#### Project Report on

# **Analysis of U-Net Architecture for Nuclei Cell Segmentation**

# **Bachelor of Technology**

in

**Information Technology** 

by

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# Department of Information Technology Heritage Institute of Technology

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## **Heritage Institute of Technology**

(A Autonomous College)

### Kolkata, West Bengal

#### Certification

(This is to certify that the work in preparing the project entitled "**Analysis of U-Net Architecture for Nuclei Cell Segmentation**", has been carried out by R*ohan Thapas* under my guidance during the session 2020-2021 and accepted in partial fulfillment of the requirement

for the degree of Bachelor of Technology in Information Technology.

Signature of the HoD with seal (Suili Roy)	Signature of the Supervisor with seal (Uttam Kumar Das)

#### **Acknowledgment**

The project work summarized in this report explores <u>Medical image segmentation technologies</u>, experienced a <u>renewed growth with the recent advancement in the field of computer vision</u>, and pattern recognition named: **Analysis of U-Net Architecture for Nuclei Cell Segmentation**,

(Nuclei segmentation contains the most significant character in the nuclei cell recognition system. An accurate Nuclei segmentation helps to increase the accuracy of nuclei recognition in biomedical image detection system.).

We hereby thank our project supervisor **Prof.** Uttam Kumar Das This is a combined endeavor of a number of people who directly or indirectly helped us in completing our project synopsis. A word of thanks also goes to all our friends for being our best critics. And finally, this documentation would never have been more educative and efficient without the constant help and guidance of our project, guide **Prof.** Uttam Kumar Das. We would like to thank him for giving us the right guidance and encouraging us to complete the project within time. We also express our deepest and sincere gratitude to all our teachers for their kind comments and advice on our project. We would also like to express our heartiest gratitude to HOD, Prof. Suili Roy and other faculties for their encouragement and kind suggestion. Who has reviewed our project work and gave his valuable feedback.

Signature of the student.		

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### Analysis of U-Net Architecture for Segmentation Nuclei Cell Segmentation

**Abstract:** Nuclei cell segmentation contains the most significant character in the nuclei detection system Nuclear medicine imaging. An accurate nuclei segmentation helps to increase the accuracy of nuclei recognition in any Nuclear medicine imaging. However, the robustness and efficiency of conventional nuclei segmentation methodologies facing massive challenges in a non-cooperative environment because of unfavorable factors, for instance, takes most of the time of researchers, human errors, off-axis and low resolution motion. These factors severely affect the accuracy of the nuclei segmentation approaches. In this paper, a nucle segmentation approach has been obtained with U-Net architectures to accurately localize the boundaries of the nuclei cells image with semantic segmentation mask synthesis. Experimental Results consolidate the fact that the nuclei cell segmentation with U-Net achieves 90.64% mean IOU value. So U-Net can outperform the existing state-of-the-art approaches on the challenging **Nuclei image dataset** Find the nuclei in divergent images to advance medical discovery.

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**Keywords:** Nuclei Segmentation, U-Net, medical image segmentation.

#### 1. Introduction

Identifying the cells' nuclei is the starting point for most analyses because most of the human body's 30 trillion cells contain a nucleus full of DNA, the genetic code that programs each cell. Identifying nuclei allows researchers to identify each individual cell in a sample, and by measuring how cells react to various treatments, the researcher can understand the underlying biological processes at work.

Image segmentation technologies [1] experienced a renewed growth with the recent advancement in the field of computer vision [2] and pattern recognition [3]. nuclei recognition has been considered as the most reliable and accurate medical image identification approach. An <u>Nuclear medicine imaging</u>

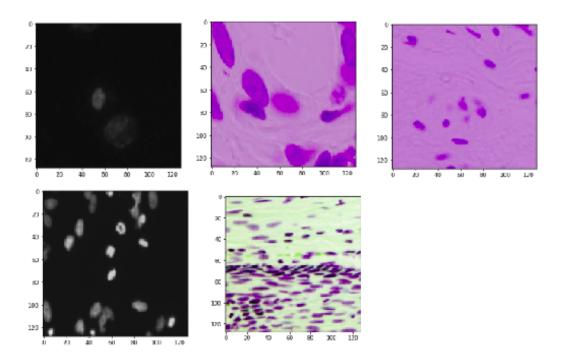


Fig. 1 Overview of Nuclei Cell Data Set.

#### 1.1 Objective and Proposed Outcome

A typical nuclei acknowledgment framework frequently comprises of the accompanying methods: nuclei picture obtaining [13], nuclei picture pre-handling [14], nuclei division [15], nuclei highlight extraction [16], and highlight coordinating for ID or confirmation [17]. In the nuclei acknowledgment framework, nuclei division is a basic and testing task in view of the flighty and sporadic state of the nuclei. By and large, nuclei surfaces are more apparent close to the space near the understudy limit. In the event that the limit of the student region isn't accurately situated, a lot of nuclei surfaces will be lost in the element extraction stage. At the end of the day, the presentation and vigor of the nuclei acknowledgment framework rely firmly upon the exactness of nuclei division. Much of the time, the impeded nuclei region would extraordinarily impact the general precision of nuclei cell division calculations. Past investigations have shown that the blunder created in the nuclei division step is communicated into all after periods of the nuclei acknowledgment, so nuclei limit assessment is as yet a vital pre-handling stage for accomplishing the high precision of the system. A basic nuclei acknowledgment framework regularly comprises of the accompanying techniques: nuclei picture procurement, nuclei picture pre-preparing, nuclei division, nuclei include extraction, and highlight coordinating for distinguishing proof or confirmation. In the nuclei cell acknowledgment framework, nuclei division is a basic and testing task due to the eccentric and sporadic state of the nuclei. By and large, nuclei surfaces are more noticeable close to the space near the understudy limit. On the off chance that the limit of the student region isn't effectively situated, a lot of nuclei surface will be lost in the component extraction stage.

#### 1.2 Organization of the Paper

The remainder of the paper is coordinated into the accompanying segments. Section 2 portrays the connected work. In Section 3, the proposed strategy is introduced. Trial results and conversation is introduced in Section 4, and Section 5 makes the inference.

#### 2. Proposed Methodology for Nuclei Cell Segmentation

This segment depicts the proposed image preprocessing model to localize the Nuclei cells, U-Net, its design, and the strategy used to prepare the model for Nuclei cell segmentation.

#### 2.1 The U-Net Architecture

**Overview:** The U-Net model addresses a mainstream CNN design for taking care of biomedical issues (for example sectioning various types of cells and identifying limits between thick cell structures) and other image interpretation assignments. The primary benefit of this model is its capacity to take in generally precise models from (exceptionally) little datasets, which is a typical issue for information scant vision undertakings, including nuclei segmentation.

**Model Architecture:** U-Net uses an encoder-decoder design as shown in **Fig. 2**. The design is partitioned into comparing encoder and decoder convolutional layers. In **Fig. 2** the left half of the model is the encoder way and the right side is the decoder way. The encoder follows a regular

CNN design, as promoted by

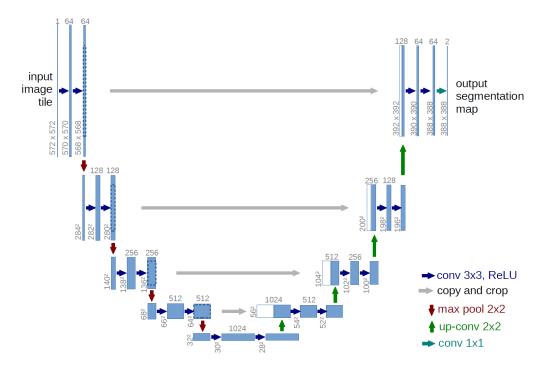
the VGG network [46]

3 × 3 convolutional

comprising of two

layers followed by a ReLu enactment layer with max pooling. Each down-examining step of the encoder duplicates the measure of highlight channels also, diminishes the picture goal considerably. The decoder part than up-examples the element guides of the lower layer while additionally connecting and editing the yield of the encoder part of a similar profundity. This interaction guarantee that data is engendered from the encoder to the decoder at all scales and no data is lost during the down-testing tasks in the encoder. The last layer of the organization is a

 $1 \times 1$  convolutional layer that blends the yield channels of the first layer and produces the division maps (one for each class - nuclei versus non-nuclei) that address the yield of the U-Net model (Note that for paired division issues the covers are supplements of one another).



**Fig. 2**. Outline of the U-Net design with a profundity of 4. The model depends on an encode-decoder engineering and uses duplicate and-harvest tasks to proliferate data from the encoder layers to the comparing layers in the decoder.

Training Details: To prepare the model for nuclei division, we first physically comment on a little arrangement of nuclei pictures and afterward gain proficiency with the boundaries of the U-Net model utilizing versatile second assessment (Adam) and paired cross-entropy as our preparation objective. For the comment strategy, we utilize an in-house instrument that first uses a couple of circles to check the nuclei (and understudy) district and afterward depends on a manual markup at the pixel level to represent the eyelids, eyelashes, and other eye subtleties that don't have a place with the nuclei. The consequence of this explanation method is a definite (pixel-level) markup of the nuclei, where the fundamental nuclei locale is limited by smooth defined second-request bends, while eye curios are concealed with nitty gritty veils as demonstrated in Fig. 1. Once the model is prepared, it takes nuclei pictures at the info and returns relating division covers at the yield.

#### 3. Experimental Results Analysis

In this part we present the aftereffects of our investigations. We initially talk about the test dataset and convention utilized for the trials, then, at that point expound on the organization preparing lastly remark on the after effects of our evaluation.

#### 3.1 Dataset and Experimental Protocol

In order to compute this experiment a total of 11,102 are annotated captured by Canon EOS 5D in sRGB format. During the experiments shutter speed (1/197 sec), lens aperture (F/7), Focal Length (400 mm), and exposure time (1/200 sec) are kept remain same all the time. All the images have and average width and height of 800 pixels and 600 pixels respectively. Whereas, the horizontal and vertical resolution are restricted to 72 dpi respectively. The images correspond to 261 distinct subject comprises with 522 different nucleies. It also contains of the different age group ([0, 20]: 6.6% [21, 25]: 32.9% [26, 30]: 23.8% [31, 35]: 21.0% [36, 99]: 15.7%), and various nuclei pigmentation (Light: 18.3% Medium: 42.6% Heavy: 39.1%). This dataset is also free from gender biasness as 54.4% Male and 45.6% Female contributed to this dataset.

We utilize an 80% and 20% split to build train and test datasets, in this way, 8880 pictures are utilized for preparing the U-Net model, and the leftover 2220 pictures are utilized to register execution measurements. We report brings about terms of accuracy, review and the convergence over-association, like [47], and additionally present accuracy review bends where relevant. Since, nuclei segmentation is treated as a double order issue for used deep learning framework, we additionally report precision esteems for the segmentation strategy.

#### 3.2 Performance and hyperparameter impact

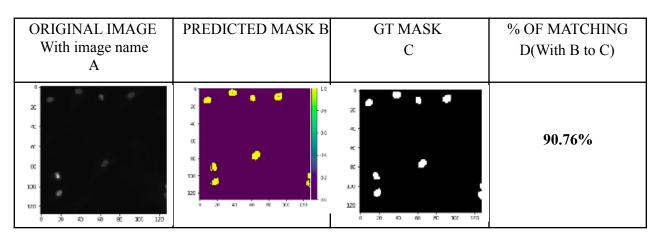
In our first arrangement of trials, we initially assess the nuclei segmentation execution of the prepared U-Net and V-Net model and survey the effect of various hyper-boundaries, i.e., the effect of model profundity and utilization of bunch standardization. Expanding the profundity of the model relates to adding an extra convolutional layer to the encoder just as to the decoder, consequently, for a profundity of 5, the model includes 5 layers in the encoder and 5 in the decoder. We utilize the code given by the creators of U-Net for all trials. Similarly, a 4-layered V-Net architecture give the highest accuracy compared to the others that's why a 4 layered V-Net architecture is chosen for all the experiments. Table 1 provides a detailed comparative study of the proposed U-Net and V-net architecture of different depth.

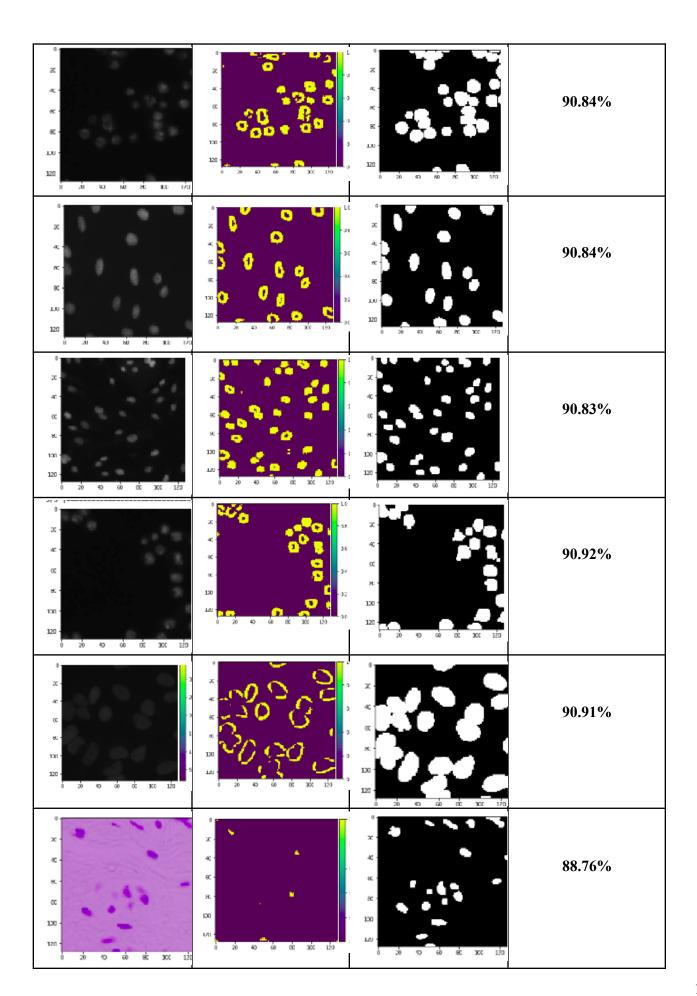
**Table 1:** Exactness for various profound U-net and V-Net architecture with and without cluster standardization (BN).

	Depth	Batch Normalization	Accuracy
	3	Yes	95.76%
U-Net	3	No	94.84%
	4	Yes	95.84%
	4	No	94.83%
	5	Yes	95.92%
	5	No	94.91%

#### 3.3 Nuclei Cell Segmentation through U-Net

The aftereffects of the main arrangement of analyses are produced on our test set of 2220 pictures and introduced as exactness review bends in Fig. 5 and as precision values in Table 1. We see that all models display expanded execution (as far as precision) with the expansion of profundity. A comparative conduct can be seen from the exactness review bend. Here, the model at profundity 5 plays out the best, followed intently by the model at profundity 4. True to form, U-Net at profundity 3 plays out the most exceedingly terrible, in any case, the exhibition of this model is somewhat better than the presentation of the model of profundity 4 at lower limits. From this we can reason that more profound models should give somewhat better execution, notwithstanding, the presentation contrasts we notice are minimal. Because of equipment limitations we couldn't assess the engineering at higher profundities. The models without group standardization by and large perform somewhat better than those with cluster standardization. When visual assessing the aftereffects of the models with clump standardization we notice recognizable smears on the outside of the nuclei, which are the reason for the lower execution. These oddities can be found in Fig. 5. What is intriguing to note is that the best performing models without cluster standardization produce nuclei locales that appear to be limited (generally) by second-request bends (i.e., ovals), which is steady with the manner in which the pictures were clarified. This experimental outcomes recommends that the organization verifiably figured out how to appraise ovals and circles as limits for the nuclei district.





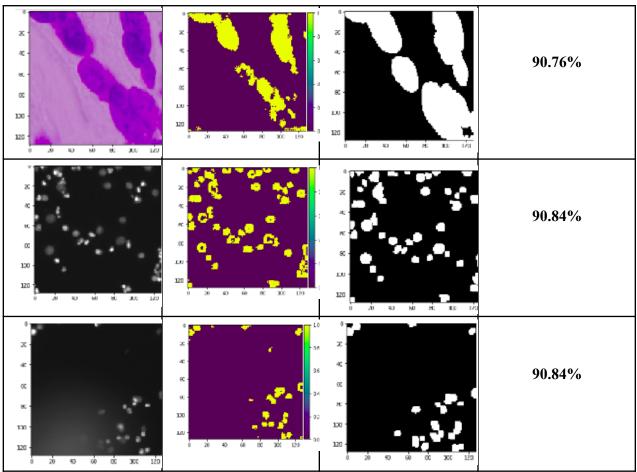


Fig. 3 nuclei segment with U-Net.

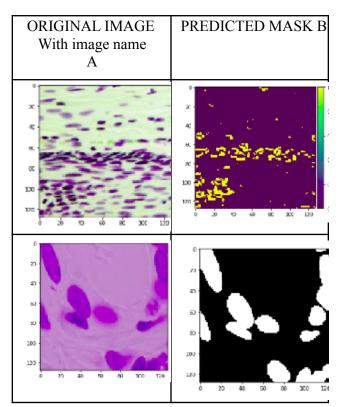


Fig. 4 nuclei segment with U-Net on test dataset.

#### 3.4 Time and space efficiency

We utilize a work area PC for the investigations running an Intel I7-2600k processor with 8 GB of RAM and a Nvidia GTX-1060 6 GB GPU. All models are tried on the GPU with the utilization of CUDA. Utilizing this equipment design we evaluate the speed of each model by taking care of them the test pictures in a circle each in turn. During this test we likewise measure the use of the GPU's assets. The outcomes are appeared in Table 2.

As can be seen V-Net utilized less measure of memory and time contrasted with U-Net. The distinction being the time it took for each model to portion the example pictures. The time expectedly expanded with profundity. During testing we likewise checked the GPU utilization. All models came to a 100% GPU utilization.

	Depth	Time/Image	Maximum Memory Used
U-Net	3	44 ms/image	5172 MB
	4	59 ms/image	5183 MB
	5	112 ms/image	5189 MB

Table 2: Existence intricacy for U-Net and V-Net models of various profundities.

#### 3.5 Comparative Study

We contrast our technique with four standard strategies. The principal standard technique (signifies as CNN [48]) utilizes the Hough change to limit the nuclei limits, then, at that point utilizes thresholding to eliminate eyelashes and specular reflections and in conclusion a flat line locator, which likewise depends on the Hough change, to recognize the eyelid limits. These strategy was picked as its source code is freely accessible. The other benchmark techniques are essential for the ResNet and DenseNet [49, 50]. The tool stash contains various nuclei preprocessing, highlight extraction and highlight correlation techniques that can be traded and consolidated to make a large number of nuclei pipelines. Normally the toolbox additionally contain various division techniques, which we used as pattern strategies. The technique (AutoEncoder)

[51] utilizes a differentiation changed Hough change. It adjusts the difference of the information picture to expand the variety between the nuclei and the sclera making edges more obvious. Likewise to CNN's strategy it additionally misuses Hough change to limit the limbic and papillary limits. The other two strategies are separated into two stages: focus limitation and limit confinement. The two strategies first limit the focal point of the student utilizing the versatile Hough change. This middle is then utilized as a beginning point from which the two techniques start their pursuit. Wahet first changes the picture into polar directions. Then, at that point an Ellipso-polar change is utilized to infer the limbic and papillary limit applicants. The change initially decides the

greatest energy even line, while expanding the vertical polar inclination. This outcomes in a smoothed bend, which is anticipated back onto Cartesian arranges and focuses are fitted to a situated oval. This is done twice, once for every limit. Conversely Ifpp utilizes twofold pooling and pushing with the utilization of the Fourier-based geometry for limit confinement. The tool stash executions of these strategies fragment the eyelids, eyelashes and reflections after standardization. As our test required non-standardized twofold veils we post-handled the sent-out covers utilizing CNN's technique for example line identification for eyelids and thresholding for reflection and eyelash division.

Table 3: Correlation with contending techniques from the writing. Normal exactness, review, and Intersection over Union (IoU) at the limit with the best proportion among accuracy and review.

Methods	Avg. Precision	Avg. Recall	Avg. IoU
CNN	$.846 \pm .0006$	$.819 \pm .0005$	$.844 \pm .0007$
ResNet	$.834 \pm .0021$	$.8563 \pm .0012$	.891 ± .0011
AutoEncoder	$.808 \pm .0013$	$.860 \pm .0004$	$.862 \pm 0.012$
U-Net	$.897 \pm .0018$	$.897 \pm .0018$	$.906 \pm .0014$

#### 4. Conclusion & Future Work

We have introduced a U-Net based methodology for Nuclei segmentation on Nuclear medicine imaging. The CNN-based architecture model ends up helpfull to medical image segmentation, while likewise outflanking all thought about gauge techniques. Taking everything into account, the utilization of profound learning strategies in nuclei cell detection may give an expansion in execution in a space of biomedical image segmentation contrasted techniques. For improving Nuclei detection remaking by upgrading the nature of pictures. We foster the U-Net design by utilizing convolution bits and changing the number of layers. The outcomes demonstrate that our proposed strategy could improve the Nuclei designs in the forefront region and decrease the effect of commotion behind the region of the scene.

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