DOI: https://doi.org/10.15276/aait.09.2026.04
UDC 004.9

Specialized recurrent U-Net architecture for immunohistochemistry image segmentation

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ABSTRACT

Microobject segmentation in biomedical images is a complex and time-consuming process, and current efforts are aimed at qualitatively separating the studied objects from the background in the image. Immunohistochemical images are used for breast cancer analysis. One of the types of images is estrogen samples. The specificity of immunohistochemical images requires a more thorough approach to segmentation, because standard algorithms or classical neural network models do not allow achieving the required accuracy. This article presents a new convolutional network architecture based on a recurrent U-network for segmentation of immunohistochemical images. The proposed architecture is specifically designed to process the unique features of immunohistochemical images. The principles of recurrent convolutional neural networks were used to develop the model and train it using open datasets. The architecture proposed in this work is based on the configuration of neural network layers, which allows to obtain the best result for a given type of image. In addition, a pipeline of continuous integration of the program code and the model was implemented to ensure continuous retraining in a cloud environment, which significantly simplified the workflow for researchers and engineers. Additionally, a mechanism for processing medical images and providing automation of the big data processing process using computer vision and deep learning was proposed. The proposed method achieved higher segmentation accuracy. The architecture allows for more accurate cell segmentation on immunohistochemical images, which is a crucial step in the diagnostic pipeline. High-quality cell segmentation increases the reliability of subsequent analyses and parameter extraction, thereby contributing to increased diagnostic accuracy.

Keywords: U-net; deep learning; segmentation; immunohistochemistry; software architecture; biomedical images

***For citation*: Pitsun O. Y., Berezsky O. M. "Specialized recurrent U-Net architecture for immunohistochemistry image segmentation". *Applied Aspects of Information Technology*. 2026; Vol.9 No.1: 51–61. DOI: https://doi.org/10.15276/aait.09.2026.04**

INTRODUCTION

Immunohistochemical images are images of tissue sections obtained as a result of the application of the immunohistochemistry (IHC) method, which is used to detect specific proteins (antigens) in the cells of a tissue sample using antibodies. The features of the use of immunohistochemical images in the diagnosis of breast cancer are shown in [1]. Analysis of immunohistochemical images for determining breast cancer is one of the key stages. Most CAD (Computer-Aided Diagnosis) systems include software modules for image processing. In most cases, both computer vision algorithms and artificial intelligence tools are used. In the diagnostic process, an important factor is the shape of the studied cell nuclei. The criteria for detecting pathologies are the shape of the cells, color, etc. Image preprocessing and segmentation algorithms are used to form automatic tissue sample analysis systems. The segmentation algorithms used are threshold segmentation algorithms, the water distribution method, and k-means. Recently, and U-net networks [2] for medical convolutional neural networks for image processing image segmentation tasks have become increasingly widespread.

With the development of hardware, U-net networks [3] are increasingly used, which allow the use of resources in the form of processor time, memory, graphics processors. The specificity lies in the large number of network architectures that show good results only for a specific type of image. Therefore, there is a need to develop new architectures for analysis, segmentation of immunohistochemical images, which would show the best results. Improving the quality of segmentation is obtained by developing new network architectures and selecting training parameters.

The article consists of the following sections:

– analysis of previous publications in this field, which allowed to highlight the current state of research;

– description of the development methodology, which includes analysis of the dataset, the proposed neural network architecture, the life cycle of biomedical images automatic segmentation;

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– results of computer experiments with analysis of the proposed solution and analogues by several metrics.

RELATED WORKS

The use of convolutional neural networks, particularly for classification and segmentation tasks, has become widespread and is currently the main machine learning technology for image processing.

In [2], the authors proposed the Attention U-net architecture. The proposed approach is based on automatic focusing on target structures of various shapes and sizes. In [3], the R2U-net network was proposed, which allows for classification and segmentation of medical images. In particular, the authors combine recurrent convolutional neural networks with convolutional ones. The peculiarity of this network lies in its feasibility of using it for processing a large amount of data. In [4], the architecture of the U-net 3+network is presented. Full-scale skip connections in the proposed network include low-level details with high-level semantics along with object maps at different scales. In [5], the authors present an approach to medical image segmentation using the transformer mechanism. The paper presents an approach for use in 2D and 3D images. The network can also be used for multi-class segmentation. Another architecture based on transformer technology is presented in [6] Swin- U-net. In most cases, this architecture is used for medium-resolution images. The use of visual transformers has significant potential. Automatic segmentation of biomedical images is considered in [7]. A feature of the paper is a comprehensive analysis of computer vision and machine learning algorithms for segmentation tasks. The authors also consider the possibility of combining algorithms and using image preprocessing.

Immunohistochemical analysis is used to diagnose various pathologies of breast cancer. An approach to diagnosing diseases related to breast cancer based on immunohistochemical images is presented in [8].

An important stage in the development of new and research of existing U-net network architectures is software implementation and approaches to resource use in cloud services. The process of training a neural network is resource-intensive, since tens of thousands of parameters can be used in the training process. Therefore, it is important to develop mechanisms for integrating algorithms into cloud environments. Considerable attention is paid to these issues in the works [9], [10]. The authors developed the MLOps approach for deploying software in cloud services, in particular DigitalOcean. In the works, the authors pay attention to the use of algorithms, the formation of datasets with masks, and the technology of continuous delivery and code integration. Terraform technologies are additionally considered.

In [11], the authors analyzed the use of ResUnet technologies for image segmentation. In total, 12 optimized ResUnet architectures using the ensemble strategy were used. U-net is often used in medical data processing systems, in particular in [12] for segmentation and object selection. The transformer mechanism is also often used in automatic segmentation tasks. Thus, in [13], the authors propose an architecture that combines the functionality of U-net and visual transformers. The proposed approach showed better results for a specific type of image. In [14], the authors proposed an improvement of the R2U-net architecture, which works on the basis of recurrent neural networks. The developed architecture is called AlexResNet + R2Unet. Scientists pay considerable attention not only to standard approaches in segmentation, but also to approaches based on GAN networks [15]. The experiments were conducted on ultrasound images. In [16], the authors propose a Deep Learning Cluster Architecture for segmentation of histopathological images. U-net networks are used as elements of deep learning in combination with other algorithms. The authors provide a comparative analysis both in the form of quantitative assessments and in visual form.

When training U-net networks for segmentation, a separate requirement is the use of annotated datasets. Annotated datasets must contain information about the pixel label of objects of interest. The annotation can be stored as binary masks or a list of region coordinates.

The PESO dataset [17] was created for the recognition of epithelial tissue on immunohistochemical samples. The data are presented as full histological slides with a size of 2500×2500 pixels and a resolution of 0.48 μm/pixel. The training set includes 62 full histological slides, as well as the corresponding masks. The masks were obtained using a pre-trained U-net network. The test set consists of 40 histological slides. The dataset contains XML files with annotations, which makes it possible to view the test regions in specialized programs, such as ASAP.

The BCSS dataset [18] consists of 151 hematoxylin and eosin (H&E) stained breast cancer histological sections. The images are taken from the

Cancer Genome Atlas archive. 25 healthcare professionals participated in the annotation, who described more than 20,000 regions of interest. A trained VGG-16 model was used to classify the 224×224 pixel regions of interest. The dataset contains JSON annotation files, binary masks, and RGB images for further processing and analysis.

Pettersen et al. in paper [19] is devoted to the implementation of deep U-net segmentation models for digital pathology of intestinal mucosal tissue images. The authors used free and open source software: QuPath, DeepMIB, and FastPathology. A dataset of 251 digitized histopathological images stained with hematoxylin-eosin and immunohistochemical staining for CD3 was created. Tissue images, including epithelium, were annotated by an experienced pathologist. The total number of annotated regions was 31,000. For classification training of the model, the original 2048x2048 regions were reduced to 512x512 pixels.

Tomar D. in [20] proposes a processed version of the CAMELYON17 dataset. The data source is 50 digitized images of complete histological sections. Each WSI is divided into fragments of 270x270 pixels. These fragments are classified as tumor and normal. For segmentation of cell nuclei, a HoVer-Ne network trained on the CoNSeP dataset was used.

Table 1 shows the main parameters of the datasets used for image segmentation.

Table 1. **Dataset parameters**

Title	Organ	Number of virtual preparations (WSI)	Annotations
PESO [17]	prostate cancer	102	Binary masks
BCSS [18]	breast cancer	151	Binary masks
Pettersen et. al. [19]	bowel cancer	251	Binary masks
Tomar D. [20]	breast cancer	50	Binary masks
IHCDBI [21]	breast cancer	500	Binary masks

***Source*: compiled by the authors**

Despite their clinical relevance, all datasets used share common limitations, including small sample sizes and binary annotations that do not capture the morphological diversity of tumor tissues. The limited number of samples increases the risk of overtraining deep models and reduces their generalization ability.

RESEARCH GOALS AND OBJECTIVES

The aim of the work is to develop convolutional neural network architecture for immunohistochemical images segmentation. To perform the task, the following architectures were investigated: Unet, AttentionUnet, and Resunet. To achieve better performance, the Resunet architecture was modified by adding additional filter layers and changing the network parameters. The criteria of accuracy and loss, which are used in the evaluation of U-net, were chosen as metrics for assessing the quality of segmentation.

To achieve this goal, the following tasks must be performed:

– analyze existing datasets for biomedical image segmentation using deep learning;

– develop a dataset structure and graphical interface for immunohistochemical images segmentation using original images and masks;

– develop a structure of the proposed modification of the R2Unet architecture for automatic immunohistochemical images segmentation;

– compare encoder architectures for immunohistochemical images segmentation.

RESEARCH METHODOLOGY

Datasets

The experiments were conducted on the basis of the “IHCDBI” immunohistochemical image dataset [21].

The dataset is intended for training a U-net type neural network. The dataset is formed on the basis of tissue samples obtained in the process of pathomorphological examination. The dataset consists of 500 immunohistochemical and histological images with a size of 4096×3286 pixels. Each image corresponds to one of 4 markers: Er, PR, HER2neu, Ki-67. Er (estrogen receptor), PR (progesterone receptor), HER2neu (oncoprotein) and Ki-67 (proliferation marker) are immunohistochemical markers that are visualized on histological images of tissues using specific antibodies. Such images allow identifying the presence and distribution of cells expressing the corresponding protein. In the images, these markers appear as areas with a characteristic color (nuclear or membrane), which serves as the basis for morphological and quantitative analysis. The images have high resolution, which allows for precise localization of morphological structures and cells with a positive reaction to the corresponding marker.

Each immunohistochemical image is accompanied by a binary mask that serves as a reference for training the segmentation model. Annotation is performed by qualified pathologists. Images are accompanied by metadata that reflect the results of morphological interpretation. In particular, the percentage of positive cells, the staining intensity score (IS), the proportion of positive cells (PS), the total score (TS) and the corresponding clinical conclusion regarding the positivity or negativity of the reaction is indicated. Such metadata allow not only to segment images, but also to quantitatively assess the level of expression of protein markers in the diagnosis of hormone-dependent tumors, in particular breast cancer. The preparation of the dataset included preliminary normalization of the color of the images to compensate for variation in staining, as well as standardization of the scale.

An example of immunohistochemical images and their corresponding masks is shown in Fig. 1.

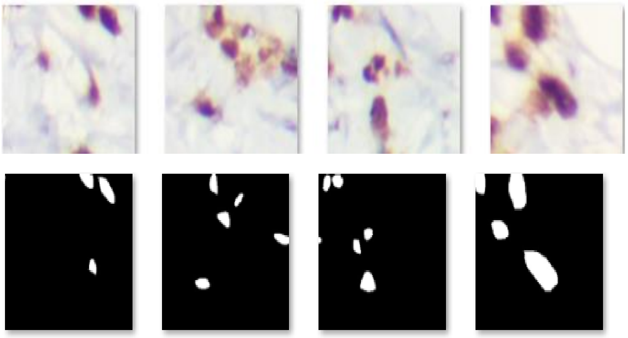


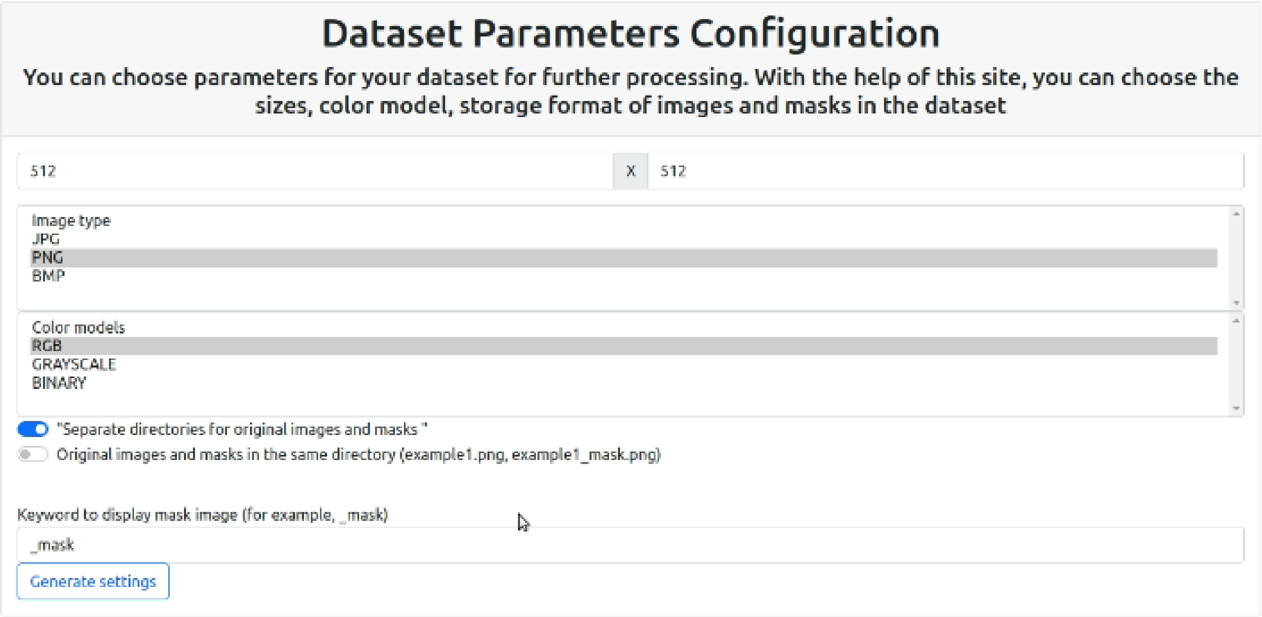
Fig. 1. **Example of immunohistochemical images and their corresponding masks (IHCDBI dataset)**
***Source*: compiled by the authors**

This study used 500 immunohistochemical images, divided into a test and training sample divided in a ratio of 80 to 20 percent, respectively.

Data preparation

Data preparation for immunohistochemical image segmentation is an important step that requires special attention. Images with a size of 4096×3289 pixels are used as the main ones. To work with a convolutional neural network, it is necessary to divide the image into smaller parts, for example, 256×256 pixels and 512×512 pixels. The principle is not to scale, which can cause the loss of important elements, but to cut the image into smaller particles. Another important step is to form the structure of the dataset, because for segmentation tasks it is necessary to make masks for each original image with cell nuclei selected by the expert. This stage requires additional attention, in particular, to form a directory and suffixes in the file name for further comparison and training. The graphical interface of the developed software module for forming requirements for the dataset is shown in Fig. 2 [22]. As a result of the setup, a configuration file is generated and this allows the use of the same dataset parameters for experiments by different scientists. The advantage of using this approach is the possibility of generating identical datasets, which will emphasize the quality of the results.

The result of the formation of the dataset parameters is a JSON file that can be further used in the software module, which will allow you to form the necessary directory structure [22]. The advantage



Dataset Parameters Configuration

You can choose parameters for your dataset for further processing. With the help of this site, you can choose the sizes, color model, storage format of images and masks in the dataset

512 X 512

Image type
JPG
PNG
BMP

Color models
RGB
GRAYSCALE
BINARY

● "Separate directories for original images and masks "
○ Original images and masks in the same directory (example1.png, example1_mask.png)

Keyword to display mask image (for example, _mask)
_mask

Fig. 2. **Graphical interface of the developed software module for generating requirements for the dataset**
***Source*: compiled by the authors**

of this approach is the ability to export and import configurations for further use of the same type and structured dataset formats to be able to reproduce experiments and create new neural network models.

As a result of the software module, the following directory structure for the dataset is initially formed (Fig. 3).

In addition, pre-processing of images takes place. For this, median filtering of the image $Im^{I}_{i,j}$ is performed to reduce the level of impulse noise.

$$Im^{I}_{i,j} = med\left[Im_{i+s,j+t}; (s,t) \in W\right]; i,j \in Z^{2}, \quad (1)$$

where $Im^{I}_{i,j}$ is element of the image matrix after filtering; Z^{2} is two-dimensional discrete spatial domain of the digital image; $W_{s,t}$ is image aperture array element with size m x n; $Im_{i,j}$ is element of the input image matrix; i,j are row and column index; med is median operator. Calculates the average of an ordered set of intensities in a window. A 3×3 window is selected for filtering with this filter.

Architecture

For the segmentation of immunohistochemical images, testing was carried out using the U-net, AttentionUnet, Resunet, R2Unet architectures. To improve the quality of segmentation, a modification of the Resunet architecture was proposed by changing the configuration of the layers and the parameters of the recurrent iteration and the activation function. In the proposed approach, there are three iterations for the recurrent layer at the encoder and decoder levels. This allows you to increase the number of trained parameters and, accordingly, increase the accuracy. In general, this allows you to highlight small details on the immunohistochemical image, which is relevant for this type of image. The structure of the proposed modification of the R2Unet architecture for automatic segmentation of immunohistochemical images is shown in Fig. 4.

Table 2 shows the Model parameters.

Table 2. **Model parameters**

Parametr	***Values***	***Description***
Input shape	(256, 256, 3)	Input 2D image size
Filters	[32, 64, 128, 256, 512, 1024]	Number of channels at each level
labels	2	Number of segmentation classes
activation	GELU	Activation in convolutional layers
output_activation	Softmax	Activating the output layer
batch_norm	True	Using Batch Normalization
pool	max	Type of downsampling
recur_num	3	Number of recurrent iterations (T)
stack_num_down	2	Number of RRCNN blocks in encoder

***Source*: compiled by the authors**

The key aspect of the proposed modification is the use of a larger number of channels, which makes the architecture deeper and allows for better results compared to analogues.

A neural network for image segmentation using U-net with recurrent blocks consists of a large number of repeating elements: convolution layers, recurrent layers, pooling functions, activation. These blocks are components of downsampling and upsampling layers.

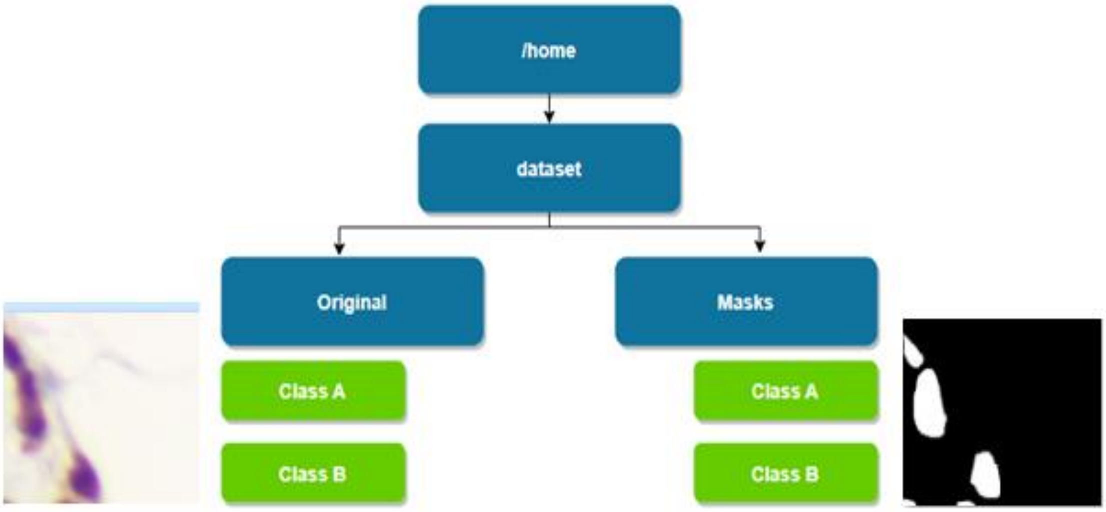


Fig. 3. **Directory structure for the dataset**
***Source*: compiled by the authors**

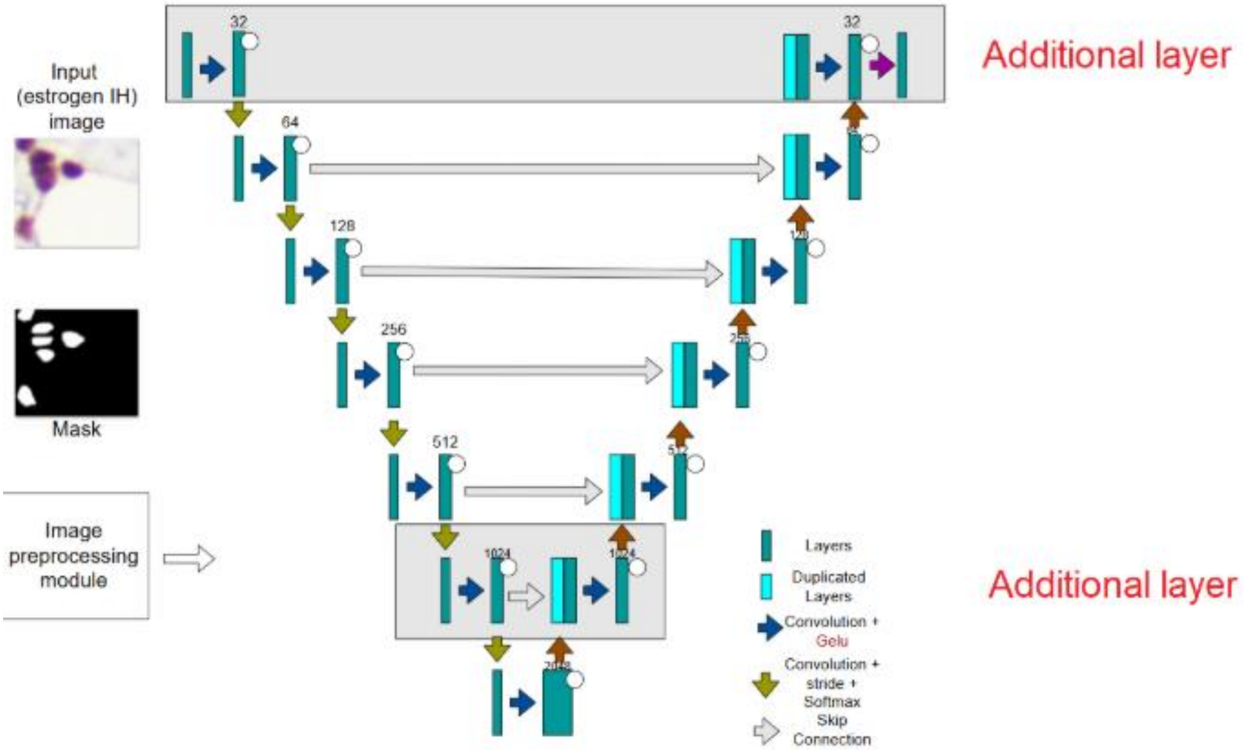


Fig. 4. **Structure of the proposed modification of the R2Unet architecture for automatic segmentation of immunohistochemical Images**

***Source*: compiled by the authors**

The image sample is divided into two parts: test and training. A feature of the U-net network is the presence of recurring blocks. Let us present the structure of the U-net network O_{cnn} as the set of operations that define the CNN:

$$O_{cnn} = \{\langle C\rangle; \langle B\rangle; \langle A\rangle; \langle Add\rangle; \langle P\rangle; S\}, \quad (2)$$

where $\langle C\rangle$ is set of convolution functions; $\langle B\rangle$ is batch normalization; $\langle A\rangle$ is set of activation functions; $\langle Add\rangle$ is multiple layers of the recurrent block; $\langle P\rangle$ is set of pooling functions; S is Skip connection.

Let's consider the key blocks in more detail separately:

Convolution block

Formally, the convolution process can be represented as follows:

$$I_{y,x} \times h = \sum_{i=-n_2}^{n_2} \sum_{i=-m_2}^{m_2} I(y-i, x-i) \cdot h(i,j), \quad (3)$$

where n_2 is half the filter height, m_2 is half the filter length, x iscolumn position pixels, y is pixel row position, $I_{y,x}$ is input image, h is convolution kernel.

Recurrent block (Add layer)

The recurrent block is designed to store information, due to the presence of feedback loops. The existence of feedback allows you to transfer data from the previous iteration of training the neural network to the current one.

The recurrent block can be described using the formulas:

$$y_l = h\big(x_l + F(x_l, W_i)\big), \quad (4)$$

$$x_{l+1} = f(y_l), \quad (5)$$

where $F(x_l, W_i)$ is recurrent block that needs to be taught; x_l and x_{l+1} are entry and exit l -th recurrent block; $f(y_l)$ is activation function; $h(x_l)$ is mapping function

Activation function GELU

The formula for finding the activation function $f(x)$ is:

$$f(x) = 0.5x\left(1 + tanh\left(\sqrt{\frac{2}{\pi}}(x + 0.044715x^3)\right)\right) \quad (6)$$

where $0.5x$ is a linear component to the function; x is input value; $tanh$ applies the hyperbolic tangent function to the input, which helps maintain a smooth transition; $\sqrt{\frac{2}{\pi}}$ is normalizing factor.

GELU allows small negative values when the input is less than zero, providing a larger gradient for error backpropagation.

Upsampling

The upsampling layers (U) in U-net restore the spatial dimensions reduced during encoding using the following transposed convolutions:

$$U = f(W^T \cdot x + b), \quad (7)$$

where W^T is transposed weight matrix; x is feature map; b is bias; f is activation function, for example *GELU*.

Skip Connections

Skip connections are key to maintaining high-resolution detail throughout the U-net processing pipeline. By combining high-resolution features from early levels in the encoder with corresponding upsampling features in the decoder, skip connections ensure that accurate spatial information is preserved.

So, the developed modification of the R2U-net architecture [3] for immunohistochemical images is that:

- additional layers with sizes 32 and 1024 for at the encoder and decoder levels were added, which allowed to increase the number of training parameters and, as a result, increase the segmentation accuracy;
- the Gelu algorithm was chosen as the activation function, which showed better results of the final segmentation accuracy compared to the classical Relu;
- in the proposed architecture, the number of recurrent layers is 3.

Metrics

To assess the quality of segmentation, we will use metrics that are typical for U-net assessment: Tversky loss and IoU loss.

Let us detail these metrics.

Tversky loss

Estimating the quality of segmentation is an important stage in the development of any neural network architecture, including segmentation. Tversky loss (Tl) [23] is used to assess the quality of image segmentation using segmented masks according to the formula:

$$Tl = \frac{TP}{TP+\alpha FN+\beta FP}, \qquad (8)$$

where FN is false positive pixels; FN is false negative pixels; TP is true positive pixels; α and β are weight parameters that control the trade-off between false positives (α) and false negatives (β).

IoU loss

Typically, for two finite sample sets A and B, their *IoU* is defined as the intersection (A∩B) divided by the union (A∪B) of A and B [24].

$$IoU = \frac{A \cap B}{A \cup B}. \qquad (9)$$

MLOps

An important element in the formation of a pipeline is the detailing of the processes of the software system. For example, to implement automatic segmentation, it is necessary to provide for the process of data preparation, the formation of original images and the corresponding masks, the direct operation of the Unet network, the selection of hyperparameters such as the number of epochs, batch size, etc. An equally important process is the visualization of the obtained results for further evaluation.

The selection of tools for the implementation of the pipeline is also an important element, which aims to organize the work in the team as clearly as possible. The main tools in this case are the choice of: containerization tools, approaches to the implementation of the infrastructure as code mechanism, CI/CD tools, such as Github CI/CD, etc. At the level of direct automatic segmentation, it is necessary to consider frameworks for working with data and U-net networks.

The life cycle of automatic segmentation is shown in Fig. 5.

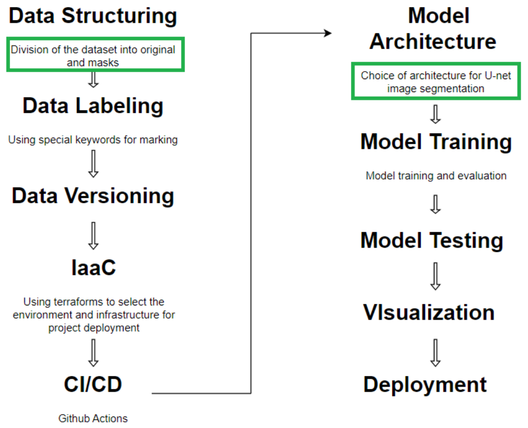


Fig. 5. **The life cycle of automatic segmentation using proposed architectures**
***Source*: compiled by the authors**

The proposed pipeline contains the main components necessary to launch a project using automatic segmentation in a cloud environment using model and dataset deployment mechanisms. The mechanism of continuous integration and continuous code delivery is a convenient mechanism for updating versions of software code on cloud systems, which allows you to maximally automate the process of delivering and deploying code on the server. This example highlights additional pipeline elements needed specifically for deploying software using U-net, distributed dataset on original images and masks. A comparative analysis of encoder architectures for segmentation of immunohistochemical images is given in Table 3. 500 immunohistochemical images were used for the experiments.

Table 3. **Comparative analysis of encoder architectures for segmentation of immunohistochemical images**

Metrics	U-net	Attention U-net	R2U-Net	Proposed modified architecture
cross-entropy loss	0.42	0.49	0.31	**0.29**
Tversky loss	0.43	0.38	0.30	**0.22**
IoU loss	0.49	0.43	0.34	**0.24**
Dice loss	0.32	0.27	0.20	**0.13**
Recall	0.80	0.80	0.88	**0.90**
AUC	0.80	0.79	0.88	**0.90**

***Source*: compiled by the authors**

The proposed model exhibits the lowest values of all loss functions (cross-entropy, Tversky, IoU, and Dice), indicating a more accurate match of the predicted masks with the reference ones. Compared to R2U-Net, which also shows competitive results, the proposed architecture provides additional improvement in both loss metrics and recognition quality indicators.

COMPUTER EXPERIMENTS

An example of segmentation results is shown in Fig. 6.

In the process of performing the experiments, tensorflow, keras, and Python programming language machine learning libraries were used. Minimum hardware requirements are hard disk capacity – 10GB, RAM capacity – 30GB, NVIDIA Tesla P100. The number of training parameters is 76,067,073, the number of epochs = 100. The training time was 2 hours 50 minutes.

The Fig. 6,a shows the original biomedical image, Fig. 6,b is the result of segmentation by proposed architecture, the image Fig. 6,c is a mask, edited by a human.

The activation function plays an important role in the training process of a neural network. In this paper, a comparative analysis of the use of the RELU and GELU activation functions for immunohistochemical image segmentation tasks is carried out. The results of the comparison are shown in Fig. 7.

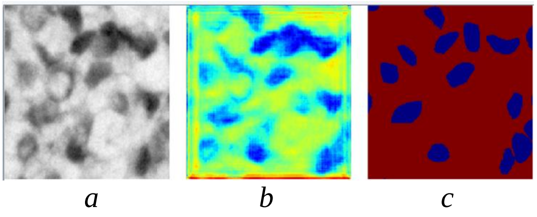


Fig. 6. **Example of segmentation results: a – original image; b – result image; c – mask image**
***Source*: compiled by the authors**

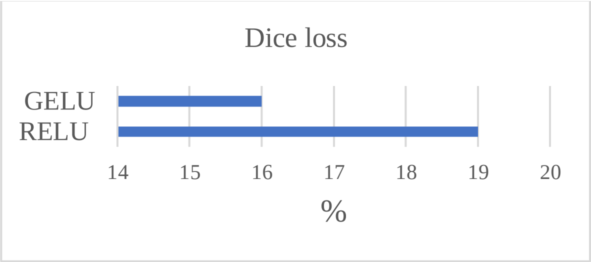


Fig. 7. **Comparison of activation functions**
***Source*: compiled by the authors**

From the presented results, it can be concluded that according to the Dice Loss indicator, the architecture presented above with the GELU activation function showed a better result, namely by 3% compared to RELU.

The results obtained demonstrate that the proposed modified architecture showed better results, namely 90 percent according to the AUC criterion compared to analogues. The proposed model exhibits the lowest values of all loss functions (cross-entropy, Tversky, IoU, and Dice), indicating a more accurate match of the predicted masks with the reference ones. Compared to R2U-Net, which also shows competitive results, the proposed architecture provides additional improvement in both loss metrics and recognition quality indicators.

DISCUSSION

The need in this study is due to the insufficient quality of segmentation of complex biomedical images for further calculation of quantitative characteristics of microobjects in the image. Their qualitative selection will facilitate the process of automatic diagnosis. Analyzing Table 3, we can conclude that the developed modified architecture showed the best result according to the focal Tversky loss, IoU loss, Dice loss criterion. When using 500 images, the proposed architecture showed the best result, namely 0.9 according to the AUC and Recall criterion. In future studies, experiments will be conducted on other types of immunohistochemical images to develop a comprehensive software solution in the CAD system.

The specialization is to develop a solution that will improve the quality of segmentation of immunohistochemical images for calculating the quantitative characteristics of cell nuclei. This type of image is significantly different from other biomedical ones. Therefore, the emphasis was placed on using a recurrent network, which is more complex in terms of the number of calculations, but demonstrates better results on this type of image. The solution used both parametric tuning and network expansion by adding additional layers, in addition, for this task the quality of segmentation is important, not the running time.

The limitations of the proposed solution are that the experiments were conducted on a limited number of open immunohistochemical datasets, which may affect the generalizability of the results. Also, the increased complexity of the proposed architecture leads to increased computational costs, which limits its application in resource-constrained settings. In addition, the metrics used do not fully reflect the clinical significance of segmentation errors.

Future work will focus on improving model generalization through evaluation on larger multi-center datasets and exploring advanced loss functions to address class imbalance and boundary sensitivity. Further research will also investigate architectural optimizations to reduce computational cost, as well as the integration of explainability and uncertainty estimation methods.

CONCLUSIONS

The proposed modified architecture showed better results, namely 90 percents by the AUC criterion compared to analogues. The modification consists in adding additional recurrent layers and increasing the number of recurrent iterations. In addition, the analysis showed that the GELU activation function increases accuracy compared to others.

From the results presented, it can be concluded that according to the Dice Loss indicator, the architecture presented above with the GELU activation function showed a better result, namely 0.16.

A “light” configuration file was developed to launch the infrastructure based on terraform technology. The advantage of the developed system is its orientation only on the process of automatic segmentation using U-net. At the same time, the stage of image processing and formation of a dataset for segmentation tasks clearly distinguishes this system from others. A web interface was developed for configuring image parameters in a convenient format. Image parameters are stored in JSON format for access via API. Functionality was developed for marking the name of mask images.

The scientific novelty of the study lies in the development and implementation of a new architecture of a convolutional neural network based on a recurrent U-net, specialized for segmentation of immunohistochemical images. Unlike classical U-net models, the proposed architecture is focused on processing specific samples, such as estrogen-stained tissues, and provides higher segmentation accuracy.

The practical significance lies in the development of a pipeline for integrating the U-net-based automatic segmentation module on cloud services with the possibility of simplifying work with masks.

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Conflicts of Interest: The authors declare that they have no conflict of interest regarding this study, including financial, personal, authorship or other, which could influence the research and its results presented in this article

Received 25.12.2025
Received after revision 12.02.2026
Accepted 19.02.2026

DOI: https://doi.org/10.15276/aait.09.2026.04
УДК 004.9

Спеціалізована рекурентна U-Net архітектура для сегментації імуногістохімічних зображень

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АНОТАЦІЯ

Виділення мікрообєктів на біомедичних зображень є складним та трудоємним процесом і соновні зусилля спрямовані та якісному відділені досліджуваних обєктів від фону на зображенні. Імуногістохімічні зображення використовують для аналізу раку молочної залози. Одним із типів зображень є зразки естрогену. Специфіка імуногістохімічних зображень вимагає більш ретельного підходу до сегментації, тому що стандартні алгоритми чи класичні моделі нейронних мереж не дозволяють досягти необхідної точності. У цій статті представлено нову архітектуру згорткової мережі, засновану на рекурентній U-мережі, для сегментації імуногістохімічних зображень. Запропонована архітектура спеціально розроблена для обробки унікальних особливостей імуногістохімічних зображень. Для розробки моделі було використано принципи рекурентних згорткових нейронних мереж та навчання її за допомогою відкритих датасетів. Запропонована у даній роботі архітектура базується на конфігуруванні шарів нейронної мережі, що дозволяє отримати кращий результат для даного типу зображень. Крім того, було реалізовано конвеєр безперервної інтеграції програмного коду і моделі для забезпечення безперервного перенавчання в хмарному середовищі, що значно спростило робочий процес для дослідників та інженерів. Додатково було запропоновано механізм для обробки медичних зображень та забезпечення автоматизації процесу обробки великих даних за допомогою комп'ютерного зору та глибокого навчання. Запропонований метод досяг вищої точності сегментації. Архітектура дозволяє точнішу сегментацію клітин на імуногістохімічних зображеннях, що є вирішальним кроком у діагностичному конвеєрі. Високоякісна сегментація клітин підвищує надійність подальших аналізів та вилучення параметрів, тим самим сприяючи підвищенню діагностичної точності.

Ключові слова: U-net; глибоке навчання; сегментація; імуногістохімія; архітектура програмного забезпечення, біомедичні зображення

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