Medical Image Registration at Pap Smear for Early Identification of Cervical Cancer

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Abstract – **The complexity of the cell structure and high overlap causes poor image contrast. Complex imaging factors in lighting differences, dye concentrations, and other variables such as drying air, excess blood, mucus, bacteria, or inflammation can make automatic visual interpretation more difficult. This study proposes an approach model by combining basic image processing techniques in deep learning for segmentation of the nucleus in the Overlap Cell Image of Pap Smear of Cervical Cancer patients. The purpose of this research is to segment by increasing the identification accuracy of Pap smear images on RepomedUNM public data. The results have the best performance as seen in the MSE value, the lowest RMSE value is 0.2024253 and the lowest PSNR is 0.04009707 and the highest PSNR is 65.3826018 dB. So, this study can be used as a reference in identifying the Cervical Cancer Nucleus as Medical Image Registration (MIR) patients.**

Keywords – **Nucleus, Cervical Cancer, Pap Smear, Early Identification, Medical Image Registration.**

1. Introduction

Medical Image Registration (MIR) is a process in digital image processing [1] for clinical purposes [2]. MIR is very necessary as accurate and complete information about the patient's disease for diagnosis and more treatment information to doctors [3]. The slightest error in the information will have very serious consequences [4].

Pap Smear (PS) Image is an MIR in early cervical cancer (CC) examination [5]. From the resulting image, abnormal cell conditions can be observed [6], but tend to be very difficult and prone to errors in manual examination [7]. Most of the cells are relatively thin and overlap [8], making it very difficult to identify [9]. For this reason, it is necessary to develop image processing techniques to assist inspections so that the accuracy results are further improved. The current technique still has weaknesses so that the accuracy is low for some cell classes and most of the techniques only work very well on one or a few images [10]. This accuracy can be improved by varying the various parameters in the technique used.

The basic step in PS image analysis for CC screening is to detect the nucleus [11]. Each cell has only one nucleus. The nucleus is indicated by CC if there is an enlarged size change and abnormal color [12]. So, it is necessary to use medical image segmentation techniques in obtaining information on the nucleus. This information is fundamental in detecting cancerous or precancerous lesions [13]. The results of segmentation can affect all processes of medical image analysis in classifying lesions [14], but the overlap of cells is still low [15] and even poor [16].

Segmentation of overlapping cells is very challenging to study. Many methods develop existing techniques in overlapping cell segmentation. Several studies that have been carried out in the development of cementation techniques in the last year (2022) are presented in Table 1.

Table 1 Research that developed the segmentation method

Authors	Developed technique	Result
Devi, et al	Active contour	Very good [17]
Mahyari, et al	Multi- layer random walker	Works very well [18]
Wang	Depth information cell	Accuracy can be improved [19]
Yang, et al	U-Net	quite high accuracy [20]
Hao, et al	Cellular Region Proposal and Pixel-level Segmentation Network (CRP- PSN)	Effective in increasing accuracy [21]

2. Materials and Methods

This research develops a segmentation model with polynomials that aims to detect and separate the core area in PS images and is continued by combining several edge detection operators by Robert. Every basic technique used strongly supports research performance where certain parameter values are obtained from the results of experiments conducted.

A. Test Images

Pap smear images that were processed as test data in this study were public data from RepomedUNM, which was obtained from PS image acquisition at the Image Processing Laboratory of the University of Nusa Mandiri (UNM) using a microscope and camera. Each slide containing cervical tissue samples was obtained in collaboration with the Bandung Veterans Pathology Special Laboratory with the stages presented in Figure 1.
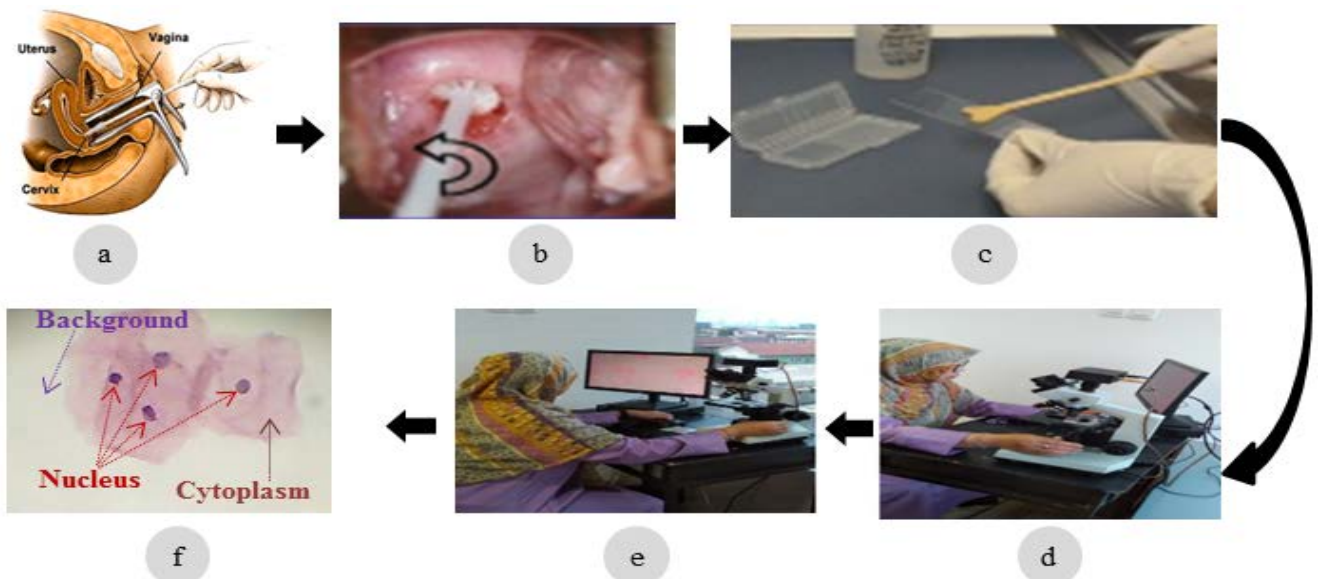

Figure 1 stages recording Image, a. Position samples, b. Sampling, c. Slide preparation, d. Slide into microscope preparation, e. Recording, f. Overlap cell image

The steps to get a PS image of a CC patient is to take a sample by inserting a *speculum* into the woman's vagina (Figure 1.a). In the speculum there is a cytobrush where the liquid is attached by rotating it (Figure 1.b). The liquid in cytobrush is placed on *a slide preparation* that has been smeared with *PreservCyt* (Figure 1.c). These preparations were placed on the Olympus CX33RTFS2 microscope and the X52-107BN microscope for observation (Figure 1.d). The observations were recorded on a computer using a Logitech HD webcam C525 camera in digital form (Figure 1.e), so that it becomes a PS image with 40x magnification.

The image format uses the Joint Photographic Experts Group (JPG) with a size of 512 x 512 pixels. The resulting image and there are overlapping cells (Figure 1.f). Many of the images obtained are presented in Table 2.

Table 2 Data set RepomedUNM

No.	Category	Num of Images
1	Normal	4,503
2	L-Shil	874
3	Koilocyt	435
4	H-Shil	357
Total		6,169

B. Enhancement

The structure of each cell consists of Nucleus, Cytoplasm and Background. To increase accuracy in segmentation, it is necessary to sharpen with enhancement techniques for the color of the nucleus to become a more significant value. The equation used is Equation (1).

$$Ce = Ci + 0.7 * (Ci_{(x,y)} - Ci_{(x+1,y+1)}) \quad (1)$$

Where Ce is the enhancement image, Ci is the input image, x is the row position of the input pixels, and y is the input pixel column position. The constant value given is 0.7 which is obtained from repeated comparisons in the test. The value of this constant may change according to the lighting quality at the time of recording.

C. Polynomial

It is a process to improve image quality by emphasizing the basic colors, namely Red, Gray, and Blue (RGB) in the image. The purpose of this technique is to identify each cell into a single cell by determining the coefficient and color degree of each cell in the overlapping area. This technique uses 2 equations which are carried out in stages, namely Equation (2) and Equation (3).

$$I_p = I_k + K(x) \quad (2)$$

$$K(x) = a_0 + a_1 x + a_1 x^2 + \dots\dots\dots + a_r x^r \quad (3)$$

Where I_p is the color intensity of the image I_k is the intensity of each color, K is a constant function in polynomial form of the degree of color layer depth, a is the coefficient value, x is the estimate, and r is the highest power variable.

Estimation on the equation using degrees up to 7, namely (0, 1, 2, 3, 4, 5, 6, 7) and the coefficient value using Gauss-Jordan elimination. The values obtained are tested using the Sum of Square Error (SSE) which is presented in Equation (4).

$$SSE = \sum_{i=1}^{n}(x_i - \underline{x})^2 \quad (4)$$

Where n is the number of tests, xi is the value of the i-th test and 0 is the average of all tests.

The resulting image from this technique produces very significant pixel values (contrast). These contrasting values can identify Nucleus and Cytoplasm objects well.

The difference in pixel values is very noticeable so that the accuracy of the object area can be recognized very precisely.

D. Edge detection

technique is the process of identifying the Nucleus object in the image. This process requires a convolution process against the edge detection kernel, namely Robert. The convolution equation is presented in Equation (5).

$$ED_{(x,y)} = \sum_{p=-m2}^{m2} \sum_{q=-n2}^{n2} k(p + m2 + 1, q + n2 + 1) f(yp, xq) \quad (5)$$

Where ED is the edge detection image, m2 is half of kernel height, n2 is half of kernel width, f represents rounding down, and k is kernel with index starting from 1 where the kernel structure is in Figure 2.

$$\begin{bmatrix} 0 & +1 \\ -1 & 0 \end{bmatrix}$$

Figure 2 Kernel Robert

3. Result and discussion

The identification stage in this study begins with the input of a single cell image resulting from the separation of overlapping cells and segmentation is carried out. The process is divided into 2 stages of data, namely training and testing. Comparison of the distribution of data is presented in Table 3.

Table 3 Comparison of training data with testing (%)

Uji ke-	Training	Testing
1	60	40
2	70	30
3	80	20
4	90	10

results obtained epoch, batch size, and dropout on the training data for a deep learning process is carried out. The model that gets the optimal value is then carried out by the testing process. The optimal results from the model will be applied to the testing data. The characteristics of the image features will determine the class of the input data.

The results of the images studied in this study are images that contain overlapping cells, where from all images obtained as many as 760 overlap cells, where the lowest Mean Square Error (MSE) value is presented in Equation (6), the Root Mean Squared Error value (RMSE) is presented in Equation (7) and the highest Peak Signal-to-Noise Ratio (PSNR) presented in Equation (8).

$$MSE = \frac{1}{MN}\sum_{i=1}^{M}\sum_{j=1}^{N}[X(ij) - Y(ij)] \qquad (6)$$

$$MSE = 0.040509$$

$$RMSE = \sqrt{\frac{1}{MN}\sum_{i=1}^{M}\sum_{j=1}^{N}((X(ij) - Y(ij))^2} \qquad (7)$$

$$RMSE = 0.2024253$$

$$PSNR = 10.log10\left(\frac{max^2}{MSE(X,Y)}\right) \qquad (8)$$

$$PSNR = 65,40869 \; dB$$

The error calculation result for the proposed model is very low, with an MSE value of only 0.040509 and an RMSE of 0.20024253. While the PNSR is greater, namely 65,40869 dB. This value indicates that the proposed model is getting better at identifying the nucleus in overlapping cells in the PS CC image.

The image presented in this article is only 1 of all processed images according to the image presented in Figure 1.f. Comparison of the results of segmentation of the nucleus object is presented. in Figure 3.
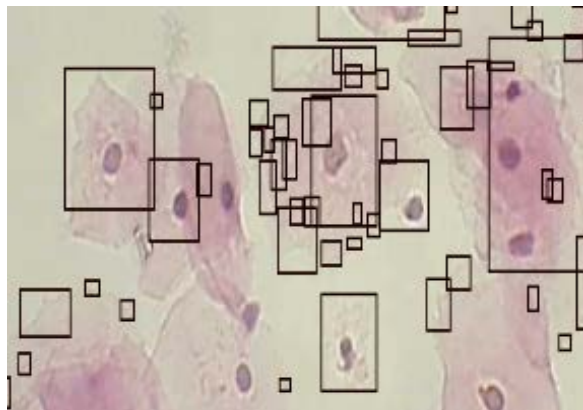
a

b

Figure 3. Image segmentation results, a) Without the proposed model, b) Using the proposed model

Based on the comparison of the resulting images, it can be observed that processing using the proposed model can correctly identify the nucleus correctly.

The performance of the proposed model was measured by the Confusion Matrix. From the results the values obtained are True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN). These values are presented in Table 4.

Table 4 Confusion matrix identification results

Actual	Positive	Negative
Positive	628	32
Negative	96	4

Evaluation values are tested using Accuracy presented in Equation (9), Precision presented in Equation (10), and recall which is presented in Equation (11).

$$Accuracy = \frac{TP + TN}{Total\ data} \qquad (9)$$

$$Accuracy = 86.8\%$$

$$Precision = \frac{TP}{TP+FP} \qquad (10)$$

$$Precision = 95.5\%$$

$$Recall = \frac{TP}{TP+FN} \qquad (11)$$

$$Recall = 99.8\%$$

There is a chance of accuracy between the data tested and the prediction results obtained by the model, namely Precision of 95.5%. Racall's results in the test probability with the model's success to find information about the Nucleus object is 99.8%. The result of accuracy in detecting the nucleus with this proposed model is 86.8%. These results indicate a very good level of accuracy against the model proposed in this study.

4. Conclusion

It is difficult to perform segmentation procedures on PS images due to color variations, complex backgrounds, irregular cell shapes, especially from overlapping cells. Combining the Polynomial model and Robert's edge detection is a very promising method. The new model proposed in this study combines basic image processing techniques to identify the nucleus more accurately. This model creates a filtering process that can better solve the problem of color contrast with a low error rate, which is shown in the three parameters tested, namely MSE, RMSE and PSNR where the PSNR value has the highest value.

This model provides a solution in detecting complex background objects in PS images against overlapping cells with various data recording features. In the future, this model can be used as a reference for research that focuses on identifying cells that overlap to form a single cell to improve the detection of nuclei in PS images. This model can be used in an image segmentation approach with a unique model to differentiate sizes.

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