

# Bi-path Architecture of CNN Segmentation and Classification Method for Cervical Cancer Disorders Based on Pap-smear Images

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# Bi-path Architecture of CNN Segmentation and Classification Method for Cervical Cancer Disorders Based on Pap-smear Images

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**Abstract**— This paper is concern about segmentation on pap smear images to use for classification cervical cancer. A cervical cancer screening by recognizing the cell shape pattern on the Pap-smear image can provide information about the presence of cervical cancer Pap-smear. The manual screening process for classifying cells is a challenging endeavor prone to the risk of error. There are several studies on the classification of cervical cell images which are sometimes not segmented first. Segmentation is very important to get the features contained in the image of cervical cells including the cell nucleus and cytoplasm. However, the segmentation results are also determined by the quality of images. This study proposed 2 paths that had a combination of image segmentation and classification. Before segmentation, image enhancement was carried out to improve image quality using Normalization, CLAHE and Adaptive Gamma Correction. The first path, the segmentation based on the CNN architecture. The second path is a classification process to test the segmentation results used by applying the KNN and ANN methods. The accuracy (ACC) result at the segmentation path was used to measure the match between the location of the segmented pixels and the results on ground truth, while the accuracy at the classification path was the success of the machine in classifying or predicting the segmentation results based on the class label for each group according normal and abnormal Pap-smear's label. The ACC result obtained in segmentation was only 0.77. However, the results of the segmentation when used in classification to classify which Pap-smears were normal and which are abnormal could provide excellent accuracy results, which were above 0.9. The results of the performance of Sensitivity (SN), Specificity (SP) and F1-score on the segmentation path also only gave results below 0.72, but the performance on the

classification path that used the results on the segmentation path gave well results, which were above 0.85. These results stated that the proposed method is quite good in detecting cervical cancer disorders based on Pap-smear images.

**Index Term**— Cervical Cancer, Classification, CNN, Image Enhancement, Pap-smear, Segmentation

## I. INTRODUCTION

THE cervical cancer is one of the most serious diseases affecting women. The World Health Organization (WHO) announced in 2019 that the 4th most dangerous and deadly type of cancer for women was cervical cancer. In 2018, as many as 570,000 women worldwide were diagnosed with cervical cancer and approximately more than 311,000 women died from the disease each year. The disease affects women in developing countries also. One of developing country is Indonesia. According to the Globocon's data in 2018, new cases of cervical cancer in Indonesia reached 32,469 people. The data showed sharp jump compared to Globocon's data in 2012 which stated that only 26 Indonesian women died of cervical cancer every year [1]. For this reason, prevention and early detection is needed to do both through vaccination and through screening.

The modern technology in the medical field makes it easy to detect the disease by detecting changes in the pattern of cervical cells based on the color and shape of the nucleus as well as the cytoplasm contained in the image [2]. Pap-smear images can provide information about the presence of cervical cancer on a Pap-smear [3]. Screening the Pap-smear image manually takes a long time. It is less thorough, has a high risk of error, and lacks adequate pathology [4]. Another problem that arises is the subjective differences of some cytologists, which sometimes give different results and can interfere with the process of screening abnormalities in the Pap-smear image [5]. Manual identification in classifying cell images has a fairly prone risk of error due to various things including image quality and subjective errors [6].

The Pap-smear cells can be grouped into 7 classes, namely Intermediate squamous, Normal squamous, Columnar, Moderate Dysplasia, Severe Dysplasia, Carcinoma In Situ, Mild Dysplasia [7]. The Groups can be classified into 2 major groups, namely normal and abnormal. Wang et al [8] classified cervical cancer cells based on Pap-smear images using hybrid Intelligent systems (HIS), which combined several artificial intelligence technologies such as Genetic Algorithm, Artificial Neural Networks as a computational

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intelligence approach, and fuzzy techniques. Various studies have been carried out to classify Pap-smear images. Ghoneim et al [9] use a method which was a combination of Convolutional Neural Net (CNN) and Extreme Learning Machine (ELM) to classify Pap-smear images into 2 classes and 7 classes. The accuracy (ACC) of the study were 0.99 for 2 classes and 0.972 for 7 classes. Another study combined the naïve Bayes classification model and Weight-Principal Component Analysis (PCA) which achieved 0.674 of the accuracy for 2 classes and 0.34 for 7 classes [10]. Zorkaflı et al [11] also conducted a classification of cervical cancer cells by applying Hybrid Multi-layered Perceptron (HMLP) trained by Genetic Algorithm (GA) and gave 0.748 for the accuracy, 0.725 for the Sensitivity (SN), and 0.867 for the Specificity (SP), while the F1-score value was not analyzed. The classification studies of cervical cancer were conducted by [9]-[11]. These studies did not enhance and segment the Pap-smear image before when doing classification. The image enhancement is an important part of image processing because it produces an image with better quality than the original image so it can provide more accurate results.

The image segmentation is crucial part to separate the background and important features in the image [12]. The image segmentation is a process of dividing an image into homogenous areas based on certain similarity criteria between the level of a pixel and the level of its neighboring. This is necessary to obtain an important part to be analyzed from an image and remove unused areas automatically. The process of cervical cancer image segmentation can be seen in Fig 1.

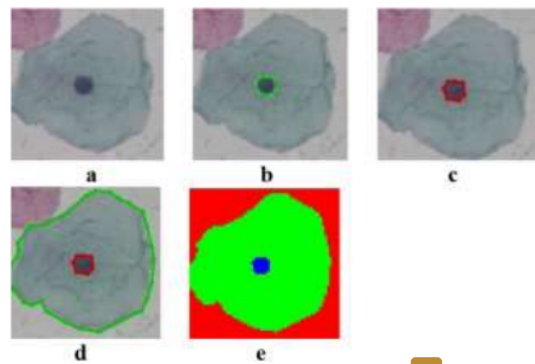


Fig. 1. The Segmentation Process on Pap-smear Image; a. Original Image. b-c. The First Feature Separation Segmentation Process on Pap-smear Image. d. The Second Feature Separation Segmentation Process on Pap-smear. e. Segmentation Output

From Fig 1, we can see the process of cervical cancer segmentation. Fig 1 (b and c) showed the image zoning process and Fig 1.d showed the segmentation results that display three different colors which were the segmentation labels. The three labels consisted of two labels for the part analyzed and one label for the unused area. This segmentation process is called semantic segmentation. If the segmentation result in only two labels, it is called binary segmentation. The results of the segmentation process are used for further high-level processes such as the image classification process and the object detection.

In the Pap-smear image, the features used for detection or classification of cervical cancer disorders are the nucleus cell.

The segmentation is needed to separate nucleus cell with other objects on image Pap-smear to extract information from cell components by identifying the region of each characteristic cervical cell [13]. Several studies performed both segmentation and classification on cervical cancer cells. Wang et al [14] applied Mean-shift clustering for image segmentation with 0.94 for the SN and 0.93 for SP. Sharma et al [15] applied normalized features and edge detection to segment the nucleus of cervical cancer cells, then classified with KNN was able to produce 0.829 for the ACC, but did not analyze the results of other performance evaluations. Sreedevi et al [16] applied an iterative thresholding algorithm for classification based on Pap-smear image. The performance classification of the study obtained the perfect result, 1 for the SN and 0.9 for the SP but this study did not analyze the performance results on the segmentation process. The segmentation of cervical cancer cells was carried out by Zhang et al [17] which used two path fusion attention feature on Binary Tree-like Network method. The results of segmentation performance evaluation were 0.94 for SN, 0.91 for SP, and 0.93 for F1-score, but it did not analyze the ACC segmentation result.

Convolution Neural Network (CNN) is one of deep neural network that extracts regional features of an image layer with the convolutional kernel and the pooling layer. The CNN architecture has a very deep network level and is usually implemented on image data. Several researchers have used CNN in a variety of applications, such as recognition, objects detection, segmentation, etc. The CNN has the advantage of being able to work very well on large-dimensional data [18], [19]. CNN can load all Spatial information from the entire scale on the object which can extract features and classify objects more accurately thereby increasing the accuracy [20]. The CNN in the segmentation of Pap-smear images was carried out by Araújo et al [18] with Mean Arterial Pressure (MAP) result is 0.936, the SN was 0.65 and the SP was 0.73, but in this study, the ACC was not analyzed. Furthermore, Song et al [19] has combined super pixel and C in cervical cancer cell segmentation with SN, SP, and F1-scores of 0.8726, 0.9143, and 0.8951 respectively. Song et al [21] also conducted a segmentation approach using multi-scale CNN to overcome overlapping problems in the cytoplasm. This study got F1-score more than 0.912 but did not analyze the results of the ACC, SN, and SP.

The segmentation was also influenced by the image quality. Often an image has poor image quality, such as blurry colors, too bright, or too much noise. Image enhancement is needed to overcome poor image quality. The Image enhancement is expected that the image obtained will have a good quality when used in the segmentation so that the required features can be captured accurately. The better the image quality the more accurate the features obtained in the segmentation [22]. One method for image quality enhancement is Normalization method which is used to stretch the contrast by taking the lowest pixel as black and the highest pixel as white so that the bright pixels will become brighter and vice versa [23]. The Normalization is a simple method by scanning image to find low and high pixel values. The Normalization is a technique to change the stretch of the pixel value in an image, for example, an image that has poor contrast because it is too glare or blurry. Normalization is



also named stretching or histogram stretching [24]. The Normalization is able to provide images containing better contrast. Another method to image enhancement is Contrast Limited Adaptive Histogram Equalization (CLAHE). CLAHE increases image contrast in the local area so that hidden features in the image can be found [25]. If the image has poor contrast or is too dark, Adaptive Gamma Correction with the appropriate gamma value can be used [26].

This study conducted a Bi-path architecture that combined two paths between segmentation and classification to identify the cervical cancer disorders. The image enhancement was needed to improve image quality in order to provide significant input for segmentation path. The image quality was enhanced by combining between Normalization, CLAHE and Adaptive Gamma Correction before segmentation. The first path was segmentation on Pap-smear images. The goal of the first path was identify the presence of cervical cells based on Pap-smear images. For segmentation, it was applied the Convolution Neural Network (CNN) method. In the study, segmentation was applied using CNN with 4 parallel layers which were divided into two parts, namely contracting part and expands part. The segmentation produced the features needed to detect cervical cancer abnormalities on the Pap-smear images.

The second was the classification path. The classification path could be said a test stage from the segmentation results to detect the presence of cervical cancer disorders on the Pap-smear images. This path was used to classify or detect which cells were normal and abnormal or which have cervical cancer disorders. The classification was used to be able to identify which cells were abnormal (have cervical cancer disorders) and which cells were normal using the segmentation result in the first path. In this path, the classification was grouped into two label categories for Normal and Abnormal Pap-smear images. For classification, it was applied Artificial Neural Networks (ANN) and K-Nearest-Neighbors (KNN) methods to detect cervical cancer disorders. The ACC, SN, SP, and F1 score of the two classification methods were measured to compare the performance of the proposed method.

## II. PROPOSED METHODOLOGY

### A. Image Dataset

The dataset used was taken from the Herlev Pap-smear dataset developed by the pathology department at Herlev University Hospital with the Department of Automation at the Danish Technical University. This dataset was obtained on link <http://mde-lab.aegean.gr/index.php/downloads>. The Herlev dataset consists of 917 images with an average size of  $150 \times 140$  pixels. Each cell was classified manually into seven classes that are Normal Superficial (NS), Normal Intermediate (NI), Normal Columnar (NC), Mild Light Dysplasia (MLD), Severe Dysplasia (SD), Moderate Dysplasia (MD), and Carcinoma In Situ (CIS). These cell labels could be categorized into 2 types of label groups, namely normal and abnormal. The labels that fall into the normal group were Normal squamous, Intermediate squamous, and the Columnar. The labels that fall into the abnormal category were Mild Dysplasia, Moderate Dysplasia, Severe Dysplasia, and Carcinoma In Situ.

The Herlev Pap-smear images consist of Blue, Green, Red

(BGR) format type's images with different resolutions. The images in the Herlev dataset had different sizes. Some images looked blurry and had poor quality. At the pre-processing, the size of all images was resized to  $64 \times 64$  so that the image has a uniform size. The images input based on their labels on Herlev dataset could be seen in Fig 2.

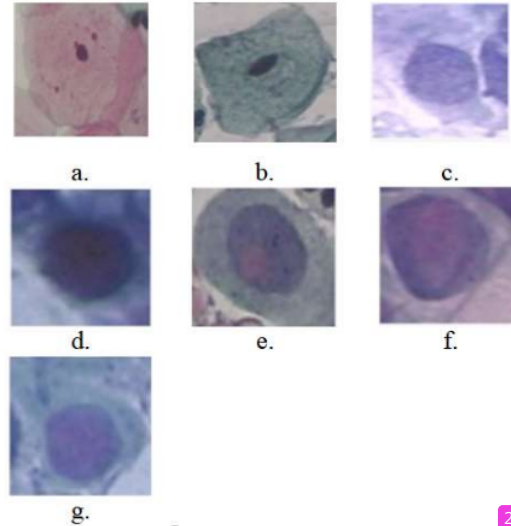


Fig. 2. Input Original Pap-smear Image of Herlev Dataset for each Label (a) Normal Superficial (b) Normal Intermediate (c) Normal Columnar (d) Severe Dysplasia (e) Mild Light Dysplasia (f) Carcinoma In Situ (g) Moderate Dysplasia.

### B. Pre-Processing

On pre-processing, the images on dataset should be enhanced to get images that have a good quality. Image enhancement had 3 stages:

#### 1. Normalization

At this stage, cervical cancer cells were normalized to improve image quality. Normalization is often called contrast stretching, which is a technique of increasing contrast in an image by stretching the intensity value to get the desired value. The equation used for stretching contrast could see on equation (1).

$$N = \frac{X - \min(X)}{\max(X) - \min(X)} \quad (1)$$

Where,  $X$  represented the input image pixel,  $N$  represented the result of normalized image, and the operators of the min and max were used to obtain value of the maximum and minimum pixel in a particular image. The Pixel valued below 0 would be dark, while pixel values above 255 would be brighter [27].

#### 2. Contrast Limited Adaptive Histogram Equalization (CLAHE)

CLAHE was used to advance the contrast of an image and to overcome color unevenness. The CLAHE limited the amplification and cut the histogram to a predetermined value and calculates the Cumulative Distribution Function (CDF). CLAHE operated in a small region that called a tile. The CLAHE tried to align 3 color components R, G, B which may not be coherent in the image. The process of calculating CLAHE is calculated by using the clip limit constraints of the histogram, where the clip limit is calculated equation (2) [25].

$$\beta = \frac{M}{N} \left( 1 + \frac{\alpha}{100} (S_{\max} - 1) \right) \quad (2)$$

where  $M$  represents area size,  $N$  is the value gray scale,  $\alpha$  is the clipping factor in percentage,  $S_{\max}$  represents the limited slope of the transformation function. The clip factor  $\alpha$  range is [0-100], thus the slope range, in each mapping, is  $[1 - S_{\max}]$ .

### 3. Adaptive Gamma Correction

After the CLAHE was applied, the image result was repaired using Adap Gamma Correction. Gamma is a non-linear operation to increase the contrast of dark images using the power-law transformation approach. Gamma correction was defined in equation (3) [26].

$$S = T(R)^{\gamma} \quad (3)$$

$S$  was the brightness value in the image and  $R$  was the brightness value in the original image which is mapped to [0,1].  $\gamma$  (gamma) was the value of the brightness level in the image. If  $\gamma < 1$  the output image would be brighter as before, while if  $\gamma > 1$  the output image would be darker.

## C. Bi-path Architecture

### 1. Segmentation using CNN

After pre-processing, the images have been ready to process for segmentation and classification. The segmentation and classification stage were combined in Bi-path architecture. The first path was segmentation. The segmentation is the process of separating features that are used with features that are not used [28]. The segmentation of an image can be considered as a pixel-based classification. It means that the pixels of the image become the labels used during training and testing, which are match the pixel on segmentation image and the pixel on the ground truth image. The enhanced Pap-smear image would be segmented by using CNN to separate the features into several regions, namely the nucleus, cytoplasm, and background. In the study used CNN with 4 parallel layers. In this study the CNN architecture used is based on UNET architecture, UNET was a CNN architect for segmentation that was originally used in biomedical imagery

[29]. The CNN architecture used was divided into two parts contracting and expansive part.

The CNN architecture in Fig 3 illustrated the training process at the segmentation stage. The CNN architecture in this method is divided into two part, namely the contracting path (left side) and the expansive path (right side). The Contractive part is the encoder function which was the first part (right side) on CNN architecture which applied convolution block combined with Max Pooling to convert the input image into the desired feature representation at various levels. The Expansive part was the decoder function in the second part (left side of the CNN architecture) which is used to map the acquired features to a pixel-dense object that had up sampling, concatenation and convolution operations.

The contracting part section consisted of 4 blocks where each block had 2 convolution layers, 2 batch Normalization layers, 1 pooling layer, and 1 Spatial dropout layer. The stride size for the convolution layer was 2. The pooling layer used max-pooling measuring  $2 \times 2$ . The number filters from the convolution layer in each block were 64, 128, 256, 512, and 1024 respectively. In the expansive part section, every 4 blocks consisted of transposed convolution, merging feature maps according to the contracting path, and 2 convolution layers with kernel size  $3 \times 3$ . Every layer except the output layer used the ReLU activation function. The ReLU activation was an activation layer on the CNN model which was very effective and simple [24]. This function was thresholding with zero value on the pixel value in the image input. This activation made all pixel values less than zero in an image become 0. The ReLU activation function was defined in equation 4 [20]:

$$f(x) = \max(0, x) \quad (4)$$

The Softmax activation function was used in the end/output layer which was usually used to calculate probabilities in multi-class classifications. The Softmax value was in the range between 0 and 1 while the number of all elements is 1. The Softmax function could be seen in equation 5 [31] :

$$P_i = \frac{e^{z_i}}{\sum_{j=1}^K e^{z_j}}, \text{ with } i=1,2,\dots,k \quad (5)$$

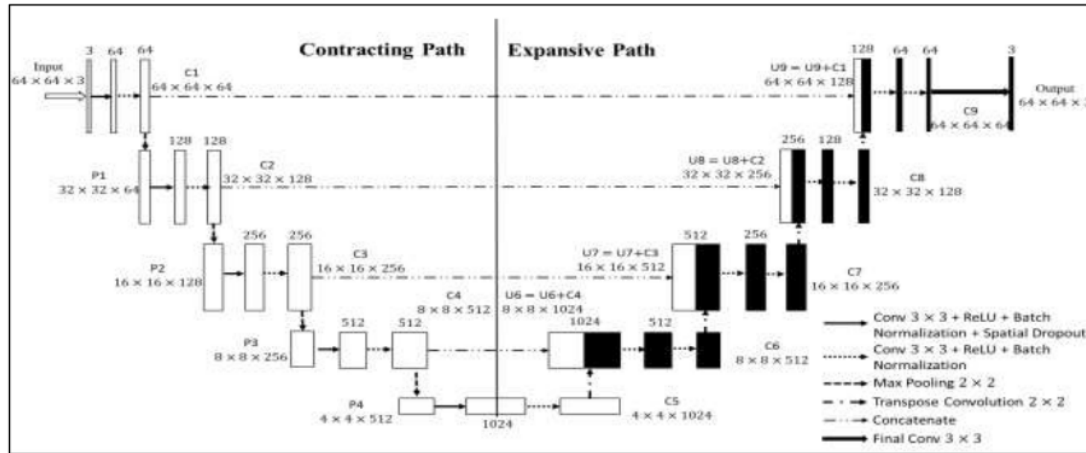


Fig 3. The Convolution Neural Network (CNN) architecture with Contracting and Expansive Part for Segmentation of Pap-smear Image in The First Path.

In the output layer, for gradient optimization, the Adam optimizer function was used by calculating individual adaptive learning rates for different parameters of each moment on the gradient [32]. Meanwhile, to calculate the loss from the training process, the categorical cross entropy function was used because the Pap-smear image used has multiple classes (Equation 6).

$$H = -\sum_{j \in \text{voxels}} \sum_{k \in \text{classes}} c_{j,k} \log \hat{c}_{j,k} \quad (6)$$

where  $\hat{c}$  represented the probabilistic prediction (after the Softmax activation function),  $c$  was the target,  $H$  is the cross-entropy function, and  $j$  is the voxels of manual segmentation and  $k$  is classes of image.

In Fig 2, the convolution Layers C1, C2, C3, and C4 on the contracting part were the main layers that underlie the CNN model with the main objective of extracting features from the input image. The feature results were obtained by multiplying the matrix from the input image to the filter, and then the results were added and saved into a matrix called a feature map. The convolution Layer function was defined in equation (7) [20] :

$$A_j = F\left(\sum_{i=1}^{16} I_i * K_{i,j} + B_j\right) \quad (7)$$

Where each input matrix  $I_i$  was multiplied by the corresponding kernel matrix  $K_{i,j}$ . The bias value  $B_j$  was added to each matrix element that has been previously generated. Next, the activation function  $F$  was applied to each matrix element resulting in a new matrix  $A_j$ . For the pooling layer, the Max Pooling layer was used to improve invariance translation because it could reduce the size of the feature map. This layer divided the output from the convolution layer into several small grids then taken the maximum value from each grid to compile a reduced image matrix [33].

In expansive parts U6, U7, U8, and U9, the input feature map used the Max Pooling index which has been stored on the feature map of the corresponding contracting part. This feature map was combined or concatenated with the filter on the contracting part which was trained to produce dense feature maps for each convolution of C6, C7, C8, and C9. This was also accompanied by the application of batch Normalization to each of these maps.

## 2. Classification

Classification with ANN and KNN were the process of the second part. The cervical cancer cells were classified into 2 classes using the features of segmentation results, namely normal and abnormal using Artificial Neural Networks

(ANN) and K-Nearest-Neighbors (KNN). A total of 917 images consisting of 7 groups were classified into normal and abnormal classes. Groups included in the normal class are the Normal Superficial (NS), Normal Intermediate (NI), and Normal Columnar (NC) groups. Meanwhile, the next 4 classes fall into the abnormal category, namely Mild Light Dysplasia (MLD), Severe Dysplasia (SD), Moderate Dysplasia (MD), and Carcinoma In Situ (CIS). The K-Nearest-Neighbors algorithm is an algorithm that performs classification based on the proximity of the location (distance) of data to other data. Near or far a location (distance) is usually calculated based on the Euclidean distance or the closest distance between two point  $x_{1i}$  and  $x_{2i}$  can calculate with equation (8) [34].

$$d(x_{1i}, x_{2i}) = \sqrt{\sum_{i=1}^p (x_{2i} - x_{1i})^2} \quad (8)$$

Meanwhile, ANN is a non-linear statistical classifier that can be used to classify data with complex relations between input and output. ANN consists of some neurons that are arranged in layers. In ANN, a multi-layer perceptron network will be used with the activation function used is sigmoid function. The sigmoid function is the most numerous and easy to use function in the ANN classification[35]. The sigmoid function was in equation (9).

$$z_j = \frac{1}{1 + e^{-z_{in_j}}} \quad (9)$$

In this study, The ANN used in this study was a multilayer perceptron with 3 layers consisting of input, hidden layer and output. The architecture ANN using MLP for the study was in Fig 4.

An image has a format of  $m \times n$ , whereas in the classification of the ANN and KNN methods only recognized data with a size of  $1 \times n$  which was grouped based on string labels, so it required a data form that has a size of  $1 \times m$ . In this case, the image must be converted into another format and the image must be flattened so that it can be used in the ANN and KNN methods for classification. The Bi-paths proposed in the study were depicted in the block diagram. The stages in the block diagram start from the procedure for image improvement and segmentation which were combined in one path and other path used to classify the cervical cancer classification based on the pattern cell on the Pap-smear image. The block diagram of Bi-path segmentation and classification in the proposed method was in Fig 5.

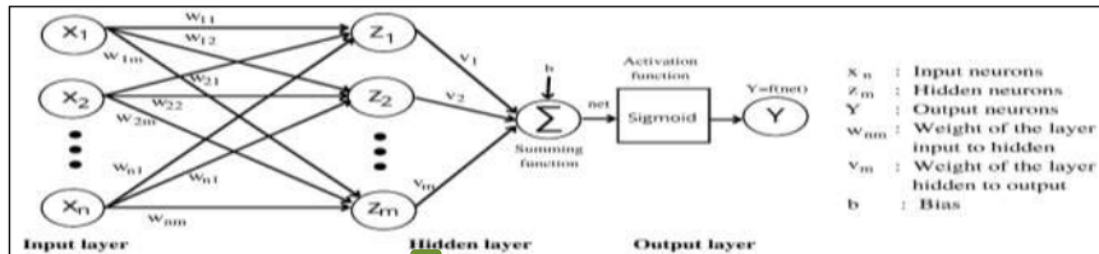


Fig. 4. ANN Architecture using MLP for Classification Cervical Cancer Detection based on Pap-smear Images in The Second Path



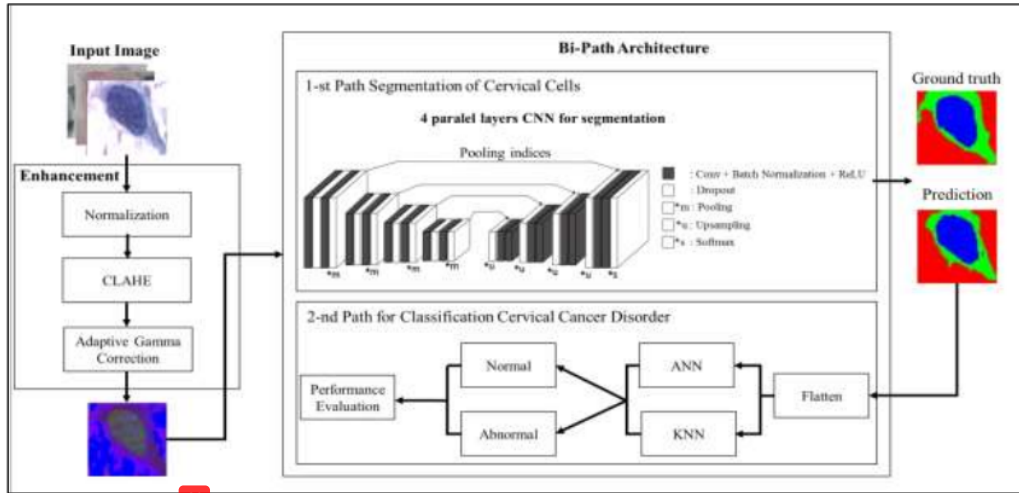


Fig 5. Bi-path Architecture of The Proposed Method for Cervical Cancer Cell Disorder Detection Based on Pap-smear Image

### III. RESULT AND DISCUSSION

In this study, the proposed method was a combination between enhancement, segmentation and classification (as Fig 8). The Herlev dataset was used on the study with 10 images for training because there were only 10 ground truth images found for Pap-smear images. The image input from the Pap-smear images has different resolutions or size of pixels, so the input data size is uniform to 128x128 pixels. Before the Normalization applied, the Pap-smear images were converted to RGB and HSV channel.

In this stage, the Normalization was applied on original image (input image) of Herlev dataset on Fig 2. Fig 6 was the result of the applied Normalization of the original images in dataset.

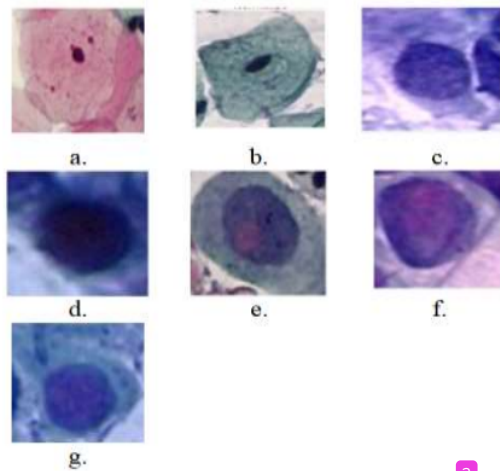


Fig. 6. Normalization for every Labels in Herlev Dataset (a) Normal Superficial (b) Normal Intermediate (c) Normal Columnar (d) Severe Dysplasia (e) Mild Light Dysplasia (f) Carcinoma In Situ (g) Moderate Dysplasia.

The image resulted from the Normalization stage looked brighter than the original image or input image. The images that had slightly blurred colors have become lighter and more vivid in color. The results of Normalization were still not a

relief. Some images show that there was still noise from the original image. In Fig 6, some of the images still looked a little dark and blurry, like the images in sections c and d of Fig 6.

To increase the image contrast, CLAHE is applied on the result of Normalization. The results of applying CLAHE could be seen in Fig 7. In Fig 7, the image produced from the CLAHE process had a clearer quality. Some images did not change significantly, but it seemed that the results of the Normalization process and CLAHE were quite helpful in improving image quality, such images c and d on Fig 7.

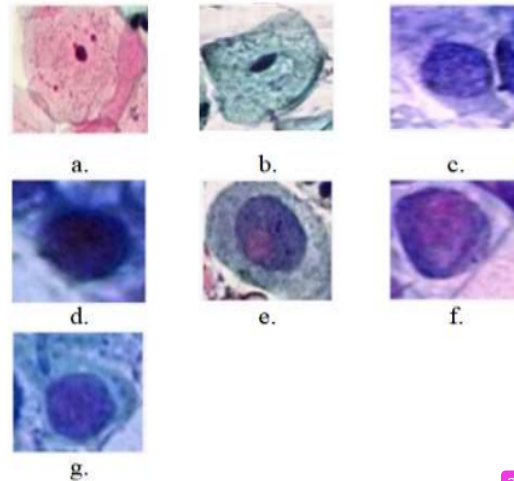


Fig 7. The CLAHE Process on Pap-smear Images for Every Labels (a) Normal Superficial (b) Normal Intermediate (c) Normal Columnar (d) Severe Dysplasia (e) Mild Light Dysplasia (f) Carcinoma In Situ (g) Moderate Dysplasia.

The result of CLAHE would be input image for Adaptive Gamma Correction. The Adaptive Gamma Correction could eliminate non-linear effects at the pre-processing stage. The results of applying Adaptive Gamma Correction could be seen in Fig 8. On Fig 8, the image quality has been increased when it compared with image on Fig 6 and Fig 7.

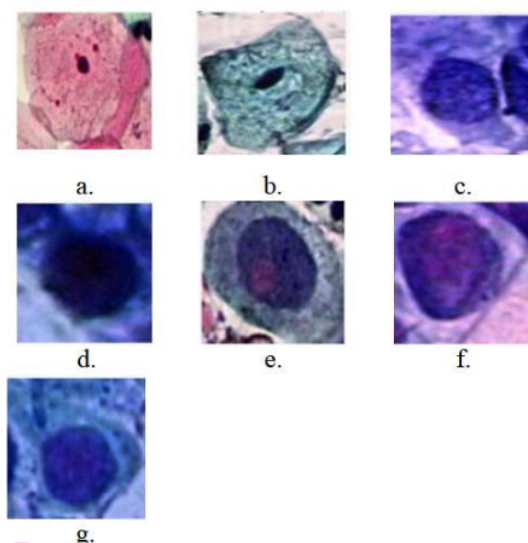
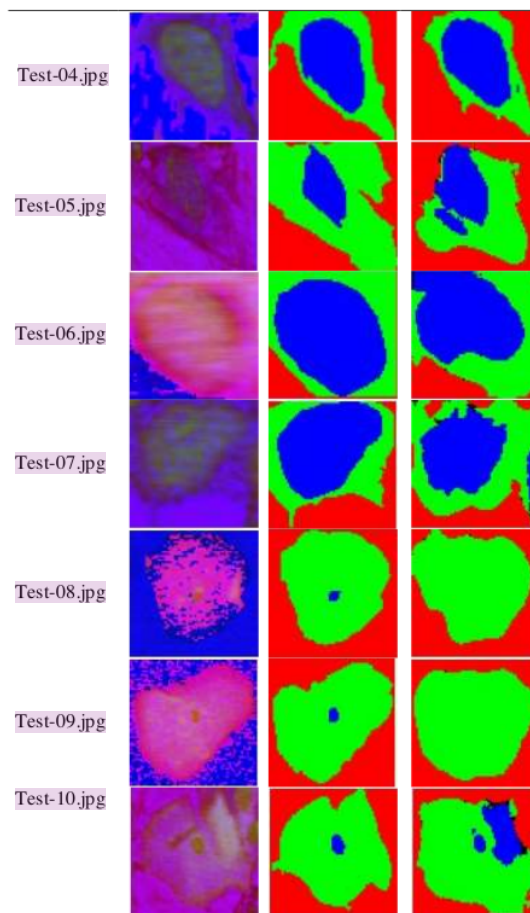


Fig. 8. Adaptive Gamma Correction on Pap-smear Images for Every labels (a) Normal Superficial (b) Normal Intermediate (c) Normal Columnar (d) Severe Dysplasia (e) Mild Light Dysplasia (f) Carcinoma In Situ (g) Moderate Dysplasia

The result of enhancement image in this process (Fig 8) would be used as input for segmentation process. The CNN method architecture applied to obtain important features that identify information regarding cervical cancer. The Pap-smear image was segmented using CNN to select parts of cervical cells on Pap-smear image. On segmentation, pixel location is used as a label based on its location. Ground truth pixels are divided into 3 parts, namely the nucleus, cytoplasm, and background. The segmentation used the CNN method with 4 parallel layers. To evaluate the performance of the results from the first path, the results of the segmentation process would be compared with the results of the ground truth for each image. The comparison was made by 10 images of ground truth and their segmentation result in Table 1. In Table 1 it can be seen that some Pap-smear images have not been segmented properly.

TABLE 1  
THE COMPARISON OF THE SEGMENTATION RESULT WITH GROUND TRUTH OF PAP-SMEAR IMAGES FOR CERVICAL CELLS

No	Original Image	Segmentation	
		Ground truth	Result
9	Test-01.jpg		
	Test-02.jpg		
	Test-03.jpg		



Based on the segmentation result in Table 1, it could be seen that some images have not been segmented properly, such as in the images Test\_03, Test\_05, and Test\_10, the nucleus, and cytoplasm sections were not selected accurately. In the images Test\_01, Test\_02, Test\_04, Test\_06, and Test\_07 the results of the segmentation look almost the same as ground truth but there were still selected areas in the wrong area but the segmentation results of the Test\_08 and Test\_09 images could not detect the Nucleus cell.

After the segmentation has been completed, the image result of this path should be calculated the performance evaluation of the method using the confusion matrix. On the segmentation the labels were a position of pixel comparing between pixel on the segmentation image and ground truth image. There are several measures that can be used to determine the performance of the proposed method, namely accuracy ( $A$ ), Sensitivity (SN), Specificity (SP), F1-score, and others. Accuracy is the ratio of true predictions (positive and negative) to the overall data.

In the training process, ACC, SN, SP, and F1-score were recorded based on the training results for each image. In Table 2, 10 examples of training results were taken from 10 images resulting from the segmentation process using CNN.



TABLE 2  
THE PERFORMANCE RESULTS OF ACCURACY, SN, SP, AND F1-SCORE FOR  
TRAINING SEGMENTATION CERVICAL CELL BASED ON PAP-SMEAR IMAGES

Name of Image	ACC	SN	SP	F1-score
Test_01.jpg	0.73	0.72	0.75	0.72
Test_02.jpg	0.85	0.86	0.86	0.86
Test_03.jpg	0.69	0.65	0.75	0.63
Test_04.jpg	0.91	0.89	0.92	0.90
Test_05.jpg	0.64	0.75	0.66	0.67
Test_06.jpg	0.71	0.75	0.68	0.70
Test_07.jpg	0.73	0.73	0.74	0.72
Test_08.jpg	0.88	0.58	0.59	0.58
Test_09.jpg	0.85	0.57	0.58	0.57
Test_10.jpg	0.73	0.75	0.58	0.57

The calculation of the total average of the trained image obtained 0.77 for ACC, 0.72 for SN, 0.71 for SP, and 0.69 for F1-score. Total average accuracy was only 0.77. It could be seen that the method used should be improved because the results were under 0.80. To find out the success of the segmentation method used, the results obtained will be compared with the results in previous research. The comparison of the segmentation results in this study can be seen in Table 3.

TABLE 3  
THE COMPARISON OF SEGMENTATION METHODS OF CERVICAL CANCER  
BASED ON PAP-SMEAR IMAGES

Method	Dataset	Result			
		ACC	SN	SP	F1-score
CNN [18]	Carl Zeiss microscope, Zeiss AxioCam MRc and BHS	-	0.65	0.73	0.69
BTTFa [17]	ISBI-14	-	0.94	0.91	0.93
Superpixel and CNN [19]	Shenzhen Sixth People's Hospital (Private dataset)	-	0.87	0.91	0.89
Mean-shift clustering [14]	Private dataset	-	0.94	0.93	-
Multi-scale CNN [21]	SZU	-	-	-	0.92
Proposed Method	Herlev	0.77	0.72	0.71	0.69

Based on Table 3, Wang et al [14] gave the highest SN and SP than other studies but did not present the accuracy and F1-score results. Whereas Zhang et al [17] had the highest F1-score but this study did not describe the results of the ACC obtained. Although the results of the SN, SP, and F1-score of the proposed method were lower than those of Song et al [19] it had better results compared to the research of Araújo et al [18]. The next step was to examine the results of the segmentation in the classification process for cervical cancer disorders on Pap-smear images.

The next path was classification the cervical cancer disorders based on Pap-smear image. In the study, the classification was grouped based on two groups. 7 labels on 917 Pap-smear images of The Herlev dataset would be grouped to normal (if there is no pattern of cervical cancer disorders on the image) and abnormal (if there is a pattern of cancer disorders on the image). There were 242 normal Pap-smear images and 675 abnormal Pap-smear images so the labels that used on the study were string type not pixel. In the classification, the KNN and ANN methods were used. Both methods were not be used on data that had m x n dimensions such as the image. The result of segmentation was an image, which is an m x n dimension of the image, so it needed to be flattened. The result of flattening was 1 x k size where k is the number of m rows that were combined into several column after the n-th column in the first row. The results of the classification evaluation carried out with ANN and KNN were compared with the result of other studies. The comparison results of the study could be seen in Table 4.

TABLE 4  
THE COMPARISON RESULTS OF CLASSIFICATION METHODS FOR CERVICAL  
CANCER DISORDERS WITH 2 CLASSES OF NORMAL AND ABNORMAL  
PAP-SMEAR IMAGES IN CERVICAL CANCER

Method	Dataset	Result			
		ACC	SN	SP	F1-score
Naïve Bayes & Weight-PCA [10]	Herlev	0.67	-	-	-
CNN and ELM [9]	Herlev	0.99	-	-	-
HMLP and GA [11]	HUSM (private)	0.75	0.72	0.87	-
KNN [15]	Fortis Hospital Mohali, Punjab (India)	0.82	-	-	-
Based on the nucleus area [16]	Herlev	-	1	0.90	-
KNN (Proposed Method)	Herlev	0.92	0.87	0.86	0.86
ANN (Proposed Method)	Herlev	0.91	0.87	0.91	0.89

On Table 4, the results of the classification evaluation using the ANN and KNN on Pap-smear images methods were very satisfactory even though the segmentation applied to cervical cancer cells is not quite satisfying. The proposed method had the highest SN and F1-score than other studies. The highest accuracy results were achieved by Ghoneim et al [9] but this research did not present the results of SN, SP, and F1-score. Meanwhile, the highest SN results were obtained by Sreedevi et al [16] but did not present the accuracy and F1-score results.

Segmentation and classification were separate path. The segmentation produced the objects needed at the classification path. The ACC, SN, SP, and F1-score results in

segmentation were carried out by checking the similarity of the location of the pixels in the segmented image with the pixels in ground truth. In classification, the ACC, SN, SP, and F1-score were measured to match the category labels predicted or classified by the machine with the label information in the dataset, in this case the labels used were normal and abnormal Pap-smears. Although the performance results on the segmentation both ACC, SN, SP and F1-score were still below 0.8 but these were able to give a very good influence on the classification results, where the ACC was above 0.9 and the results of SN, SP, and F1-score were above 0.85 both using the KNN method as well as ANN.

#### IV. CONCLUSION

The Bi-path architecture proposed in this study combined the segmentation CNN and classification with ANN and KNN methods. The proposed architecture included various stages of image processing starting from image enhancement, segmentation, and classification to recognize cervical cancer patterns on the Pap-smear image. The results of the performance in the segmentation with CNN were not very satisfying but still have a good influence on the classification process by ANN or KNN. From the results of the final evaluation on the classification, it can be concluded that the proposed architecture method is robust enough to be used to classify which Pap-smear images are normal without cervical cancer and which are abnormal and possibly have cervical cancer based on the segmentation CNN result.

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