SEMARAK ILMU PUBLISHING

Journal of Advanced Research in Applied Sciences and Engineering Technology

Journal homepage:
https://semarakilmu.com.my/journals/index.php/applied_sciences_eng_tech/index
ISSN: 2462-1943

Edge Enhancement and Detection Approach on Cervical Cytology Images

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ABSTRACT

Cervical cancer is a prevalent and fatal disease that affects women all over the world. This affects roughly 0.5 million women annually and kills over 0.3 million people. Recently, a significant amount of literature has emerged around the advancement of technologies for identifying cervical cancer cells in women. Previously, diagnosing cervical cancer was done manually, which could lead to false positives or negatives. The best way of interpreting Pap smear images and automatically diagnose cervical cancer are still up for debate among the researchers. Method used in this study is the contrast enhancement technique for pre-processing and edge detection-based for segmentation of the nucleus. In this study, the average performance results of the method showed an accuracy of 96.99% in the seven-class problem using Herlev dataset. The present finding also support this study which concluded the results of accuracy achieved for the algorithm used for nucleus detection is improved by 6.15% when comparing to previous work. The accuracy value is in the lines of earlier literature that achieved accuracy of the approach used above 90% for seven class of cells. The major feature of the suggested approach is an improvement in the ability to anticipate which cells are aberrant and which are normal. Adding more classifiers could improve the suggested system even further. Therefore, a cervical cancer screening system might utilize this framework to identify women who have precancerous lesions.

Keywords:
Edge Detection, Nucleus, Cytology image

Received: 13 June 2022 **Revised: 22 August 2022** **Accepted: 2 September 2022** **Published: 15 Sept. 2022**

1. Introduction

Women all across the world are exposed to cervical cancer, which is now the most prevalent cancer in developing nations. Numerous causes, including population growth and ageing, have contributed to the rise in the burden of cancer. In the early 20th century, cervical cancer cells had to be manually systematised, which took some time and offered misleading results [1,2]. The second

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https://doi.org/10.37934/araset.28.1.4455

most dangerous aggressive tumour to develop in a woman's cervix is cervical cancer. There may be a lower mortality rate from cervical cancer if it is properly treated and discovered at an early stage [3–5].

In recent years, it has been common practise to screen for diseases like colorectal cancer, breast cancer, and cervical cancer using cell images from pap smears. Important phases in the diagnosis and analysis is the need of the accurate segmentation of cells nuclei [6]. The straightforward screening test known as a Pap smear is typically used to detect cancer. Cervical cancer is divided into normal and abnormal cancers, which have cells and cytoplasm in a same structure for accurate screening and detection. Recognizing a malignant nucleus in a cell is a challenging task. The most especially challenging and time-consuming task is medical image processing. The Pap test is a preventive measure that requires specialist and time-consuming analysis of cytological preparations in order to find potentially abnormal cells from the internal and external cervix surface. The task of a cytopathologic is to examine numerous microscopic fields while looking for aberrant cells [7].

Cell segmentation has become a crucial stage in determining the course of cervical cancer led to the massive use of computer-aided detection tools in cervical cancer screening [8,9]. The problem driven on by a lack of medical resources is somewhat alleviated by traditional manual treatments. Although technological advances considerably increase the early detection of cervical cancer, proper diagnosis is still challenging due to a number of variables [10]. Segmentation of nuclei in cervical cytology pap smear images is a crucial stage in automated cervical cancer screening. Segmentation also become difficult due to the presence of cervical cells with spurious edges, overlapping cells, neutrophils, and artifacts [11].

Nevertheless, the complicated technique seems unable to provide an automatic diagnosis due to the relatively low segmentation accuracy for abnormal cells. Artificial intelligence is becoming more and more popular in computer-aided diagnosis due to the ability of various deep learning techniques to automatically extract image features with high accuracy and less error. The commonly used method is segmentation of the cell images. There are several segmentation techniques available for detection of cell nuclei has been studied and reviewed. This study aims to contribute a better performance method of nucleus detection method.

Image segmentation is used in medicine to quantify tissue volumes, advise surgeons during surgery, find and identify cancer cells, and virtually mimic operations. Image segmentation has a variety of uses in the medical field. Once the affected areas are located, treatments can be devised for them. Hence several studies have been reviewed related to images segmentation in nucleus detection of cervical cell based on pap smear images.

Several image processing-based methods have been put further to obtain pap smear images and detect cervical cancer in pap smear images. Accuracy is frequently the primary concern when evaluating these systems' performance. In 2022, Fekri-Ershad and Ramakrishnan [12] published a paper in which they described the method of segmentation by using an appropriate threshold. This research presents a two-stage approach for classifying pap smear images. The first stage's goal is to jointly extract texture data from the cytoplasm and nucleus. The pap smear image is further segmented using the suitable threshold for this purpose. The local textural elements are then described using a texture descriptor called modified uniform local ternary patterns (MULTP). Second, the pap smear images are classified using an enhanced multi-layer feed-forward neural network. The number of hidden layers and hidden nodes in the proposed deep neural network are tuned using genetic algorithms. In order to address these parameters, a novel chromosomal representation and cross-over technique is developed. The findings demonstrate that the method has a higher detection accuracy than the methods that were compared. The finding is consistent with the study by Hoque *et al*., [11] which in the method proposed, the image goes through a convolution filter after the initial

adaptive thresholding pre-processing steps to remove some noise. Then, a nucleus size recovery process based on the average intensity value of the contours, the contours from the resulting image are filtered according to their individual contour properties. The outcomes demonstrate that our algorithm performs better in nucleus segmentation than other state-of-the-art techniques.

The research study by Prianka and Celine Kavida [13] also found that by extracting and removing the background space from the pap smear image to obtain a clear image of the damaged cervical cells, the malignant cells were identified a positive and negative values are obtained as the nucleus cells were segmented. The background spaces and cervical area cytoplasm were eliminated in order to obtain the primary images. Eliminating extraneous cytoplasm revealed the squamous and basal cells. The super pixel cells for analysis were collected along the process. The framework for the procedure was built with a succession of segmentations and the extraction of core nuclei to remove unwanted space and discover the cancerous area. The cancer cells discovered on the cervix's surface are explained in stage 0 of the disease. Segmentation was done on the cancerous cells that were found [14]. Each frame's segmentation will be tagged as positive or negative depending on whether a cancer cell is present. If there is no malignant cell present, the frame will be designated as negative. It is easier to determine the number of cancerous cells in the area by analysing the segmentation and extraction. With the same objective, a new finding demonstrates the advantages of Neutrosophic Graph Cut-based Segmentation (NGCS) over previously processed cervical images in a study by Anousouya Devi *et al.*, [15]. This NGCS-based segmentation is mostly used to examine the overlapping contexts of pre-processed pictures from cervical smears in order to improve classification accuracy. With the help of this NGCS-based segmentation, the input pre-processed image is divided into a variety of non-overlapping parts, improving perception at the user's convenience. According to the estimated indeterminacy value, which incorporates the intensity and spatial information from the pre-processed input image, the pre-processed input image is turned into a Neutrosophic set and indeterminacy filter in NGCS-based segmentation. The indeterminacy value related to each intensity and piece of spatial information is minimised by the indeterminacy filter that is being used. Comparing the outcomes of this NGCS-based cervical cancer detection method to the conventional graph cut orientated cancer detection methodologies, the results are shown to be excellent on average by 13%.

In another study by Waly et.al, [16] proposed the Gaussian filter (GF) approach is initially used to improve data by removing noise from the Pap smear image. The segmentation of an image is decided by the Tsallis entropy approach with the dragonfly optimization (TE-DFO) algorithm in order to correctly identify the sick regions. To extract deep-learned features, the cell pictures are loaded into the DL-based SqueezeNet model. That is crucial to properly screen pap smear images in order to aid in the earlier detection and diagnosis of cervical cancer. Deep learning (DL) techniques may be used to create computer-aided systems for the detection of cancerous cells. Utilizing biological pap smear pictures, this study offers an intelligent deep convolutional neural network (IDCNN-CDC) model for cervical cancer diagnosis and classification. The results of the experiments confirm that the proposed technique performs better in terms of sensitivity, specificity, accuracy, and F-Score. In addition, Chuanyun *et al*. [17] proposed adopting the gradient vector flow approach to segment nuclei and cytoplasm areas (GVF). It does not, however, address the problem of the overlapping cells. The issue of overlapping cells has been addressed by numerous different techniques [7]. One of the most popular of these is marker-controlled watershed transition. Over-segmentation issues are the main issue with this approach [18]. Shape, texture, and colour features are the most frequently employed features in feature extraction [19], [20]. The practicality of using the texture attribute is its major draw. Support vector machine (SVM), LDA (Linear Discriminant Analysis), k-nearest neighbour (KNN), and ANN (Artificial Neural Networks) are the most frequently utilised classifiers in multi-cell

cervical image analysis [21–26]. Numerous research studies have been conducted on the detection of cervical cancer, however the majority of these studies only focused on the segmentation of nuclei regions [27]. Cytoplasmic area segmentation is also crucial. For the classification of aberrant cells, the characteristics that are retrieved from cytoplasm areas are useful [28]–[30]. Table 1 illustrate the summary of prevailing works. The outcomes of this study indicate that appropriate system design and tuning, machine learning methods is able to detect nucleus of cervical cancer cell accurately and efficiently in its early stages using clinical data. Therefore, better performance of nucleus detection method is needed to provide a good data for classification in determination of cervical cancer.

Table 1
Summary table of prevailing studies

Author /Year	No. of image/ Dataset	Accuracy	Precision	Sensitivity	Specificity
Chitra & Kumar. [31]	DenseNet	98.38%	99.3%	98.58%	98.83%
Rahaman *et al*. [32]	Herlev	2-Class 98.32% 7-Class 90.32%	-	-	-
Khamparia *et al*. [33]	CRIC Searchable Image Database	2-Class 96% 3-Class 96% 6-Class 95%	2-Class 96% 3-Class 94% 6-Class 85%	-	2-Class 96% 3-Class 97% 6-Class 97%
Wang *et al*. [34]	143 whole slide images	-	93%	-	-
Novitasari *et al*. [35]	Colposcopy data	95%	-	-	-

3. Methodology

3.1 Image Acquisition

Herlev is widely used dataset and this image databases have been used to design the detection technique. Most researchers used the Herlev University image datasets to improve the design and development process. Herlev Pap database is compiled by Herlev University Hospital (Denmark) and the Technical University of Denmark. The database contains 917 pictures that were manually sorted into groups by professional cytotechnicians and physicians. Surface squamous, intermediate squamous, columnar, mild dysplasia, moderate dysplasia, extreme dysplasia, and in situ cancer are among the seven cervical cell classifications in the database. Various cell and nucleus properties are extracted [36].

In this study, 105 pas smear images were used. The database falls under the category of NiSIS or Nature inspired Smart Information System (EU coordination action, contract 13569), with a particular focus on the group “Nature-Inspired Data Technology”. The data is accessible over the internet (http://fuzzy.iau.dtu.dk/download/smear2005). Table 2 provides the details of the dataset used for the nucleus detection method. There are seven types of cells that falls under the category of normal cells and abnormal cells. The normal cells consist of normal superficial, normal intermediate and normal columnar type. While the abnormal cells consist of mild dysplastic, moderate dysplastic, severe dysplastic and carcinoma in situ type of cells. The total numbers of images in this dataset is 917.

Table 2
Descriptions of seven-classes cells from the Herlev (single cells) dataset

Class	Type	Number of cells
Normal cells	Normal superficial cells	74
	Normal intermediate cells	70
	Normal columnar cells	98
Abnormal cells	Mild dysplastic cells	182
	Moderate dysplastic cells	146
	Severe dysplastic cells	197
	Carcinoma in situ	150
	Total	**917**

3.2 Image Enhancement

Most of the pap smear images contain noise and low contrast which can affect the accuracy of the detection method. Image enhancement is applied as to remove the noised and increase the contrast [37]. There are three functions that can be applied to adjust for contrast enhancement in image processing which are 1) *imadjust* function – adjust image intensity values and colormap, 2) *histeq* function – enhance contrast using histogram equalization and 3) *adapthisteq* function – contrast-limited adaptive histogram equalization (CLAHE). Cell segmentation was simpler and more accurate with high contrast images when compare to a low contrast image [38]. Table 3 has demonstrated the results from the contrast enhancement procedure that has been done on seven types of cervical cell.

3.3 Nucleus Cell Detection

Segmenting the cell's regions from the source images was the aim of this step. Critical features of the cell area include the nucleus and cytoplasm. In a Pap smear screening system, cytologists examine at microscope images of cells and classify them as cancer or healthy cells depending on how the cells' constituent parts seem. The automated screening method follows the same steps. An essential stage in the automatic detection method is the segmentation of cell components. The process of segmenting many cells involves several challenges, such as overlapping cells and undesirable artefacts. Segmenting the nuclei is simpler than segmenting the cytoplasm. Studies have primarily concentrated on nuclei segmentation, with cytoplasm segmentation being a rare topic. The segmented images are presented in Table 4. As Table 4 shows, there is a clear proof that this method of edge detection for nucleus of cells is able to segmented the cell between the nucleus and cytoplasm.

Table 3
Image enhancement results

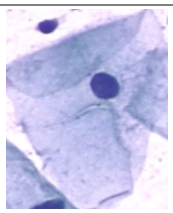
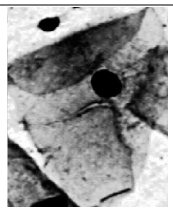
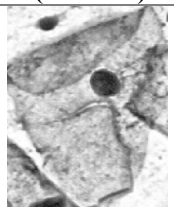
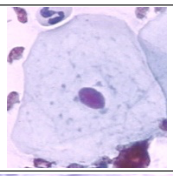
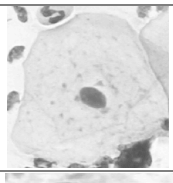
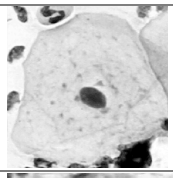
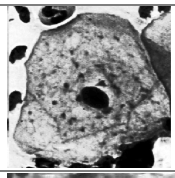
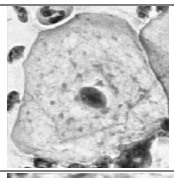
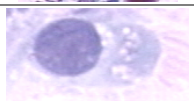
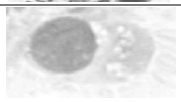
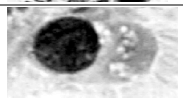
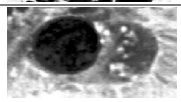
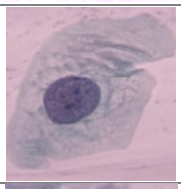
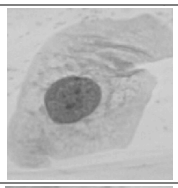
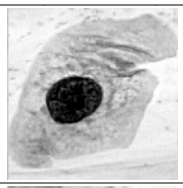
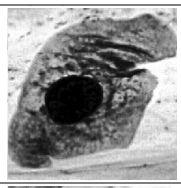
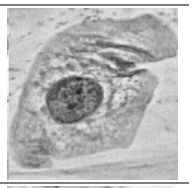
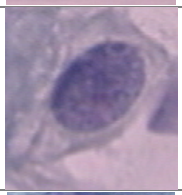
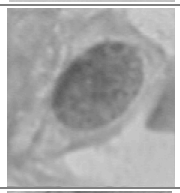
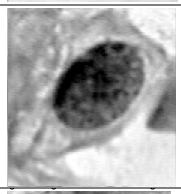
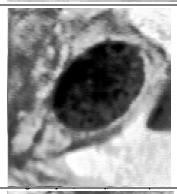
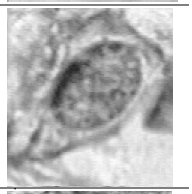
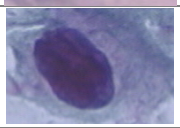
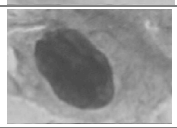
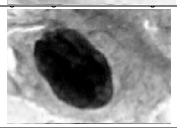
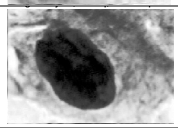
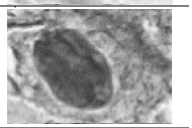
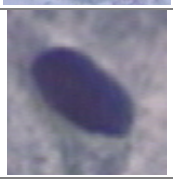
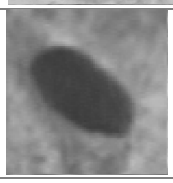
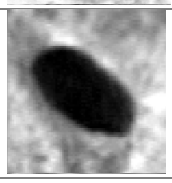
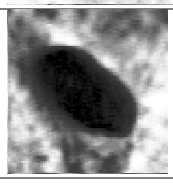
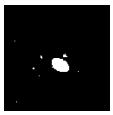
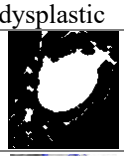
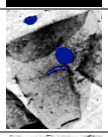
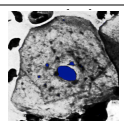
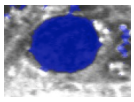
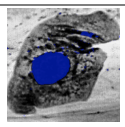
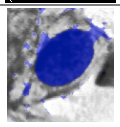
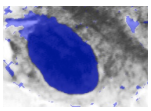
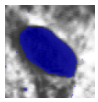
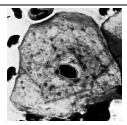
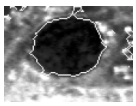
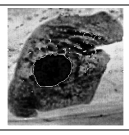
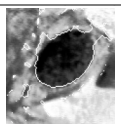
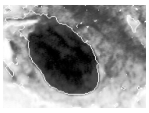
Type of cells	Original Image	Contrast enhancement image			
		Original grayscale	**imadjust**	**histeq**	**Adapthisteq (CLAHE)**
Normal superficial					
Normal intermediate					
Normal columnar					
Mild dysplastic					
Moderate dysplastic					
Severe dysplastic					
Carcinoma in situ					

Table 4
Segmented image, mask over segmented images and outline original image

Type of cells	Normal superficial	Normal intermediate	Normal columnar	Mild dysplastic	Moderate dysplastic	Severe dysplastic	Carcinoma in situ
Segmented image							
Mask over segmented image							
Outline original image							

4. Results

The Quantitative analysis is a numerical-based way for obtaining information on an algorithm's performance without involving any human interaction. Smear photos have a lot of debris in the background, and the nucleus and cytoplasm are in the foreground. The number of items, precision, sensitivity, F-measure, specificity, accuracy and PSNR are calculated in such a complicated context (see Table 5). Image quality assessment is done to measure the accuracy of the algorithm used to detect the nucleus of the cell.

Table 5
Qualitative results based on precision, sensitivity, F-measure, specificity, accuracy and PSNR

Type of Cells	Precision	Sensitivity	F-measure	Specificity	Accuracy	PSNR
Normal Superficial	0.98	100.00	99.11	50.10	98.26	17.60
Normal Intermediate	1.00	99.95	99.78	79.55	99.57	23.64
Normal Columnar	0.97	99.53	98.23	88.09	97.15	15.45
Mild Dysplastic	1.00	99.91	99.71	94.05	99.46	22.71
Moderate Dysplastic	0.93	99.64	95.96	76.59	93.75	12.04
Severe Dysplastic	0.91	99.94	95.02	76.77	92.77	11.41
Carcinoma In Situ	0.98	99.03	98.67	94.28	97.94	16.86
Average	0.97	99.71	98.07	79.92	96.99	17.10

The calculated values can be calculated based on the segmented images. These findings demonstrate the importance of validating image quality using the suggested techniques on the Pap smear dataset [39]. The process is evaluated subjectively by comparing the segmented pictures pixel by pixel with the ground truth images, and quantitatively by counting the number of cells (objects) in the images [40]. Figure 1 shows the calculated values for performance assessment metric on algorithm applied to detect the nucleus of the cervical cells based on edge detection method.

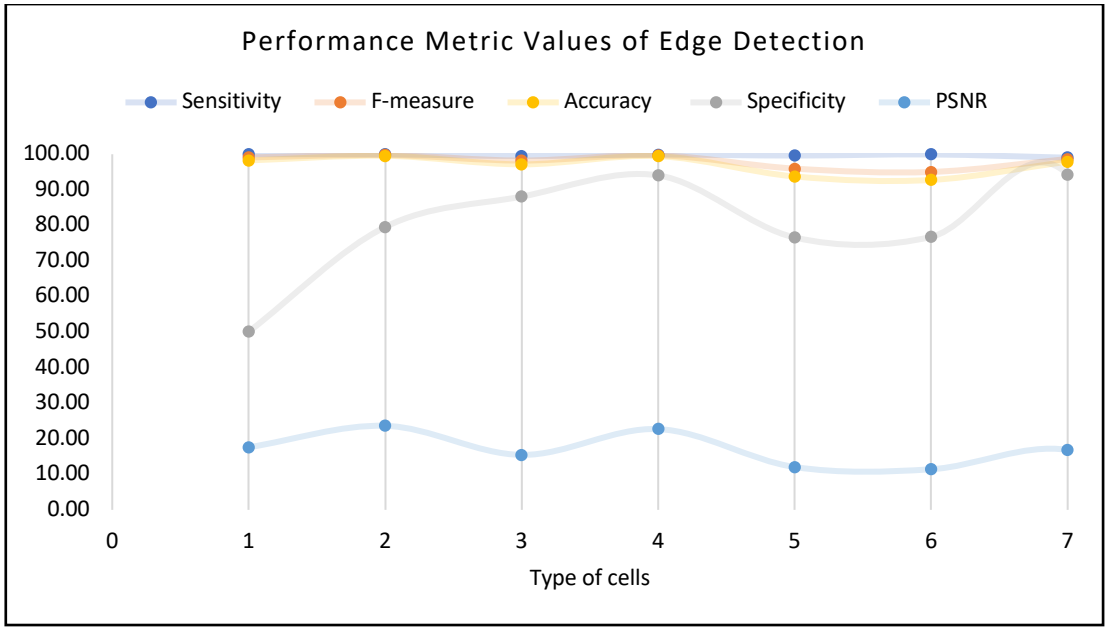


Fig. 1. Performance metric values of edge detection-based segmentation method

* 1 = Normal Columnar
2 = Normal Intermediate
3 = Normal Superficial
4 = Mild Dysplastic
5 = Moderate Dysplastic
6 = Severe Dysplastic
7 = Carcinoma in Situ

Based on the graph in Fig. 1. Performance metric values of results shows that the method of edge detection-based on segmentation give a good performance with high values more than 90% in sensitivity, F-measure, and accuracy. The specificity also provides a satisfying value more than 50% for all cell types. The highest specificity values are for the carcinoma in situ type of cell with a value of 94.28% followed by mild dysplastic with 94.05%. The peak signal-to-noise ratio for both images was determined by the PSNR block in decibels. The performance between the original and the segmented image was calculated using this ratio. The quality of the compressed or segmented image increases with the increasing PSNR. The image's compression quality was evaluated using peak signal-to-noise ratio (PSNR) [41]. The PSNR values showed better consistency value with more than 10% for each type of cell even though the value may not be high compare to other values. The present finding also support this study which concluded the results of accuracy achieved for the algorithm used for nucleus detection is improved by 6.15% when comparing to previous work done by Win *et al.*, [1]. The accuracy value is in the lines of earlier literature that achieved accuracy of the approach used above 90% for seven class of cells [14].

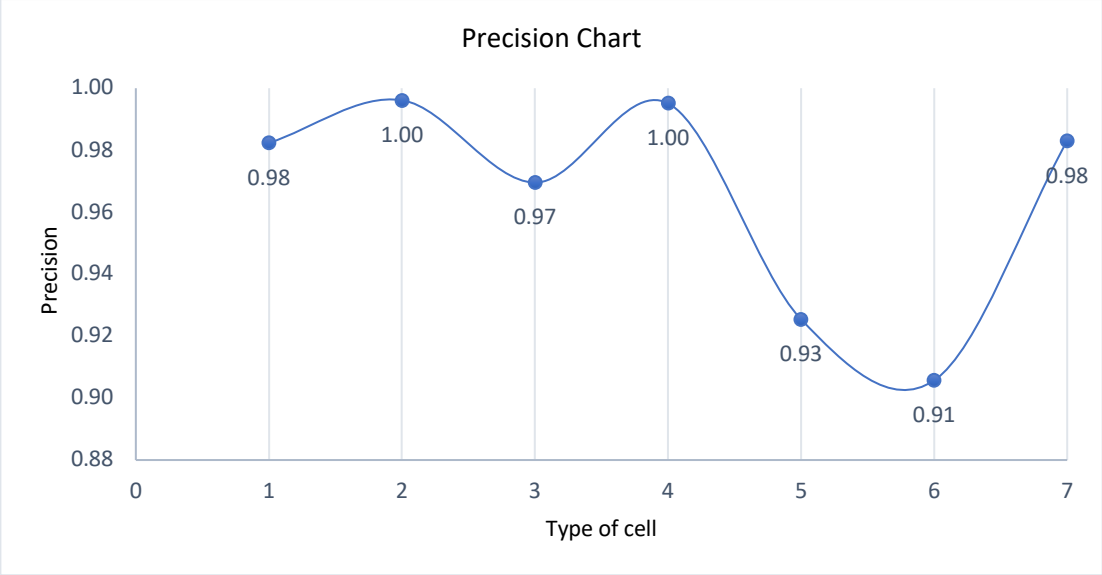


Fig. 2. Precision chart

* 1 = Normal Columnar
2 = Normal Intermediate
3 = Normal Superficial
4 = Mild Dysplastic
5 = Moderate Dysplastic
6 = Severe Dysplastic
7 = Carcinoma in Situ

Precision is a ratio between the number of positive samples to the total number of samples classified as true positives and false negatives and classified the model's accuracy as positives. The higher the precision the better the performance of the model. In this study, Fig. **2** illustrates the precision values for the approach tested to detect the cell nucleus of different type of cells. Method applied has showed a consistent and higher values of precision which is more than 0.9 for each type of cells. The most obvious finding to emerge from the graph is that the value of the precision is a good performance measure that can be used to analyse the detection method of cell nucleus.

4. Conclusion

This paper proposed a method for detection of cell nuclei using segmentation. Approach used is edge detection-based segmentation with the aid of contrast enhancement. There are several methods have been introduced in the past for this field. However, the accuracy has not been found to be significantly accessible. In this study, the average performance results of the method showed an of 96.99% in the seven-class problem using Herlev dataset. The present finding also support this study which concluded the results of accuracy achieved for the algorithm used for nucleus detection is improved by 6.15% when comparing to previous work done. The accuracy value is in the lines of earlier literature that achieved accuracy of the approach used above 90% for seven class of cells. This method seems to be able to detect the nucleus with better performance metric. The major feature of the suggested approach is an improvement in the ability to anticipate which cells are aberrant and which are normal. Adding more classifiers could improve the suggested system even further. Therefore, a cervical cancer screening system might utilize this framework to identify women who have precancerous lesions.

Acknowledgement

This research was supported funding by the Ministry of Higher Education (MoHE) Malaysia under the Fundamental Research Grant Scheme (FRGS/1/2021/SKK0/UNIMAP/02/1).

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