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Fusing Expert Knowledge and Deep Learning for Accurate Cervical Cancer Diagnosis in Pap Smear Images: A Multiscale U-Net with Fuzzy Automata

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Abstract: Ovarian cancer is a severe disease that impacts many women in developing countries. Increasing screening capacity is the most effective strategy for lowering cancer risk and saving people's lives. Early stages of cervical cancer often lack symptoms, making it the fourth leading cause of mortality among women. Although cancer cells grow slowly in the cervix and can be effectively treated if detected early, detecting it before it rapidly spreads are a major challenge for the medical community. Segmentation is a critical screening step as it enhances our comprehension of cell morphological properties. This study provides a technique to segment multi-class cells into Nucleus and Cytoplasmic areas. Multi-resolution U-Net (MRU-Net) is provided for medical image segmentation to bypass the constraints of U-convolution Net's kernel with a restricted receptive field and undetermined ideal network width. First, additional semantic information is extracted from the images using a series of recurrent convolutions. Second, to distinguish the characteristics, a convolutional unit with distinct receptive fields is utilized. The effects of network width inconsistency may be mitigated by integrating a convolution layer with a large number of receptive fields. The effectiveness of the research was measured against state-of-the-art methods using the Herlev dataset and classification structures were used to get excellent results. Effectiveness indicators for both groups suggest that the method is reliable enough to complete the task. The approach may enable doctors to identify cervical cell anomalies and provide improved medical care. MRU-Net is evaluated using varied medical image segmentation datasets.

Keywords: *Segmentation, Fuzzy Automata, Pap smear images, Multiscale U-Net*

1 Introduction:

Ovarian cancer is a type of cancer that starts in the cervix, the lower part of the uterus that connects to the vagina. It is one of the most common types of cancer affecting women worldwide. According to recent statistics, cervical cancer is responsible for approximately 7.5% of all female cancer deaths globally. In 2020, an estimated 604,000 new cases of cervical cancer were diagnosed worldwide, and it caused 342,000 deaths. The majority of these cases (around 90%) occur in developing countries, where access to screening and treatment is limited. In developed countries, screening programs have been successful in reducing the incidence and mortality rates of cervical cancer.

Most women who contract HPV do not develop cervical cancer, but for some, the virus can lead to abnormal changes in the cells of the cervix, which can then develop into cancer if left untreated. Smoking tobacco, immune system compromise, protracted use of contraceptive pills, are further contributors to the development of cervical cancer.

The absence of signs in the disease's early stages is one of the most difficult aspects of dealing with cervical cancer. Indications of a vaginal cancer progression include vaginal discharge, discomfort during sexual activity, and abnormal vaginal bleeding. It is challenging to identify cancer through signs alone since these symptoms might be affected by other illnesses as well. Thus, cervical cancer screenings should be performed regularly to ensure early diagnosis and treatment. A Pap smear is a screening procedure used to diagnose cervical cancer by taking cells from the cervix and analysing them under a microscope. In recent years, HPV testing has also been employed in screening. There are more effective treatment options for cervical cancer if it is caught early. Surgical, radiation therapy, immunotherapy, or a combination of these may be used to treat cervical cancer. Ovarian cancer is still a major public health issue all over the globe, despite the fact that vaccinations and reliable detection and management alternatives are available. Most women in poor and middle-income nations do not know how to

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protect themselves against cervical cancer, and few have access to screening or treatment. As a result, it is important to work towards expanding access to cervical cancer screening and treatment, as well as making accessible effective preventative measures like vaccination. Cervical smear tests and biopsies are two examples of the types of medical imaging data that may be analysed by deep learning algorithms to look for signs of cervix cancer. The necessity for invasive diagnostic procedures may be reduced by training these algorithms to distinguish between malignant and non-cancerous cells. Convolutional neural networks (CNNs) are one use of deep learning in cervical cancer diagnosis; these networks can analyse digital pictures of cervical cells to find aberrant patterns that may signal the presence of cancer. Recurrent neural networks (RNNs) are another method, since they can analyse time-series data such as the size and shape of cervical cells over time to detect trends that may signal the existence of cancer. Therefore, efforts are needed to increase awareness about cervical cancer, improve access to screening and treatment, and ensure that effective preventive measures, such as vaccination, are widely available. Deep learning algorithms can analyse large amounts of medical imaging data, such as cervical smear tests and biopsies, to identify abnormalities in the cells of the cervix that could indicate the presence of cancer. These algorithms can also be trained to differentiate between cancerous and non-cancerous cells with high accuracy, potentially reducing the need for invasive diagnostic procedures. One example of deep learning in cervical cancer detection is the use of convolutional neural networks (CNNs), which can analyse digital images of cervical cells and identify abnormal patterns that may indicate the presence of cancer. Another approach is the use of recurrent neural networks (RNNs), which can analyse time-series data, such as changes in the size and shape of cervical cells over time, to identify patterns that could indicate the presence of cancer.

Moreover, deep learning algorithms may be used to create prediction models that can determine which women are at a particularly high risk of having a certain health condition based on their medical history, lifestyle factors, and genetic markers. These models can help healthcare providers to target screening and prevention efforts to those who are most at risk, potentially improving early detection rates and reducing the number of deaths from cancer. Despite the promise of deep learning in l cancer detection and prevention, there are also challenges that must be addressed. One of the main challenges is the lack of large, high-quality datasets for training and validating deep learning algorithms. Another challenge is the need to ensure that these algorithms are unbiased and do not perpetuate existing disparities in cervical cancer detection and treatment.

Awais Majeed, et al. (2021) The author reviewed various deep learning algorithms, including Convolutional Neural Networks (CNNs), Support Vector Machines (SVMs), and Random Forest (RF).Here, various publicly available datasets, including the Cervix Segmentation Dataset (CSD), the ISBI 2016 Cervix Segmentation Challenge Dataset, and the SIIM-ACR Pneumothorax Segmentation Challenge Dataset. The authors noted that most studies focused on the binary classification of normal vs. abnormal, and more research is needed on multi-class classification. Siyu Liu, et al. (2021)The paper reviewed various deep learning algorithms, including CNNs, Long Short-Term Memory Networks (LSTMs), and Autoencoders.The authors used various publicly available datasets, including the Cervix Segmentation Dataset (CSD), the Kaggle 2018 Data Science Bowl Cervical Cancer Screening Challenge Dataset, and the ISBI 2016 Cervix Segmentation Challenge Dataset.In this paper most studies were conducted on small-scale datasets, and more research is needed on large-scale datasets.Sathya Devi Rajendran, et al. (2021)In this paper algorithm reviewed various deep learning algorithms, including CNNs, SVMs, and K-Nearest Neighbors (KNN).

The authors used various publicly available datasets, including the Kaggle 2018 Data Science Bowl Cervical Cancer Screening Challenge Dataset, the Cervix Segmentation Dataset (CSD), and the TCGA Cervical Cancer Dataset.Here that most studies focused on only one type of deep learning algorithm, and more research is needed on ensemble models. Zhe Chen, et al. (2021) The paper reviewed various deep learning algorithms, including CNNs, Recurrent Neural Networks (RNNs), and Multilayer Perceptron (MLP).The authors used various publicly available datasets, including the TCGA Cervical Cancer Dataset and the Kaggle 2018 Data Science Bowl Cervical Cancer Screening Challenge Dataset. The authors noted that most studies did not use external validation datasets, and more research is needed on the interpretability of deep learning models. P. N. Mishra, et al. (2021)The paper reviewed various deep learning algorithms, including CNNs, MLPs, and KNN. including the TCGA Cervical Cancer Dataset and the Kaggle 2018 Data Science Bowl Cervical Cancer Screening Challenge Dataset It is noted that most studies were conducted on retrospective data, and more research is needed on prospective studies. They also noted that the lack of standardized evaluation metrics made it difficult to compare results across studies.

According to Roth et al., 2018 the U-Net framework is the most common encoder-decoder method used for medical image segmentation. Many scientists have contributed to

U-Net throughout the years after its first publication, improving it in a variety of ways. Several variants of the initial U-Net design have so been proposed. Nevertheless, the original U-Net had two restrictions that later versions didn't. Initial loss of variation in attributes is due to the convolution kernel's inflexible receptive field. Scale feature maps with the same convolution filter might have various semantic implications when using different receptive fields. Hence, the network's performance may vary depending on the variables of the convolution filter, especially the receptive field size. According to Luo et al., 2016, redundant features are retrieved if the receptive field of the convolution filter is too small. If the receptive field of the kernel is too big, smaller targets are not processed. As an example, in pulmonary tumor, the edge information of the smaller lesion or organ is hidden by the wide receptor field, while the shape of the lesion or organ is hidden by the narrow receptor field. Thus, a filter with independent receptive fields is required for image processing. Combining numerous receptive fields by convolution may provide promising solutions in the natural picture analysis problem (Seif and Androutsos, 2018). There are just a few studies on the use of varied visual field in medical picture segmentation tasks that we are aware of. Second, there is a risk of information loss if features are extracted at different scales using the same convolutional sequence. The use of several convolutional sequences enables for a greater quantity of feature data to be collected. The loss of feature information during down-sampling and up-sampling may be minimised by using well-structured multiple convolutional sequences. Hence, the learning capability of the network is enhanced by many convolutional sequences (He et al., 2015). In order to overcome these restrictions, we develop a novel architecture for image analysis in this work called multi-scale-Net. The architecture of this particular design is distinguished by segmentation generalisation.

2 Related Works

Cervical segmentation is a difficult task that even the most skilled physicians struggle with. Medical imaging performance, especially for cytological abnormalities, is crucial for diagnosis. In cervical cell segmentation study employing classic image understanding methods, active contours were used to define the nucleus' boundaries. Nonetheless, there was a chance that defects and cytoplasm might spread during this treatment. Cells were segmented at a rate of 99.64% over the 20300 images used in this experiment.

It is one of the first efforts in the field, hence it lacks accurate measurements that might be used to evaluate it against more recent methods [5]. Examples of conventional image interpretation methods involve graph cuts, which may segment images including many cervical cells. Examining histograms and cell boundaries are included in this technique, which is based on thresholds and binarization. The Dice Similarity Coefficient (DSC) for segmenting the cytoplasm and nuclei was 0.93. This endeavour failed to distinguish cells. [6] A private database verified this method.

Using Watershed method, K-means clusterting, a 0.86 DSC segmented nuclei and cells. To ensure the quality of this work, we put it through its paces on the Herlev dataset and in SIPaKMeD. There are many moving parts in an ensemble technique, and some of them must be randomly initialised; K-means and some other clustering algorithms often contain this stochastic quality [7]. By a combination of morphological reconstruction and a technique to locate prospective Nuclei candidates [8], FCM and SVM clustering achieved excellent Sensibility and Specificity 0.70 for FCM, 0.93 for SVM at the cost of requiring more than 1.5 minutes each segmentation. Fuzzy C-Means segmented Herlev dataset nuclei with a 0.82 (ZSI) for each class.

Pre-processing includes techniques for reducing noise, as well as determining expensive computational parameters such as the area for each image [9]. Additional FCM-based techniques, including morphological modifications such dilation [10], were also able to attain 0.82 ZSI. Li's et.all strategy included spectrum analysis, machine learning, and picture interpretation in CIELAB color spaces [11].

Shape attributes may be retrieved and identified as Nuclei with an accuracy of 0.81, 0.91, 0.86, and 0.83 using the Regression Techniques, Conditional Random fields, Decision trees, and Nearest neighbor algorithms, respectively. K-Means segmented the image with 0.72 IoU [12], however K may vary. Semi-automated identification using Random Forests yielded impressive results in a cytoplasm nuclei and background investigation.

In order to get almost flawless performance ratings, human pre-processing was required [13]. For the purpose of analysing the picture spectrum and separating the nuclei, Braga et al. suggest a hierarchical median narrow band. These algorithms are superior than others in most computer vision tasks, but they are more difficult to train and take more time to calculate. 0.89 F1 score. [15] In this technique, nuclei were segmented using a private data set. It is possible that ensemble Deep Learning approaches for nuclei segmentation, which need three concurrent models to run simultaneously, will also reach great performance (0.92 ZSI). Segmentation performance may be improved by employing dense blocks and adaptive convolutions [16]. With a ZSI of 0.9 on the Herlev Dataset, Learning with Convolutional Networks outperforms previous methods.

The networks were used to extract low-level properties, which were then further classified [17]. In whole-cell cervical segmentation experiments, recent image segmentation architectures like Mask CNN performed well [18]. In particular, most of these techniques are devoted to isolating cell nuclei by segmentation.

3 Materials and Methods

3.1 Cervical cytology and the study of cells

All the actions that make life possible are carried out by the cell, the smallest structure in the body. The study of cells, their clinical features, structure, and internal organelles, as well as their interactions with the environment, cell growth, and cell death, is known as cytology or cellular biology. The study of cytopathology is a subspecialty of pathology that focuses on the diagnosis of illnesses at the cellular level through the examination of morphological and phenotypic alterations in diseased cells. The membrane, the cytoplasmic, and the nucleus are the three major components of a cell.

The nucleus, which serves as the cell's central nervous system, contains genetic material and deoxyribonucleic acid (DNA) in the form of chromatins, a structure resembling a web inside the nucleus. The nucleus contains one nucleoid, which is a densely packed area of ribonucleic acid (RNA). Normal cells develop, divide to create new cells, and eventually perish after serving their purpose. When cells begin to develop and generate new aberrant cells without dying, this is referred to as abnormality. Modifications to the cell's dimensions, morphology, texture, alignment, and colour are all brought on by this anomaly. Specifically, this method may raise the efficiency of testing facilities, reduce hectic workloads, and improve screening quality. We believe that this approach will have a major impact on reducing mortality and occurrence rates. When these components are segmented accurately, automated screening systems and human experts are able to identify normal, pre-cancerous, and cancerous cells inside a pap smear. As a consequence of this, dissecting a cervix cell is an essential part of current research, and it may be simplified into the following four steps:

Segmentation by individual region, as in Nuclei.

- Background subtraction and whole-cell segmentation to isolate cells from their surroundings in a picture.
- Segmentation of many regions, including nuclei and cytoplasm, per cell.
- Segmentation of cells that overlaps.

To better understand how to segment cervical images, this research employs Deep Learning to ease the process of dissecting a single cell into its nucleus and cytoplasm automatically. The proposed architecture for cervical segmentation outperforms prior attempts at a more difficult problem by combining Efficient Net and FPN, two of the most prominent structures in segments and classification for computer vision. As a benchmark, the Herlev Dataset [20] may be used to evaluate a broad range of methods. It was created by Dr. Jan Jantzen of the Danish Herlev University Hospital at the University of the Aegean [21]. The background, nucleus, and cytoplasmic of individual cells are all included as ground facts for segmentation operations, and the tool was designed specifically for evaluating categorization algorithms.

- shortest-to-longest diameter ratio
- Nucleus and cytoplasm perimeter length
- How centralized the nucleus is in the cytoplasm
- Count the maximum/minimum pixels inside a 3-pixel radius.
- Nuclei and cytoplasm pixels count
- Cell size vs. nucleus size
- The smallest dimensions of nuclei and cytoplasm
- Average brightness
- The longest dimensions of nuclei and cytoplasm

Table 1: Most notable aspect of data collection

Above Table 1 summarises some of the key features of this dataset, including the fact that there is a significant imbalance between the classes due to a higher percentage of aberrant cells than normal ones. This can be problematic for classification and object recognition, and it also affects segmentation since the number of pixels in each class is not evenly distributed. It also demonstrates the difficulties that this dataset's semantic segmentation poses. For instance, the photos contain a sizable amount of trash. There are overlapping cells and low-quality photos, and the ground-truth masks don't always accurately reflect the number of cells present. This below figure 1 explaining the characteristics of different categories from Herlev dataset

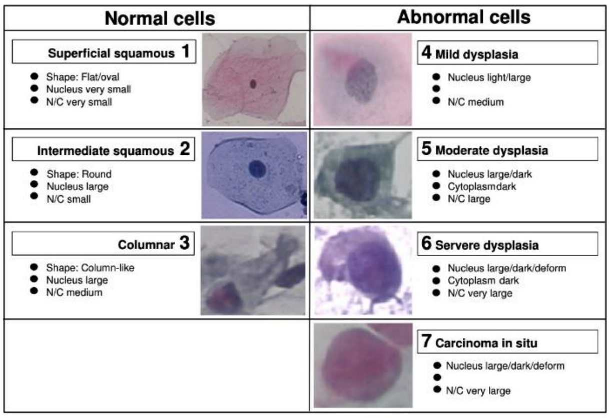


Fig 1: Sample images with their Nucleus and cytoplasmic feature from Herlev Dataset

4. Proposed work

4. 1 Multi-resolution U-Net (MRU-Net)

It comprises of multi-scale building pieces made up of convolution sequences with various receptive fields. These benefits are made possible by MRU-innovative Net's multi-scale block. First, the network's many convolutional sequences structure allows for the collection of additional feature data. Though their convolution inputs are same, their convolution kernels are not. Not only does this layout speed up the learning process for the network during training, but it also boosts segmentation performance. For another, the features gathered from the multi-scale block are varied. This is due to the multi-scale block's usage of numerous convolution sequences, each of which has a unique receptive field.

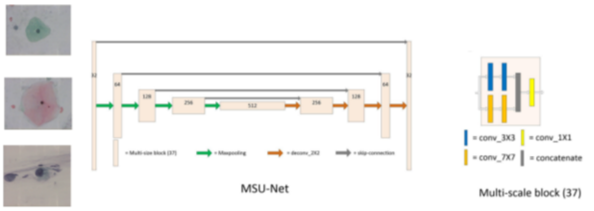


Fig 2: Multiscale -U Net

Semantic data is derived from a feature map constructed using a convolutional sequence in which receptive fields of varying sizes are used. Having the network laid out in this way improves feature extraction by the encoder and feature restoration by the decoder. By below figure 2 We build a variety of multi-scale blocks utilising many widely-used convolution kernels. Three segmentation datasets are used for a thorough analysis of various multi-scale blocks. In this work, findings show that semantic segmentation is much improved by MRU-Net, which was created by integrating numerous convolution sequences with various receptive fields.

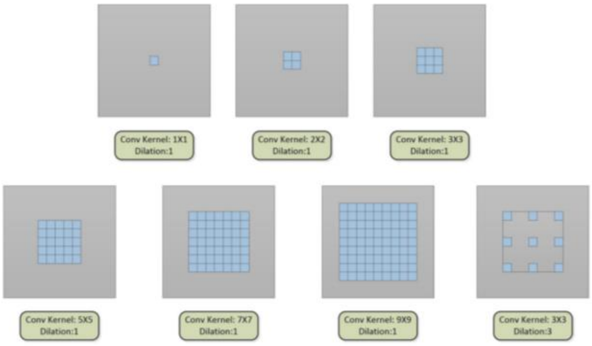


Fig 3: Several convolution kernels with Multiscale block

The above Figure 3 shows the several varieties of convolutional kernels are seen in the image above. Various multiscale block types are proposed by merging more than seven convolutional kernels. One of MRU-key Net's advantages over the standard U-Net structure is that it allows for the combination of various convolution sequences with varying receptive field widths. With forward propagation, this enhancement makes object characteristics more obvious. The suggested multi-scale block is also easily adaptable to pre-existing network architectures.

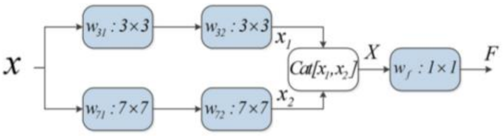


Fig 4: Detailed description of multi-scale block

Figure 4 above provides a comprehensive explanation of a multi-scale block. Features are extracted using a pair of convolution kernels, first a 3x3 and then a 7x7. After that, the feature by cat is used to combine the extracted characteristics. Ultimately, following dimensionality reduction using 1x1 convolution, the combined features are sent to the user.

In conclusion, this paper's most significant contributions are as follows:

(1) We present multi-scale blocks that are built on top of many popular convolution kernels. With multi-scale block, you may extract more detailed feature maps and a wider variety of feature information from your image.

(2) MRU-Net is offered as a novel segmentation architecture for medical images. That is a step forward from U-original Net's design. The suggested approach is more effective than previous methods in resolving the issues of class imbalance and overload.

(3) Dense prediction tasks necessitating specific spatial information rely heavily on receptive fields that vary in size and shape. It has the potential to increase the network's resilience and bolster its learning ability. The experimental findings show that the suggested technique

outperforms the state-of-the-art algorithms in the medical picture segmentation job under various imaging modalities.

(4) We provide a solution to the cervical cell segmentation issue by enhancing the past's state-of-the-art applications to handle a more difficult challenge.

4.2 Fuzzy Automata:

Fuzzy automata are mathematical models that are used to describe complex, uncertain, and vague systems. In the context of medical image analysis, fuzzy automata can be used to develop diagnostic systems for conditions such as cervical cancer smear images are commonly used for cervical cancer screening and can provide valuable information about the health of the cervix. However, the distinction between healthy and cancerous cells in these images can be subjective, making it challenging to develop an accurate diagnostic system. Fuzzy automata provide a powerful tool to address this challenge by capturing the uncertainty and vagueness in the relationship between the input pap smear images and the output diagnosis. The use of fuzzy sets and rules allows the diagnostic system to account for multiple perspectives and opinions, making it more robust and flexible.

In a fuzzy automata-based diagnostic system for pap smear images, the input image is mapped to the diagnosis using a set of rules that describe the relationship between the input and output. The transition function updates the state of the system based on the input and output, providing a continuous and dynamic assessment of the diagnosis. By using fuzzy automata in the analysis of pap smear images, we can develop a more accurate and reliable diagnostic system for cervical cancer, improving the ability to detect this condition early and providing better outcomes for patients. A Residual Attention Neural Network (RANet) is a type of neural network architecture that combines the concepts of residual networks and attention mechanisms.

Imagine a diagnostic system that takes a pap smear image as input and outputs a diagnosis of cervical cancer. The input is fuzzy, as the distinction between healthy and cancerous cells in the image can be subjective. To capture this uncertainty, we can define a fuzzy set A for the input image, with the membership function:

A(x) = {0, x = healthy cells (x - healthy) / (cancer - healthy), healthy < x < cancer 1, x = cancer cells}

Similarly, we can define a fuzzy set B for the diagnosis, with the membership function:

B(y) = {0, y = negative (y - negative) / (positive-negative), negative < y < positive 1, y = positive}

Next, we define the rules that describe the relationship between the input and output. For example:

If the image has many healthy cells, then the diagnosis should be negative:

$$\text{If } x \text{ is } A \text{ then } y \text{ is } B$$

If the image has many cancer cells, then the diagnosis should be positive:

$$\text{If } x \text{ is } A \text{ then } y \text{ is } B$$

Finally, we define the transition function that updates the state of the system based on the input and output:

$$S= f(S, x, y) =S+y$$

where S is the state of the system, x is the input image, and y is the diagnosis. Figure 5 gives the overview of the proposed work.In this example, the fuzzy automaton maps the input image to the diagnosis using the rules and transition function. The use of fuzzy sets and rules allows for the modelling of uncertainty and vagueness in the relationship between the input and output, making the diagnostic system more robust and flexible.

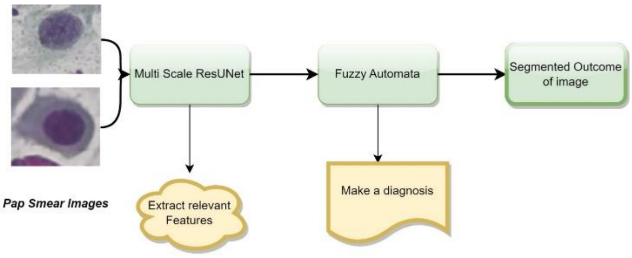
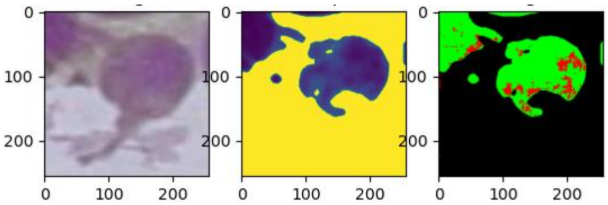


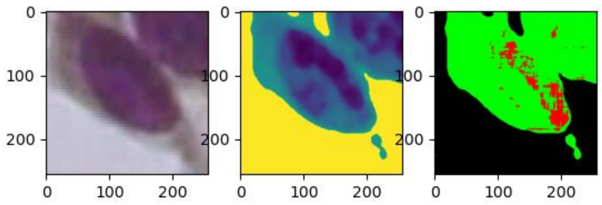
Fig 5. Workflow of proposed model

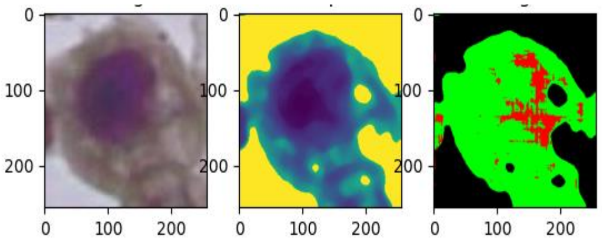
One approach could be to use a Multiscale ResUNet to extract features from the input image at different scales, and then use a fuzzy automaton to make decisions about the segmentation based on those features. The fuzzy automaton could be trained to consider the uncertainty and imprecision present in the image data and use fuzzy logic to make more robust and adaptive segmentation decisions.

5. Results

Sample Image   Pre-processed   Segmented
Image







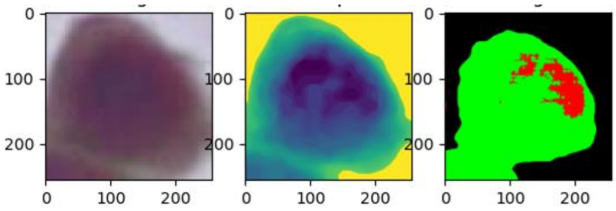


Table 2 Experimental Parameter

Name	**Value**
K	5
Batch size	8
Weight decay	0.001
Epochs	150
Loss Dice Learning rate	0.01
Momentum	0.99
Optimizer	SGD
Pyramid block filters	2048

The above Table 2 displays the final rainfall hyperparameters. A small batch size is maintained due to memory restrictions. In order to minimise overfitting in such a short dataset, a larger L2 regularising term is included. Training continues for 150 epochs without interruption. Dice loss was chosen because it performs well on unbalanced datasets [38], which is important given the heterogeneous pixel distribution across classes. Using the conventional optimizer stochastic gradient descent, we were able to avoid local minima with a high learning rate and momentum. Finally, the size of the filters in the Pyramid Block is raised to 2048 in order to improve the model's capacity.

6 Performance Metric

By calculating the projected mask's difference from the actual mask, segmentation metrics calculate the model's performance. First, each pixel in the expected mask is examined to see whether it matches to its ground truth equivalent, and then record the outcomes according to the following conditions.

- True Positives (TP): The number of pixels whose class has been accurately detected.
- True Negatives (TN): The number of pixels accurately detected as not belonging to their class.
- False Positives (FP): The number of pixels that have been misclassified.
- False Negatives (FN): The number of pixels that were wrongly detected as not belonging to their class.

Precision, Recall, Specificity, F1-score, and Intersection over Union are the performance measurements (IoU).

$$precision = TP/(TP + FP) \qquad (1)$$

$$recall = TP/(TP + FN) \qquad (2)$$

$$specificity = TN/(TN + FP) \qquad (3)$$

$$F1\ score = 2(TP)/(TP + TN + FP + FN) \qquad (4)$$

$$IoU = TP/(TP + FP + FN) \qquad (5)$$

The term "precision" refers to the ratio of accurate detections to total detections; so, a 100% precision would mean there were no false positives. The percentage of correct predictions may be measured by a metric known as "Recall" or "Sensitivity," with 100% representing no false negatives. The term "specificity" is shorthand for "true negative detection rate," with a Specificity of "100%" indicating that no false positives were found. Harmonically averaging Precision and Recall gives us the F1-score, the Indenols Similarity Index [40]. Hence, an F1-score over 70% implies a well-fitting prediction, as stated by Zijdenbos et al. [41]. How well the expected mask fits the underlying reality may be measured using the Jaccard Score.

TABLE 3 | Ablation study for AttU-Net, MSAttU-Net, U-Net++, and MRU-Net++.

Architecture	BUL	EM	NS
	M ± SD	M ± SD	M ± SD
AttU-Net	0.607 ± 0.039	0.853 ± 0.043	0.655 ± 0.020
U-Net++	0.670 ± 0.020	0.885 ± 0.013	0.665 ± 0.012
MRU-Net++ (Ours)	0.687 ± 0.009	0.895 ± 0.002	0.691 ± 0.022
IoU (AttU-Net, U-Net++ MRU-Net++)	0.791	0.811	0.642
Dice (AttU-Net, U-Net++ MRU-Net++)	0.871	0.902	0.913
Precision (AttU-Net, U-Net++ MRU-Net++	0.893	0.895	0.872

The multi-core variants of Attu-Net and U-Net ++, MSAttU-Net and MRU-Net ++, respectively. According to Table 3, our suggested MRU-Net performs better than state-of-the-art methods when it comes to semantic segmentation. For all five segmentation tasks (SL (0.01), CXR (0.01), BUL (0.1), EM (0.016), NS (0.027), MRU-Net obtains a considerable IoU increase over both designs.

7 Conclusion:

The results of the study show that the proposed method outperforms existing deep learning models and achieves high accuracy in classifying Pap smear images. The use of fuzzy automata to incorporate expert knowledge improves the accuracy of diagnosis and provides explain ability to the model's decision-making process. The multiscale U-Net architecture enables the model to extract features at different scales and capture fine details in the images, further improving the accuracy of diagnosis. The proposed approach of fusing expert knowledge and deep learning for accurate cervical cancer diagnosis in Pap smear images is a promising development in the field. The combination of deep learning and expert knowledge can provide a more accurate and consistent diagnosis of cervical cancer, which can ultimately lead to better patient outcomes. The use of fuzzy automata for incorporating explain ability is a novel approach that improves the explain ability of the model's decision-making process. Further research can explore the application of this approach to other medical imaging tasks and the development of more sophisticated fuzzy automata systems for incorporating expert knowledge.

Authors contribution statement

Jeyshri J and Kowsigan M contributed to this work in different ways and provided the study idea and designed the experiments. Both authors contributed to the interpretation of the results and approved the final version of the manuscript.

Conflicts of interest

The authors declare no conflicts of interest.

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