of the signal input and output interface, which is called the coaxial to waveguide adapter. This paper first processes eight kinds of data of the fourth-order Chebyshev impedance transformation steps in the coaxial to waveguide adapter according to the working frequency band of the pyramidal horn communication terminal. The eight kinds of data are processed separately according to the length and height data of the four impedance transformation steps, and select a group of data that conforms to the best working state. Then process the two dimensional data in the opening direction of the terminal itself according to the working frequency band. Finally, the simulation model of the pyramidal horn communication terminal is established using the processed data, and the standing wave ratio pattern of the communication terminal are obtained.**

***Keywords:* pyramidal horn antenna, Chebyshev impedance transformation, waveguide adapter**

I. INTRODUCTION

Pyramidal horn communication terminal is one type of aperture antennas. The radiation fields from aperture antenna can be determined from the knowledge of the fields over the aperture. The aperture fields become the sources of the radiated fields at large distances [1]. Its radiation pattern in one plane can be adjusted by changing the aperture dimensions or length of the horn in that plane with negligible variations in the radiation pattern in another plane [2]. The pyramidal terminal is fabricated by flaring a hollow pipe of rectangular or square cross section to a larger opening.

Engineers commonly adopt the terminal as a standard gain antenna for calibration purpose of other antennas [3]. Pyramidal terminal is also used as a feeding element for large reflector and lens antennas in communication systems [4].

In particular, The terminal has the advantages of higher gain, better directivity, lower voltage standing wave ratio, better frequency characteristics, larger power capacity and simpler structure.

In order to obtain the above advantages, appropriate working frequency should be selected [5], and then the excitation type should be selected. Typically, a pyramidal horn communication terminal is an open horn excited by a waveguide [6].

In this paper, we present the data processing in the design of pyramidal horn communication terminal working at 4.8–6.2 GHz in detail. By employing the processed data to simulate the terminal, it has a Voltage Standing Wave Ratio (VSWR) of less than 1.6 within the working frequency band, indicating excellent working characteristics.

II. DATA PROCESSING

A. Dimensions of coaxial to waveguide adapter

The physical model of adapter is shown in Fig. 1. The data processing of the adapter involves the radial parameters of the coaxial probe, as well as the height and length parameters of the four steps. The traditional design method deals with the above parameters simultaneously, but it consumes huge computing resources and takes a long time. This paper adopts the method of processing one by one, so that ordinary

personal computers can be successfully completed. The specific methods are as follows.

For the step height parameter (h) and length parameter (l) in Fig. 1, l_1, l_2, l_3 and l_4 are processed one by one in order, then h_1, h_2, h_3 and h_4.

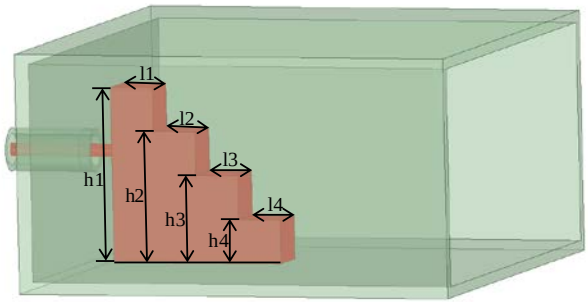

Fig. 1. Structure of the coaxial to waveguide adapter

Parametric scanning analysis is carried out for parameter l_1. The scanning range is set to 2.5~4 mm, and the scanning interval is 0.1 mm. The results are shown in Fig. 2a. It can be seen from the figure that when l_1 is 3.1 mm, the VSWR is the optimum. Therefore, the length of the first step is selected as 3.1 mm. Using the same method, the scanning range and interval of l_2 are 3.5~4.5 mm and 0.1 mm, the l_3 scanning range is 4.5~5.5 mm with the interval 0.1 mm, the scanning range of l_4 is assigned 3.5~4.5 mm, and the scanning interval is set to 0.1 mm. The specific scanning results are shown in Fig. 2(b)–(d), and it can be obtained that the optimal dimensions of l_2, l_3 and l_4 are 4.1 mm, 5.5 mm and 5.5 mm, respectively. From Fig. 2, we can see that the overall VSWR within the communication frequency band decreases in turn during the processing of each step length, indicating that the data processing method is feasible.

Therefore, this method is applied to the processing of step height parameters and the optimal dimensions of processed h_2, h_2, h_3 and h_4 are 15.9mm, 11.9mm, 8mm and 5.5mm, respectively. The optimal dimension of the coaxial probe can be obtained by the same method as well.

B. Dimensions of horn structure

The data of the horn structure size is processed according to the waveguide size. The length and width data of the waveguide radiation port are expanded along the electric field vector direction and the magnetic field vector direction respectively.The optimal aperture size in line with the frequency band is obtained according to the size relationship of the pyramid horn terminal. This size is used for modeling to obtain the final VSWR of the pyramidal horn communication terminal, and the VSWR is shown in Fig. 3.

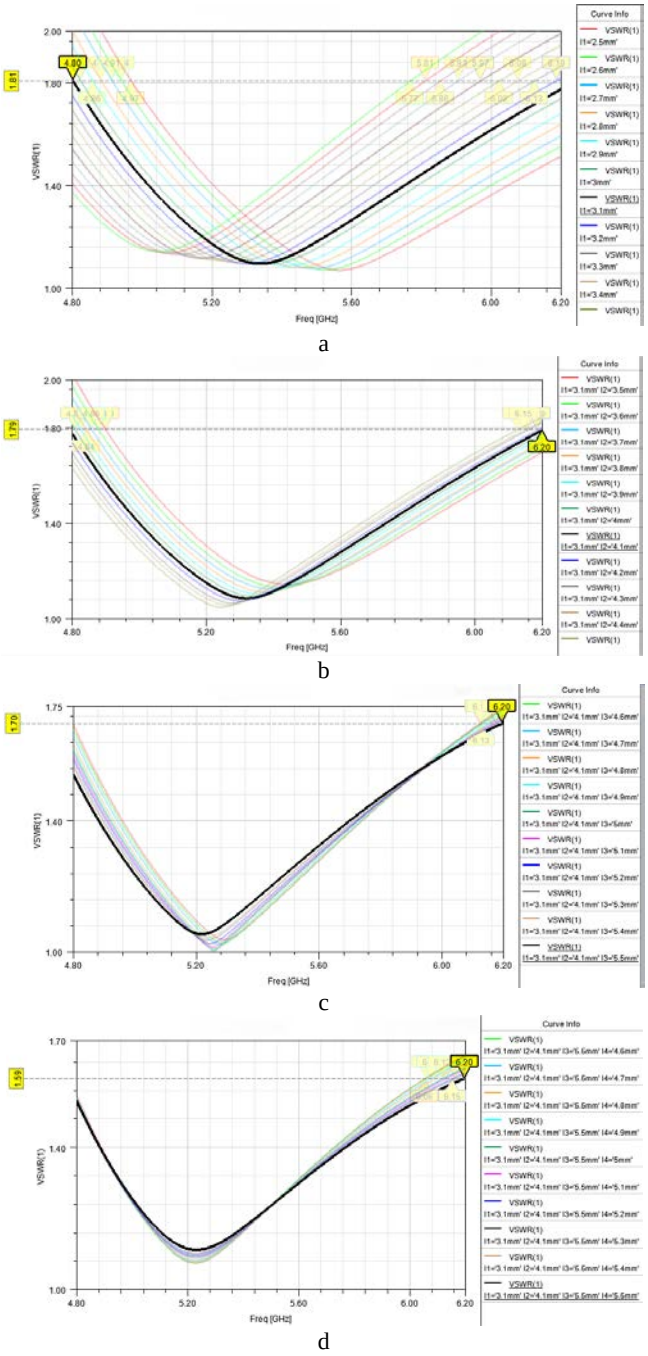

Fig. 2. VSWR of the processed l_1 (a), l_2 (b), l_3 (c) and l_4 (d)

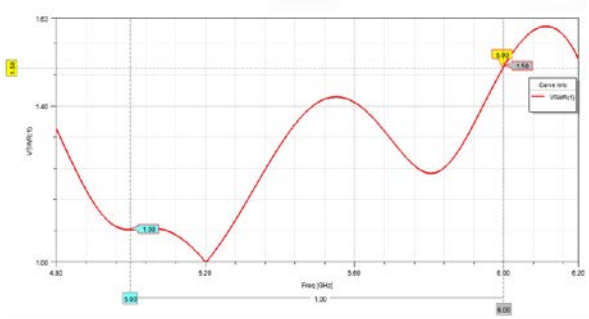

Fig. 3. Final VSWR of the processed data of horn structure

III. Conclusion

In this work, data processing of the structure parameters in the design of pyramidal horn communication terminal including the coaxial to waveguide adapter and horn is presented. Employing the processed data to simulate, the VSWR is less than 1.63 within the working frequency band which indicates the result meets the need of engineering application.

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Hybrid Deep Semi-Supervised Learning Model for Sparse Distributed Object Recognition in Multi-Parameter Data

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Abstract. **Advancements in deep learning have greatly enhanced visual pattern recognition, driving progress in areas such as robotics, urban planning, and geospatial analytics. While current methods perform well in detecting densely distributed objects in urban aerial imagery, identifying sparsely located and visually subtle targets remains a significant challenge, especially when annotated data is scarce. This paper addresses these issues by proposing a hybrid deep semi-supervised learning model that combines an ensemble of classifiers with a YOLO-based detection framework, further improved through two rounds of pseudo-labeling. Experiments were conducted using a satellite imagery dataset focusing on a single target class – ships. The results demonstrate the effectiveness of the hybrid approach for detecting sparse objects and highlight its potential for adaptation to other object types in similar tasks.**

Keywords: **hybrid deep learning, deep learning, object recognition, ensemble, semi-supervised**

I. INTRODUCTION

Recent progress in machine learning has significantly improved the ability to detect and analyze patterns in visual data, supporting a wide range of applications including robotics, urban development, and geospatial analytics. Numerous previous studies have demonstrated strong results in detecting densely distributed objects within aerial images of urban areas [1–3]. However, additional challenges arise in scenarios where objects are sparsely located, have low visual distinctiveness, or where labeled training data is time and cost consuming [4–6]. These difficulties are especially relevant for tasks involving anomaly detection in multi-parameter datasets or identifying rare objects – such as inspecting nuclear facilities for unusual activity, detecting private aircraft at less monitored airstrips, or spotting ships amidst complex oceanic backgrounds. To explore these challenges further, this study focuses more precisely on a representative example: detecting single ships on ocean or sea surfaces using satellite imagery, as it fittingly illustrates the selected problem criteria.

Detecting ships in such contexts is especially challenging because the top-down satellite perspective offers limited variation in visual features, making it difficult to distinguish ships from their surroundings. Moreover, the complex and often noisy maritime background – including waves, reflections, and varying water textures – adds further complexity to the detection process. The low density of ships in these images results in fewer positive samples for training, limiting the ability of machine learning models to learn robust and generalizable features.

Consequently, even state-of-the-art deep learning networks struggle to accurately identify and classify ships under these conditions. These challenges, highlighted in [7, 8], are further exacerbated by factors such as occlusions from clouds or shadows, varying ship sizes and orientations, and the presence of other objects with similar shapes or colors, like marine debris.

From an industry standpoint, this specialized field offers one of the most promising opportunities for practical deployment, with projected growth exceeding 10 % over the next 10 year [9]. In the area of maritime vessel analytics, the focus has shifted toward identifying moving targets at sea, understanding complex logistics flows, analyzing route utilization, and detecting anomalies – rather than simply identifying stationary vessels in ports. This approach is particularly relevant for industries such as logistics, insurance, and navigation safety. Additionally, object detection capabilities are often integrated with tracking methodologies [10–12], as demonstrated in recent technological developments.

In summary, sophisticated object detection methods encounter difficulties when dealing with images that contain only a small number of relevant targets, making effective pre-processing crucial for thorough analysis. The top-down view provided by satellites often lacks detailed resolution, which can obstruct accurate identification of maritime vessels and lead to a higher rate of false positives caused by unrelated features. Moreover, the complexity of scanning vast geographic

regions is intensified by fluctuating environmental conditions and background noise. These obstacles underscore the importance of developing tailored approaches for analyzing satellite imagery, especially in the context of maritime vessel detection.

To address the challenges outlined above, this study introduces a hybrid deep semi-supervised learning model designed for recognizing sparsely distributed objects within multi-parameter datasets, such as images.

II. Methodology

The analysis of target objects was conducted using a dataset combining optical imagery from Pléiades, SPOT, etc. satellite sources coupled with radar satellite systems [13]. This dataset includes more than 200k images with a resolution of 1.5 meters. Although many images depict relatively uniform water surfaces, the background conditions vary widely due to differences in weather and maritime environments. This variation presents significant challenges in reliably detecting objects – particularly ships, which can vary greatly in size, shape, and contrast. Furthermore, additional complications arise from visual obstructions such as clouds or floating debris, which can interfere with accurate recognition. As previously noted, a major challenge in this case is the considerable imbalance within the dataset, where only one-quarter of the images contain relevant objects. To address this, the dataset was rebalanced so that only a quarter of the images are empty, increasing the representation of images with target objects. A subset of empty images was intentionally retained to help the model learn to recognize cases where no objects are present. During preprocessing step, cropping with overlap was done in a way that ensured objects remained intact and their entire shape was preserved within each training or validation example. To make the model more robust to various transformations and improve its generalization while mitigating overfitting, a range of data augmentation techniques were applied.

The hybrid method introduced for analyzing multi-parameter data follows a two-stage framework. Initially, a classification part is used to screen the images and flag regions that are likely to contain objects of interest. In the second phase, these selected regions undergo detailed processing through an object detection algorithm to confirm and accurately locate the objects. This approach reduces the computational load by preventing the application of complex models to images without relevant content, helping to minimize false detections caused by artifacts like sea surface glare or floating debris.

As classifier an ensemble was used, combining two deep learning architectures: one based on a densely connected model [14] and another using a residual network [15] with a reduced stride configurationm, smaller kernels on first layers and integrated average pooling layers. Both classifiers were independently trained on the training dataset. These averaged scores were then used to identify samples for the next stage of processing, which employed the YOLO-based architecture [16]. To further enhance performance, two rounds of semi-supervised learning were conducted using pseudo-labeling with incorporating into the training set 15 % of most confident predictions of the original testing data.

III. Results

The hybrid deep semi-supervised learning model's performance was assessed by measuring prediction accuracy against ground truth data via averaged F2 score over set of thresholds measured using Intersection over Union ranging from 0.5 to 0.95. The model was trained on Nvidia Quadro RTX 6000. The dataset was evaluated using 5-fold cross-validation. Accuracy of sparse distributed object recognition improved by 6 % and 7.1 % over the original augmented baseline after the first and second cycles of semi-supervised pseudo-labeling, respectively, ultimately reaching a level of 0.92.

IV. Conclusion

This paper tackles the challenge of detecting sparsely distributed objects in multi-parameter data, within a case on ship identification in satellite imagery. It introduces a hybrid deep learning framework that integrates densely connected networks with one-stage detectors, further enhanced by semi-supervised pseudo-labeling to utilize unlabeled data effectively. The model achieved a recognition accuracy 0.92 by the F2 score. The results indicate strong performance in large-scale remote sensing applications. Furthermore, the proposed methodology is adaptable to other object types under similar task conditions.

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Controlled Image Generation with Generative Adversarial Networks

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***Abstract*. Generative Adversarial Networks (GANs) have become a prominent framework for high-quality image synthesis in different domains. This research covers controlled image generation using GANs; evaluation and comparison of various architectures (including the novel approach of R3-GAN) to identify models with the best performance under specific constraints. To enable control over high-level semantic features we incorporate auxiliary neural networks for feature extraction and feature-latent spaces mapping. Our approach addresses the challenge of controlled generation when trained on unlabeled datasets. Additionally, we explore latent space manipulation and dimensionality reduction techniques, enabling visualization and interpretation of GAN latent representations. Our contribution includes a structured evaluation methodology for GANs, an analysis of metrics correctnesses with respect to different objectives and a pipeline for controlled image generation, which does not require manually annotated dataset.**

***Keywords:* Neural network model, image generation, image generation methods, metric, generative adversarial networks, dimensionality reduction methods**

I. Introduction

Generative neural networks, particularly Generative Adversarial Networks (GANs), have significantly advanced the field of image generation by exhibiting remarkable capabilities in synthesizing diverse and realistic images. Nevertheless, due to the complexity of the internal data representations, these models often exhibit limitations in precise control over specific attributes of the generated images. In this study, we undertake a systematic investigation of image generation performance across different variants of GAN architectures. Furthermore, we design and implement a pipeline that enables controlled image generation compare it with the existing methods [1]. Additionally, the research studies dimensionality reduction methods and their application with clustering algorithms to obtain more control over the generating process.

II. GAN architecture choice. Datasets

The specific GAN architecture for the controlled image generation pipeline is chosen based on its image generation quality and training stability. Image quality is assessed using Inception Score (IS), Fréchet Inception Distance (FID), Learned Perceptual Image Patch Similarity (LPIPS), and Perceptual Path Length (PPL) metrics. IS rely on class labels obtained from the prerained Inception-V3, FID rely on feature vectors extracted from the penultimate layer of the same pre-trained Inception-V3, while LPIPS and PPL can utilize both the AlexNet or VGG networks as their backbones [2, 3]. To assess metrics correctness and image generation quality we use a dataset consisting of 6,000 histopathological images (2,000 healthy and 4,000 with cancer cells) and MNIST dataset in the controlled image generation section.

III. Training results. Comparison of the architectures

In this section, we provide a comparative evaluation of different GAN architectures in terms of convergence behavior and ability to produce high-quality images. The examined models include different strategies for enforcing the 1-Lipschitz constraint on the critic's function (fundamental for WGANs). These strategies include weight clipping, gradient penalty (GP), spectral normalization (SN) and a combination of both (SNGP) [4–6]. Additionally, we examine R3-GAN. WGAN failed to converge (weight clipping is highly sensitive to dataset the model was trained on), WGAN-GP converged to a local minima (the gradient norm penalty effectively enforces the 1-Lipschitz constraint). WGAN-SN failed to converge (when applied only to critic and both generator and critic). While spectral normalization imposes a direct constraint on weight matrices, it does not necessarily ensure bounded gradient norms, thereby potentially violating the 1-Lipschitz constraint. WGAN-SNGP converged to a local minima. The recently proposed R3-GAN also converged to a local minima, demonstrating competitive stability and image quality.

METRICS VALUES

Metric	GAN Architecture				
	WGAN	**WGAN-GP**	**WGAN-SN**	**WGAN-GP-SN**	**R3-GAN**
IS	-	**2.29**	-	1.18	2.10
FID	-	273.53	-	**263.94**	267.90
LPIPS	-	0.69	-	0.70	**0.67**
PPL	-	1.5	-	1.51	**1.45**

Table presents the values of metrics. Such values can be explained by the specific domain of medical images and the specific nature of the metrics. For example, IS relies only on the knowledge obtained from the pretrained network (probability distribution over the ImageNet classes), and since there are no histopathological images in the ImageNet dataset, the network may not be able to classify images confidently enough, leading to low metric values. The LPIPS metric computes pairwise weighted comparison of neural network activations on each layer between generated and real images (in the absence of class-aligned image pairs, the metric may produce values that do not accurately reflect the true quality of the generated images).

IV. PIPELINE FOR CONTROLLED IMAGE GENERATION

Achieving control over the attributes of generated images remains a key challenge in generative modeling. To address this limitation, we propose a new approach for controlled image generation. It is based on the usage of pretrained feature extractor to establish a base for mapping from feature space to the latent space. This allows for controlled image generation by specifying concrete feature vectors, rather than random latent. The overall process can be formalized as follows: The GAN is trained to learn the underlying data distribution and generate high-quality images; Afterwards, a set of latent vectors is sampled from the prior distribution, and corresponding synthetic images are generated from them; These generated images are then passed through a pre-trained feature extractor to obtain high-level feature representations; Additional neural network (we used MLP with batch normalization) is trained on the dataset, where the inputs are extracted feature vectors and the targets are the original latent vectors. The objective is to minimize MSE between true and predicted latent vectors; Upon completion of training, this model enables the mapping of any given feature vector into the latent space, allowing for conditional image generation based on desired feature attributes.

An overview of the pipeline is presented in Fig. 1. The main advantage of this method is its interpretability and simplicity with no need of additional classifiers to identify specific directions in latent space or complex analysis of GAN weights [7, 8].

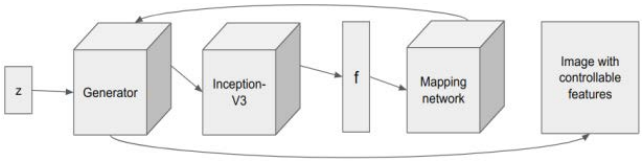

Fig. 1. Controlled image generation pipeline architecture

Rather than directly manipulate latent vectors this pipeline explicitly defines the desired image attributes in the feature space before mapping them into the latent. This modification ensures that the changes correspond to more meaningful, high-level changes in the final image. Unlike Conditional GAN, this method does not require annotated images. Additionally, this method does not modify the training process of GAN (like Path Length Regularization in StyleGAN2 which is a computationally-expensive process, since it requires the Jacobian computation) [9].

We experimented with Inception-V3, EfficientNet-B0 and a self-trained MNIST classifier as feature extractors. The mapping of feature-vectors obtained from the last one failed to converge (we assume it is due to the significant dimensionality difference). While Inception-based and EfficientNet-based mappings converged with no significant difference. Fig. 2 illustrates the difference of performing operations in the feature and latent spaces. In the feature-based approach, the final image receives the expected features unlike the latent-based approach (we add and subtract feature-vectors of different “3” and then add feature-vectors of “0” and expect to get “0” as a resulting image). We also obtained a side-effect of such a method (image restoration). The application of different dimensionality reduction methods in combination with clustering algorithms didn’t result in accurate split since, as we assume, the dimensionality of the feature vector is too high and is the field for further research.

Fig. 2. Results of operations in latent space (upper row) and feature space (lower row)

V. NEGATIVE RESULTS AND FUTURE WORK

We report that the application of such a method on the histopathology dataset was not that successful, which can be explained by the usage of specific pretrained backbones for feature extracting. Since they were trained on ImageNet dataset (which lacks histopathology images). As an idea suitable for future

study, we propose the application of self-supervised representation learning method. Such an approach has the potential to enable the pre-training of a robust backbone for obtaining the feature-vectors. This could enhance the quality and controllability of generated images.

VI. Conclusion

This work introduced experimental evaluations of an image generation using GAN architectures with the aim of identifying a suitable model for usage in a controlled image generation pipeline. Subsequently, a pipeline for controlled image generation was designed and implemented, targeting cases when the image labels are not complete. The developed pipeline enables structured manipulation of high-level image features through an interpretable mapping from feature space to latent space, thereby facilitating controlled generation.

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Assessing Carbon Absorption in Drone Images

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Abstract. **The article describes an algorithm for solving the problem of estimating carbon uptake by vegetation in an image. It covers the main properties of an orthophoto as a possible input data format, and the scope of its application, as well as provides solutions to several intermediate tasks: isolating vegetation zones, calculating their volume, and conducting a comparative analysis of two vegetation indexes based on various classification metrics.**

Keywords: **orthophoto, vegetation index, image segmentation, vegetation volume, carbon absorption**

I. ORTHOPHOTO

One of the main ways to obtain high-quality aerial photographs and eliminate problems associated with image distortion is to create an orthophoto, which is ideal for creating accurate maps of the region. An orthophoto is an orthogonal representation of an area with georeferencing to a specific coordinate system. Such a map is compiled from multiple aerial photographs taken from a given height by an unmanned aerial vehicle (UAV) and combined using special software. It differs from standard aerial photographs in that it provides a strict image from above and has no distortion caused by optics. Its correction is carried out taking into account three aspects: perspective, camera tilt, and lens distortion. This allows you to scale the map, measure the characteristics of objects located on it, calculate their volume, etc.

The scope of accurate digital terrain maps includes the following tasks: creating topographic plans; monitoring the ecological state of vegetation and identifying areas at risk from droughts, diseases, etc.; planning fertilizers and irrigation in agriculture; forecasting field yields; accurately determining the area and estimating the volume of forests, which can be used for calculating carbon absorption. The solution to the latter task is examined in this article.

II. PROBLEM STATEMENT

The source data includes multispectral images captured using 5 camera sensors mounted on the drone. The research was conducted on the campus of one of the universities in China [1]. As a result, the coverage area was 78.3 hectares, and the shooting was carried out at an altitude of 115 meters, resulting in a series of five-channel frames (red R, green G, blue B, near infrared NIR and Red Edge channels). Using special software, an orthophoto of the terrain and a corresponding height map with a range from 0 to 28 meters were created (Fig. 1).

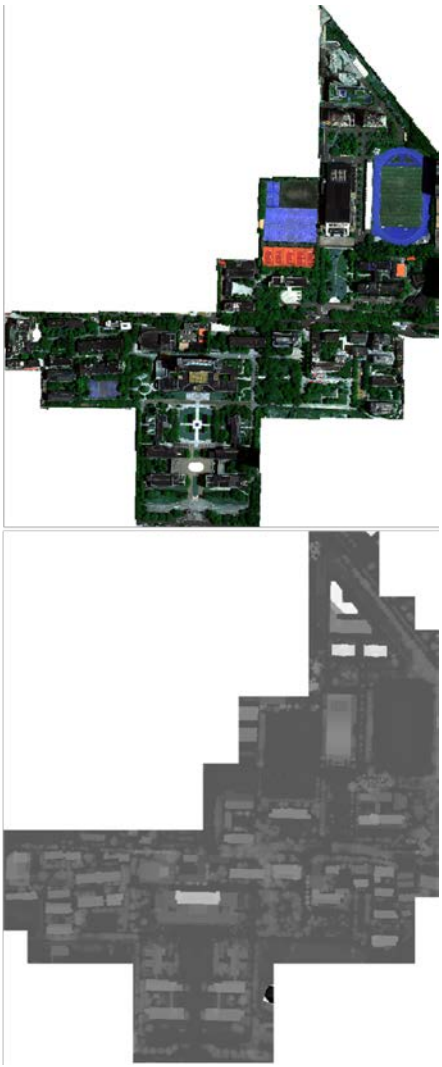

Fig. 1. Orthophoto (higher) and height map (lower)

III. CARBON ABSORPTION ESTIMATION ALGORITHM

As a result, a method for calculating carbon uptake was developed, which includes the following sequence of steps.

A. Separate vegetation from other orthophoto objects

After threshold binarization of the Normalized Difference Vegetation Index, a vegetation mask was obtained, while the optimal threshold value $\tau = 0.56$ was found by maximizing classification metrics on a validation sample of points. It was built using the manual labeling acceleration program, and the final metrics for several threshold values are presented in Tabl. I.

B. Calculate the vegetation volume

The task does not imply an exact solution due to the unlimited degree of refinement of the shape of each plant. To estimate the volume value, an approximation of the double integral calculated from the surface function, which is formed by the height map, is chosen (Fig. 2). Finally, the result takes the following form of upper bounds for the true volume value:

$$V \approx \sum_{i=1}^{N} h(i) \cdot \Delta x \cdot \Delta x. \quad (1)$$

In equation (1) summation is performed over all pixels of the image; h(i) – height value of pixel i; Δx – size of the pixel (76 mm).

C. Calculate the mass of vegetation and use it to derive the mass of carbon dioxide absorbed

The article suggests two approaches, where the second is preferable in case additional information is available about the plant species diversity and the illumination under the tree crowns. The first one is based on the idea of using empirically established data, which eventually leads to the formula (2):

$$CDM = C_{CO_2} \cdot 0.5 \cdot 0.725 \cdot \rho \cdot V. \quad (2)$$

In equation (2) $C_{CO_2} \approx 3.67$ from the ratio of the atomic masses of oxygen (16 Da) and carbon (12 Da) in a CO_2 molecule; 0.5 – experimentally determined proportion of carbon mass relative to dry biomass; 0.725 – dry biomass proportion in $M = \rho \cdot V$. $\rho = 600\ {}^{kg}/_{m^3}$ was used in the article as the average vegetation density in the China region considered [2].

The second approach allows us to obtain a more accurate estimate of the annual absorption of CO_2 using the following formulas basing on the leaf surface index I_{LA} and its linear dependence on plant height:

$$Q_{CO_2} = \sum_{i} I_{LA} \cdot W_{co_2} \cdot \frac{E}{365}, \quad (3)$$

$$I_{LA} = \frac{-\ln(a_1 \cdot NDVI + b_1)}{a_2 \cdot NDVI + b_2} \cdot H, \quad (4)$$

$$W_{CO_2} = W_{CO_2}^{ref} \cdot \left(1 + 0.5 \cdot (NDVI - 0.56)\right) \cdot S. \quad (5)$$

TABLE I. CLASSIFICATION METRICS VALUES FOR OPTIMAL THRESHOLD

Threshold	Accuracy	Precision	Recall	F1-measure
0.56	0.975	0.979798	0.970	0.974874
0.58	0.975	0.979798	0.970	0.974874
0.60	0.975	0.984694	0.965	0.974747
0.62	0.975	0.984694	0.965	0.974747

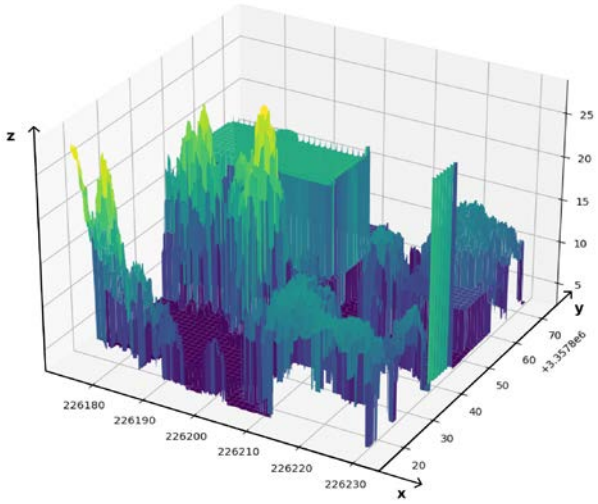

Fig. 2. Representation of a height map for calculating vegetation volume

TABLE II. CARBON ABSORPTION ASSESSMENT RESULTS

NDVI threshold	Mass of CO_2 absorbed (1 approach), tons	Yearly mass of CO_2 absorbed (2 approach), tons	Territorial proportion of vegetation, %	Volume fraction of vegetation, %
0.55	787 133.8	5 369.9	12.64	37.55

In equations (3)–(5) H is the pixel height value, a_1, b_1, a_2, b_2 are selected empirically as $0.306, -0.065, -0.534, 0.541$, respectively, in [3], $E \approx 172$ is the effective photosynthesis time per year. The calculation results for both approaches and the optimal NDVI threshold are presented in Tabl. II.

IV. RESULTS

The results obtained in the article (Tabl. II for numerical results) are relative in nature, which is the result of the input data format. The article shows, that despite the relative nature of the results, they produce a wide scope of their application. The described method is effective for comparative analysis of several territories in terms of biomass and carbon uptake. Regarding this, it is possible to determine the influence of various parameters on the state of vegetation and, in particular, its ability to absorb carbon dioxide. These

parameters include the species diversity of vegetation, relief features, the presence of large sources of CO_2 emissions, and many others. The second approach to estimating carbon uptake also demonstrates how to get more solid results by incorporating additional info to the data already available.

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Machine Learning Approach in Searching Novel Human Aromatase Inhibitors

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***Abstract*. Human aromatase (CYP19A1) presents a key target for treatment hormone dependent breast cancer due to its role in regulation of estrogen biosynthesis. Recently aromatase inhibitors have gained considerable attention in field of drug design and pharmacology because there is a need for novel inhibitors in order to decrease side effects and drug resistance of existing generation of aromatase inhibitors. The main idea of our work is to build and evaluate machine learning models for identification molecules with high probability to inhibit human aromatase. The machine learning models were built on comprehensive CYP19A1 inhibitors datasets using PubChem fingerprints for model training. Five machine learning models were built, based on the algorithms of Random Forest, Adaptive Boosting, Extra Trees, Light Gradient Boosting and Support Vector Machine and presented the following metrics of accuracy on the test set: 0.85, 0.77, 0.86, 0.85 and 0.83 respectively. The Extra Tree model demonstrates the best performance agreeing with metrics of accuracy, precision and ROC-AUC. This model will be implemented for further screening of novel human aromatase inhibitors for treatment hormone-dependent breast cancer and presents a promising instrument to predict the bioactivity of new molecules in a short period of time and at a reasonable cost.**

***Keywords:* human aromatase, machine learning, predictive models, aromatase inhibitors, PubChem fingerprints, chemical space analysis**

I. Introduction

The human cytochrome P450 19A1 (CYP19A1, aromatase) is a heme-containing enzyme that plays essential role in steroidogenesis and is responsible for conversion of androgens to estrogens. At the same time aromatase presents a major target in treatment of hormone dependent breast cancer (the most common cancer among women worldwide) [1]. Recently, aromatase inhibitors have gained considerable attention in field of drug design and pharmacology because of their, on the one hand, distinctive characteristics such as high enzyme specificity and prolonged inhibitory action. However, on the other hand, treatment using third-generation aromatase inhibitors is accompanied with serious side effects, including arthralgia, decrease of bone mineral density, musculoskeletal symptoms, high blood pressure, neurological symptoms, etc. Another problematic issue that arises during aromatase inhibitors administration is drug resistance (innate or acquired) [2]. Consequently, there is still a need for new generation of aromatase inhibitors with minor side effects and decreased drug resistance [3]. The main idea of our work is to explore non-steroidal aromatase inhibitors data, to train multiply machine learning (ML) classification models for the prediction of inhibition of human aromatase and reveal, which of machine learning approach will be the most suitable for application in practice.

II. Materials and Methods

To build predictive models for aromatase inhibition we used reliable sources of the target enzyme inhibition activity data (IC_{50}), which are represented in literature, patents and curated ChEMBL database. A total of 2900 aromatase inhibitors were retrieved along with their structures in SMILES and IC_{50} values in nM range. All compounds from the dataset were preprocessed and standardized, including tautomer canonicalization, removal of stereoisomer information and elimination of salt components. Duplicated, unqualified or missing data values were removed. The final dataset includes 2586 molecules. To achieve better distribution of the obtained data, the IC_{50} values were converted to a negative logarithmic scale, referred to as pIC_{50}. Compounds with $pIC_{50} \geq 6$ were labeled as active (1), and molecules with $pIC50 < 6$ as inactive (0) to prepare dataset for binary classification. Exploratory data analysis of the dataset was performed in order to obtain the chemical space of CYP19A1 inhibitors and correlation of physicochemical properties with pIC_{50} values.

We implemented PaDELPy Python software for calculation molecular features – PubChem fingerprints (881 molecular features were generated), which represent molecules in binary way, providing insights into the atomic indices of molecules. Then we used feature selection technique with random forest algorithm to identify and extract 250 significant

fingerprints, according to their feature importance values. Selected fingerprints were used for training machine learning models. To avoid overfitting, caused by imbalanced data, balancing with Synthetic Minority Oversampling Technique (SMOTE) was performed.

In order to obtain model with the best performance, 5 representative classification algorithms: Random Forest (RF), Adaptive Boosting (AB), Extra Trees (ET), Light Gradient Boosting Machine (LGBM), Support Vector Machine (SVM) have been employed independently for model construction. A random 70:30 split was used for training and test sets. All the classifiers were developed using the scikit-learn Python library with optimal hyperparameters, that were found by Grid Search. We performed 5-fold cross-validation for training set for each model. The performance of 5 binary classification models was evaluated on the external test set via the following metrics: the accuracy, the recall, the precision and the area under the receiver operating characteristic curve (ROC-AUC).

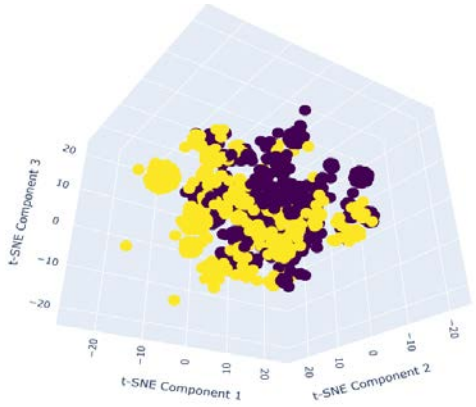
III. Results and Discusion

The performances of the final models are listed in Table (the best metrics for test sets are highlighted in red). According to the Table, Extra Trees algorithm provides the best performance for training set with accuracy 0.86, precision 0.84 and recall 0.91; the best performance for recall metrics by LGBM model is shown. It should be noted, that the main aim of the trained model will be identification of active compounds among chemical databases, including millions of compounds, that's why the most valuable metrics would be accuracy and the most suitable one for further implementation in drug design appears ET model, which demonstrates the best performance agreeing with metrics of accuracy, precision and ROC-AUC.

Performance metrics for ML models, built with 5 classification algorithms

Algorithm	Accuracy		Recall		Precision		ROC-AUC	
	Training set	Test set	Training set	Test set	Training set	Test set	Training set	Test set
RF	0.91	0.85	0.89	0.85	0.92	0.82	0.97	0.91
AB	0.79	0.77	0.75	0.78	0.78	0.73	0.87	0.85
ET	0.93	0.86	0.90	0.85	0.94	0.84	0.98	0.91
LGBM	0.93	0.85	0.91	0.87	0.94	0.82	0.99	0.90
SVM	0.88	0.83	0.86	0.84	0.88	0.79	0.96	0.90

t-SNE analysis was performed over the distribution of significant fingerprints with matplotlib and seaborn Python libraries (Figure). It demonstrates the comparison of chemical space of the active (yellow) and inactive (purple) compounds *via* clustering. From the Figure it's clearly visible that active compounds form specific clusters in chemical space (by projecting in the three t-SNE components), which are significantly different from clusters of inactive compounds. This circumstance explains and confirms the fact that models trained on fine-tuned training data due to feature selection technique, show high quality metrics and are less prone to errors.



t-SNE visualization of the chemical space, occupied by active (yellow circles) and inactive (purple circles) nonsteroidal aromatase inhibitors

According to the results obtained, the ET model with the best performance metrics will be implemented for further screening of novel human aromatase inhibitors for treatment hormone-dependent breast cancer.

Acknowledgment

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Behavior-Driven Dynamic Visual Adjustment: A New Approach to Mitigating Virtual Reality Motion Sickness

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Abstract. **This paper presents a behavior-driven visual adjustment model for mitigating motion sickness in virtual reality. By dynamically adapting the field of view, calculating real-time gaze points, and applying personalized post-processing based on user movement and gaze behavior, the proposed method enhances visual comfort and immersion. Compared to a fixed field of view baseline in an experiment involving 65 participants, the adaptive method significantly reduced motion sickness and improved comfort, immersion, and user satisfaction. This approach highlights the value of embedding behavioral intelligence into visual systems and offers insights into user-centered virtual reality optimization.**

Keywords: **virtual reality, behavior-driven adjustment, Adaptive FOV, motion sickness, embedded systems**

I. INTRODUCTION

Virtual Reality (VR) technologies are increasingly used across gaming, education, healthcare, and industry. Despite advances, motion sickness remains a major barrier to widespread adoption. Symptoms include dizziness, nausea, and visual discomfort, often due to mismatches between visual and vestibular signals [1]. Previous studies proposed static field of view (FOV) restrictions, blur effects, and gaze anchoring to reduce discomfort [2–4]. However, these solutions often lack real-time adaptability and compromise immersion.

This paper introduces a behavior-driven visual adjustment framework that integrates adaptive FOV, gaze point fusion, and dynamic post-processing to optimize comfort. Main contributions include: (1) A dynamic FOV adjustment model based on user movement and controller input; (2) Gaze point estimation via head and controller direction fusion; (3) Real-time visual effect tuning based on behavior; (4) Empirical validation with 65 participants showing significant improvements across user experience metrics.

II. PROPOSED FRAMEWORK

A. Dynamic Field-of-View Adjustment

The FOV angle is modulated in real time by the controller's pointing angle and the user's movement speed, fused through a dynamic weighting factor α [3–5]. Let

$$FOV_{final} = (1-\alpha)FOV_{angle} + \alpha FOV_{speed}, \quad (1)$$

where α is updated continuously to balance directional intent against locomotion intensity.

B. Gaze Point Calculation

The instantaneous gaze direction combines head orientation (d_{gaze}) and controller orientation (d_{hand}) via a weighted average:

$$d_{focus} = (1-\beta)d_{gaze} + \beta d_{hand}, \ \beta = 0.4. \quad (2)$$

The empirical value β=0.4 yielded the most stable focus in pilot tests.

C. Post-Processing Optimization

Image-space effects are driven by the user's state to reduce visual strain and heighten immersion:

- Depth of field (DoF): focus distance derived from *d* focus [6].
- Vignetting: intensity proportional to translational speed to emphasize central vision during rapid motion.
- Color saturation: modified by proximity to scene geometry, easing color contrast when objects approach the user [7].

III. EXPERIMENTAL SETUP

A. Apparatus

The experiment ran in Unity 2022.3 on an Oculus Quest 2 head-mounted display (HMD). Two FOV modes were implemented: (i) a dynamic FOV that adapts in real time, and (ii) a fixed 60° FOV baseline.

B. Participants

Sixty-five volunteers (18 ⩽ age ⩽ 60 yr, 29 female) took part under a within-subject design. All reported normal or corrected-to-normal vision and no vestibular disorders.

C. Procedure

Each participant experienced both FOV conditions in counter-balanced order. A short practice session preceded data collection to familiarize users with the HMD controls and virtual-reality environment.

D. Measures

After each condition, participants rated:

- motion sickness,
- visual comfort,
- sense of immersion, and
- overall satisfaction

on a five-point Likert scale (1 = strongly disagree, 5 = strongly agree).

IV. Results and Analysis

A. Overall Effects of Dynamic FOV

Paired t-tests indicated significant improvements for the dynamic-FOV condition on all four subjective measures (all $p < 0.001$):

MEAN DIFFERENCES AND EFFECT SIZES FOR DYNAMIC VS. FIXED FOV

Metric	Mean Δ (Dynamic – Fixed)	Cohen's d
Motion sickness	–0.48	0.54
Visual comfort	0.97	1.11
Immersion	0.52	0.55
Satisfaction	0.8	0.88

[a] All improvements favor the dynamic-FOV condition.

Non-parametric Wilcoxon signed-rank tests yielded consistent results ($p<0.001$), confirming robustness to deviations from normality.

B. Predictors of User Satisfaction

A multiple-linear regression on change scores (dynamic – fixed) identified visual comfort (ΔVC) as the primary driver of user satisfaction (ΔUS):

$$\Delta \text{US} = 0.55\Delta\text{VC} + 0.31\Delta\text{SP}, \quad R^2 = 0.57, \qquad (3)$$

where ΔSP denotes the change in simulator sickness symptoms. The standardized coefficient for ΔVC was nearly twice that of ΔSP, underscoring comfort's dominant role.

C. Order Effects

Independent t-tests comparing first- vs. second-condition scores revealed no significant sequence effects on any measure ($p > 0.10$), indicating successful counter-balancing.

V. Conclusion

A behavior-driven, dynamic visual-adjustment framework was introduced that combines adaptive field-of-view control, head-and-hand gaze fusion, and state-dependent post-processing. In a within-subject study the system reduced motion sickness, improved visual comfort, and heightened immersion and satisfaction relative to a fixed-FOV baseline. Future work will integrate physiological signals (e.g., heart-rate variability) for closed-loop adaptation and validate the approach in larger-scale, real-time VR applications with more diverse locomotion tasks.

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Adaptive Control System Based on Deep Neural Networks

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Abstract. **A new approach to adapting control signals of the automated production control loop to external control actions and environmental factors based on deep learning neural networks is proposed. A new generation intelligent computer system has been developed to stabilize the parameters of the technological cycle within the framework of the requirements of the technical regulations for technological operations. An algorithmic model for the synthesis of neuroregulators and control feedbacks has been proposed to reduce the sensitivity of the parameters of technological operations to random disturbances and the influence of external environmental factors in real time. Method for formally describing the components of the technological process model and their interrelations using the logical inference mechanisms of the ecosystem of new generation intelligent computer systems are presented.**

Keywords: **neural networks, machine learning, adaptive control**

I. Introduction

In the operation of complex technical systems, including within automated production systems, the task of accounting for and compensating the influence of external destabilizing factors in real time is of current relevance [1]. Ensuring the stability of technological parameters while complying with the requirements of technical regulations and normative documentation is of significant importance. In this context, the development of hardware and software tools aimed at reducing the sensitivity of technological process parameters to random external disturbances holds both scientific and practical value. Within this task, a new approach is proposed for adapting control signals in the control loop of an automated production process, based on the use of an intelligent adaptive control system. This system implements neuroregulator synthesis algorithms built on deep learning principles, enabling dynamic adjustment of control actions under conditions of a changing external environment and stochastic disturbances.

This solution increases the robustness of the control system to external control influences through the intelligent processing of current process parameters. The application of deep learning models enables the generation of adaptive control signals that account for both stochastic and deterministic changes in the external environment, ensuring compliance with the technical regulation requirements and improving the overall efficiency of the production cycle.

II. General Scheme of Adaptive Control

Adaptive control of the technological cycle in the context of this work is considered as the process of generating corrective influences on the control variables of the technological process control system (TPCS) [1] in order to ensure its stable operation under external disturbances while complying with the requirements of the technical regulations.

To ensure compatibility and integration capability of the developed control adaptation method with other information-control tools, a formalization of the control loop is proposed based on OSTIS technology [2], using an ontological description of the subject domain "technological processes with probabilistic characteristics" [3], which ensures system scalability, increases its interoperability, and enables inclusion in broader intelligent production environments.

The developed intelligent adaptive control system implements procedures for the synthesis of neuroregulators [2], capable of performing real-time correction of control parameters (Fig. 1).

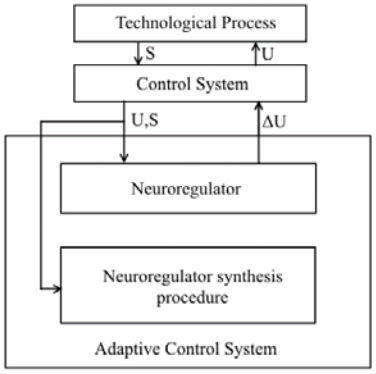

Fig. 1. Scheme of the proposed adaptive control loop

Within the neuroregulator synthesis procedure, numerical criteria for evaluating adaptation quality are introduced [4], taking into account both the dynamics of technological parameters and regulatory constraints. The constructed neuroregulator generates control signals based on which decisions are made regarding the necessary correction of controlled variables in the TPCS, thereby ensuring adaptive compensation of deviations and enhancing the stability of the production process.

III. Neuroregulator Synthesis Procedure

The neuroregulator synthesis procedure in the developed intelligent adaptive control system includes the following sequence of stages:

- Definition of numerical criteria for control adaptation quality – formalization of target performance indicators based on analysis of the technical regulation, involving expert evaluation by domain specialists.
- Formation of the training environment – construction of a simulation model of the technological process control system, used as the environment for training the neural regulator through deep reinforcement learning.
- Search for optimal neural network architecture – automated search for the best neuroregulator architecture using an evolutionary algorithm [5], ensuring a balance between model accuracy and computational efficiency.
- Training, validation, and testing – execution of the training process for the selected neuroregulator architecture based on the constructed training environment, followed by validation and testing to assess generalization capability and robustness to disturbances (Fig. 2).
- Integration and practical application – connection of the trained neuroregulator to the real control system of the automated technological cycle, enabling adaptive correction of control actions in real time based on the current system state and external factors.

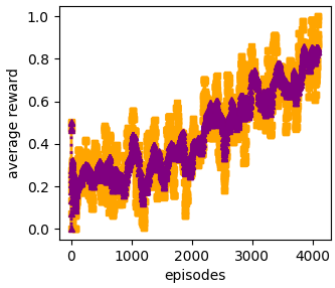

Fig. 2. Reward function dynamics during the neuroregulator training process

IV. Examples of Practical Application of Control Adaptation Technology

The use of the intelligent adaptive control system in the context of laser thermal cleaving technology (Fig. 3) represents a promising direction for increasing process efficiency. In the implementation of this technology, it is critical to ensure the required thermal regime, including strict adherence to heating and cooling parameters of the processed item. The control system generates a stream of observed data that includes key responses of the technological process – such as peak temperature values and tensile stresses in the laser exposure zone. This data is fed into the adaptive loop, where the neuroregulator operates.

The neuroregulator, using current observations of the system state (including both control variable values and process responses), evaluates the necessity of corrective actions. Based on its output signals, a decision is made either to maintain the current parameters or to perform a targeted adjustment of one of the control variables. This approach allows for compensation of deviations from target processing regimes, ensuring high quality and repeatability of laser processing results.

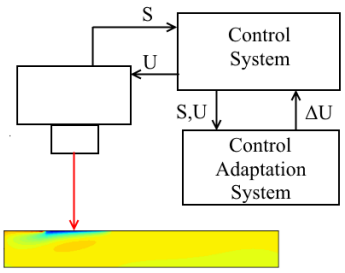

Fig. 3. Adaptive control scheme for the laser material processing system

V. Conclusion

A new approach to adaptive control of operational parameters in automated technological production processes has been developed and implemented based on an intelligent system employing deep learning neural networks. The proposed solution ensures stability and correctness of the control system operation under external disturbing factors while strictly complying with technical regulation requirements. The constructed algorithmic model for neuroregulator synthesis enables real-time generation of corrective control actions based on current responses of the technological process, demonstrated by the example of controlling modes in laser thermosplitting processing.

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TCS: an Algorithm for Focusing on the Segmentation of Tree Crowns and Trunks in Forest Point Clouds

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***Abstract*. Forest tree crown and trunk point cloud segmentation enables accurate acquisition of tree morphological parameters, supporting forest growth assessment. However, traditional methods are inefficient and destructive, existing algorithms suffer from accuracy limitations due to noise and data sparsity, and deep learning-based methods lack generalization and robustness. This paper proposes the TCS network, combining soft density grouping and fusion density clustering. Using U-net as the backbone, it processes point clouds via semantic, offset, and density prediction branches. The clustering stage adaptively adjusts radii based on density for feature clustering, and the refinement stage employs deformable convolution upsampling to enhance accuracy. Experiments on datasets from Dongtai Huanghai Forest Farm using backpack, ground station, and UAV point clouds show TCS outperforms other methods in IoU, precision, recall, and F1-score, improving deep learning robustness and generalization in tree segmentation.**

***Keywords:* Point cloud segmentation, Deep learning, Clustering algorithm, TCS network**

I. INTRODUCTION

Tree crown and trunk point cloud segmentation provides key parametersfor forest growth assessment, resource statistics, and vegetation mapping. Traditional on-site measurements are time-consuming, labor-intensive, and destructive. Clustering algorithms, affected by noise and point cloud irregularity/sparsity, have limited accuracy. Deep learning automates feature learning but lacks generalization and robustness. Thus, we propose TCS, integrating soft density grouping and fusion density clustering to enhance performance on diverse forest point clouds.

II. METHOD

A. Backbone Net

In this paper, TCS uses U-net as its backbone network. The network takes point sets as input, first converts disordered points into an ordered voxel grid, then implements U-net via submanifold sparse convolution. This effectively handles the sparsity of point cloud data, reduces computation while retaining geometric information, and then recovers point features from voxels for subsequent branches.

Semantic prediction branch: It takes point features extracted by the backbone, processes them through fully connected layers, and outputs the probability of points belonging to different categories, providing a basis for subsequent instance clustering, with Focal Loss used for evaluation. Offset prediction branch: It takes point features, predicts 3D offset vectors from points to the geometric centers of their affiliated instances via fully connected layers, evaluated by smooth L1 loss. Density prediction branch: Based on point features output by the backbone, it connects a multi-layer perceptron. Input features are processed through linear transformations and activation functions, outputting predicted density values of each point, with mean square error loss used for supervision.

B. Clustering

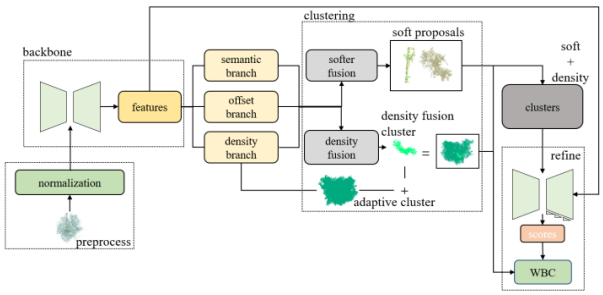

Fig. 1. The overall structure of the TCS network

The clustering module adopts a serial combination of density-based adaptive adjustment of clustering radius and density-fused feature clustering. First, using point cloud density information and preset mapping rules, the density values of points are converted into corresponding clustering radii. Then, the DBSCAN algorithm is used for preliminary clustering of the entire point cloud data to obtain preliminary clustering results.

After initial clustering, the stage of density-fused feature clustering begins. Density-fused features of points in each initial cluster are extracted to more comprehensively describe point attributes. Then, based on algorithms like K-Means, secondary clustering is performed using distance metrics designed for these fused features. During secondary clustering, clustering centers are updated through multiple iterations to further subdivide initial clusters into more accurate sub-clusters, or merge and adjust unreasonable clusters in initial results, ultimately achieving more precise clustering outcomes.

C. Refine

In the fine-grained segmentation network, this paper designs deformable convolution upsampling: the sampling positions of convolution kernels can adaptively change according to input features, and control sampling positions by learning offsets. This enables more flexible capture of irregular structures and complex shapes in point clouds, better restoring details. For forest point clouds, where tree shapes and distributions are often irregular, this convolution can adaptively adjust sampling positions for more accurate upsampling, retaining details such as branch curvature and leaf distribution to improve segmentation accuracy.

The input of the top-down refinement module is the union of trunk and canopy clusters, along with point set features extracted by the backbone network. These are input into the fusion network for fine segmentation, and a score is assigned to each cluster to indicate associated clustering quality. This helps retain complete clusters in subsequent instance prediction, thereby completing individual tree instance segmentation.

III. EXPERIMENT ANALYSIS

A. Dataset

The forest point cloud was collected from an artificial forest in Dongtai Yellow Sea Forest Farm, Yancheng, Jiangsu Province. The two plots investigated are both poplar forests, covering approximately 10,000 square meters and 3,600 square meters respectively, with differences in diameter at breast height and tree height, and certain representativeness.

B. Results

In this paper, the LiDAR point clouds of the TLS were selected from the sample plots for experiments. The experimental visualization results are as follows:

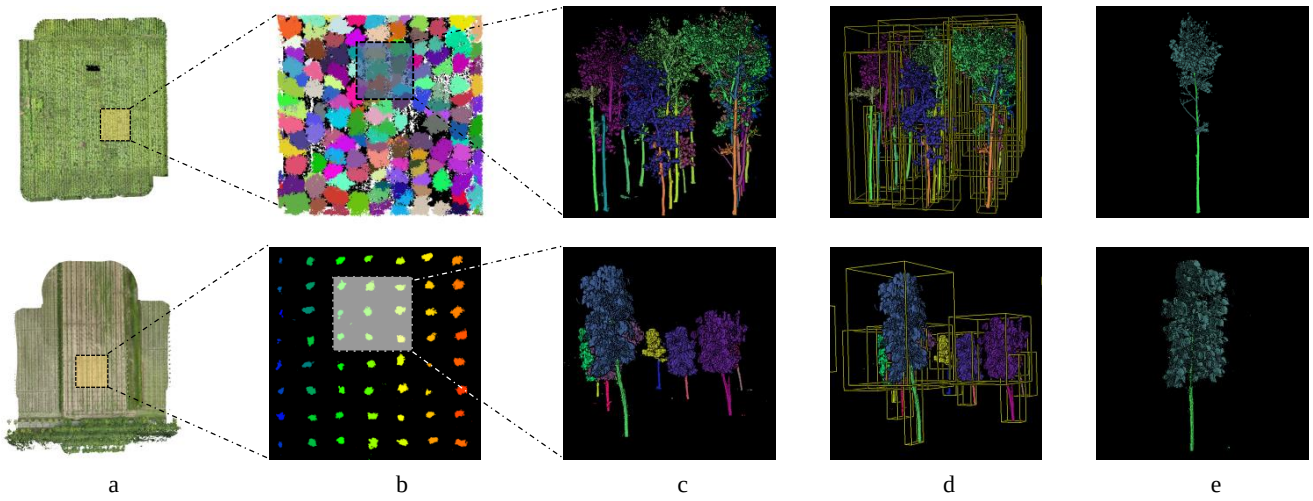

Fig. 2. The experimental results of the TLS dataset, where (a) is the original data, (b) is the high-altitude top view after the segmentation of the experimental area is completed, (c) is the side view of the small area, (d) is the examples of different tree crowns and trunks in the (c) area, and (e) is the segmentation of the tree crowns and trunks of individual trees

II. CONCLUSIONS

This paper proposes the TCS network for segmenting forest crown and trunk point clouds. The network integrates soft density grouping, fusion density clustering, along with a U-net backbone network, semantic, offset, density prediction branches, and deformable convolution up sampling in the refinement stage, effectively handling the irregularity and sparsity of point cloud data. Experiments on forest point cloud datasets from Dongtai Huanghai Forest Farm in Jiangsu Province. Research indicates that the TCS network performs excellently in forest point cloud segmentation, enhancing the robustness and generalization ability of deep learning in this field. With the development of LiDAR technology and the growing demand for accurate forest resource assessment, this network can play an important role in forestry applications. Future work will focus on optimizing the network structure, exploring combinations with more advanced deep learning techniques, and expanding application scenarios.

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