

IDENTIFICATION OF CERVICAL MALIGNANCY AND CERVICAL CELL CATEGORIZATION

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Abstract—

In World Wide Many Woman are affected by the cervical malignancy. So, Most of the Researchers and collegiate have found many no of elucidation to identify this malignancy from the test images of pap smear test. But their results were represented only that women are affected by malignancy or not with less accuracy. According to the obtainable report, I proposed not only to identify the malignancy but also classify the particular Cells as normal or abnormal. The proposed work is based on segmentation, feature extraction and classification process. Test results shows that the mean value based classification of the normal and abnormal cell. Thus the results would be more useful for the pathologist.

Keywords — cervical cancer; segmentation, feature extraction; classification;

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I. INTRODUCTION

Cervical malignancy is the most common malignancy in women of developing countries. Cervical malignancy develops over a prolonged period covering two to three decades [1]. Cervical malignancy is the most common form of malignancy in women under 35 years of age and the second most commonly occurring malignancy in women of all ages, worldwide [2].

Cervical malignancy is a preventable disease, and, unlike most other cancers, it can be easily detected by a routine screening test. Currently, cervical smear screening is the most popular method used to detect the presence of abnormal cells developing in the cervix. The method is as follows: Using a small brush, a cotton wad stick, or a wooden stick, a specimen is taken from the uterine cervix, smeared onto a thin rectangular glass plate—a slide, and colored, making it easier to examine the cells under a microscope. The purpose of the smear screening is to diagnose premalignant cell changes before they progress to a cancer.

Pap test is the most popular and effective screening test for cervical cancer. By extracting and observing morphological of cervical cells, doctor will classify cervical cells based on Bethesda system; normal, *low grade squamous intraepithelial lesion (LSIL)* or *high grade squamous intraepithelial lesion (HSIL)* cell [3].

Automation of diagnosis of malignancy cell image has been studied for a few decades in the field of medical image processing technology. Most of studies involved development of diagnosis support system that solved problems of pathologist shortage [4]. Many techniques of image processing were proposed to handle the problems such as cell segmentation and classification in the development of these systems. Segmentation is one of the most important technique and it was used in all cell segmentation, each nucleus was segmented from its surrounding cytoplasm using a series of automated fast morphological transforms with octagonal structuring elements [5].

The detection and segmentation of the nuclei in images containing cell overlapping and cell clusters has been successfully addressed by several studies [6]. Classification of Pap smear images are based on the calculation of features extracted from the areas of the nucleus and the cytoplasm [7]. These features are usually based on shape and intensity characteristics of the objects of interest.

Basically a malignancy cell was having large nucleus area that means it contains more severity of the lesion like low grade or high grade squamous intraepithelial lesion. Based on this

percent of lesion that occurs in the nucleus, the cancer stage could be classified. The stage of the malignancy could be under the given four stages. That is 1. CIN 0 (Normal), 2. CIN 1 (Mild dysplasia) 3. CIN 2 (Moderate dysplasia) & 4. CIN 3 (Severe dysplasia).

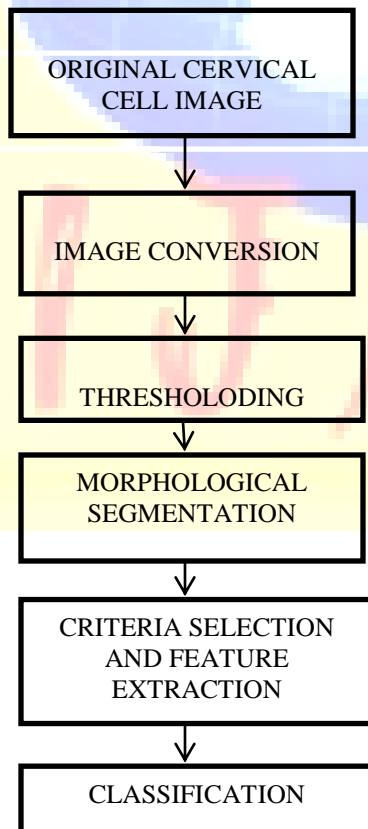
The goal of this research was to develop a cervical malignancy detection system that is able to detect and categorize cervical cells into normal and cancerous cells based on mean value of the nucleus in an image.

II. METHODOLOGY

The proposed methodology and the working process of the proposed method was explained briefly under the following sections.

A. FLOW CHART

The following Flow chart that represent the work flow of how to detect the cervical malignancy from the test images of Pap smear screening test images.



A. IMAGE CONVERSION

Original Cervical cell color image is converted into gray scale image (I).

B. THRESHOLDING AND MORPHOLOGICAL SEGMENTATION

Then the gray scale image (I_G) was first locally thresholded by using given equations 1. that is the mean value of the original input image was multiplying with the factors α , by adjusting the value of this factors we got somewhat segmentation of the nucleus. So Cytoplasmic regions were removed by performing a Morphological closing of the image using a structuring element smaller than the smallest nucleus, and nuclear in homogeneity was corrected by an Morphological opening of similar size. The resulting segmented image for identifying the nucleus with more details than the original image and it is given in equations 2.

$$TI = MEAN(I_G) * \alpha \quad (1)$$

$$SI = ((TI \bullet MC) \circ MO), \quad (2)$$

Where SI is the resulting segmented image. TI is the threshold image, MC & MO are structuring elements. The symbols \bullet and \circ denote morphological closing and opening, respectively. where SI is the resulting segmented Image.

B. FEATURE EXTRACTION

After segmented the nucleus, we must extract the features of the nucleus to find the growth of the nucleus that is normal or abnormal because then only to identify the given cell was affected or not affected by the cancer.

For this reason I go for nucleus feature extraction process. In this process, I was extracted some of the features like area, mean, perimeter, standard deviation of the nucleus by using XROI command in IDL Language.

The use of this command can be exactly to find out the feature values of the nucleus from the gray scale image.

c. CLASSIFICATION


After the features of the nucleus was extracted then it is further move into the classification process.





In this classification process is mainly focused on main features of the nucleus like mean value. By using this value we can identifying the given cell is affected by a malignancy or not and also based on this value the particular cell was further classified into normal or abnormal cell.

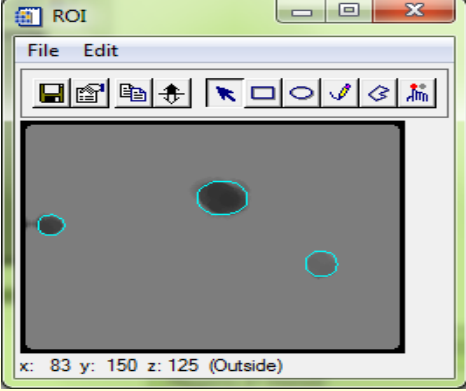
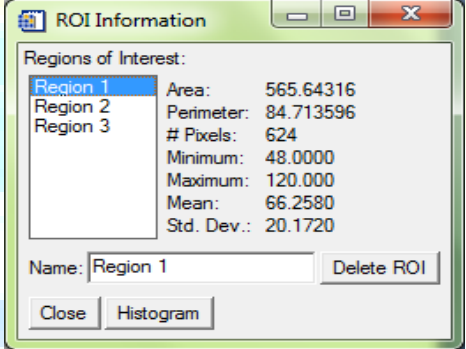
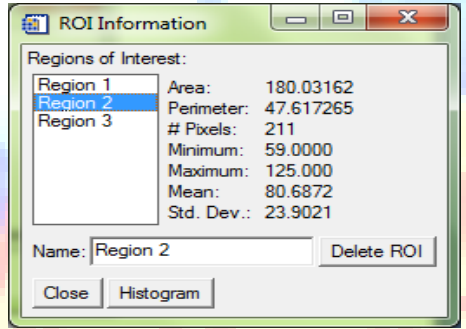
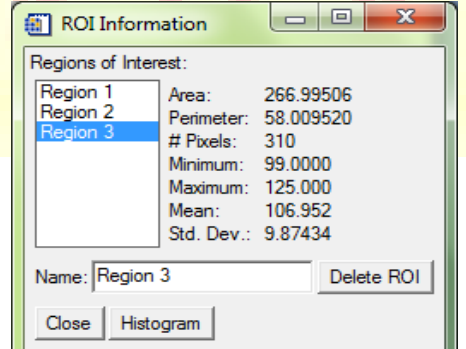
RESULTS AND DISCUSSION

In this section a detailed explanation of digital image processing techniques with the corresponding image results were discussed based on the following two tables namely Table1 for detecting cancer.

Table .1 – System Methodology and Results Table

S.No	Image Names & Important Factors	Images
a)	Input Image	

b)	Color Conversion	
c)	Segmentation	  <p>(d)</p>  <p>(e)</p>

<p>d)</p>	<p>Criteria Selection</p>	 <p>(f)</p>
	<p>Nuclei Feature Extraction</p>	 <p>(g)</p>  <p>(h)</p>  <p>(i)</p>

In the above table Fig. a represents the Input image, Fig. b represent gray scale image. Fig. C represents threshold image, Fig. d and Fig. e represents closing and opening operation image. Fig.F represents nuclei criteria selection, Fig. g,h and Fig. i represents Region of interest information of R1,R2and R3.Then the classification results are applied in table.2.

Basically, how was the malignancy might detected means, Mainly it depends upon decreased mean value of the region of interest (ROI).

As compared to the previous researches conducted by Eko Supriyato and Jeremiah, color intensity level of normal cell ranges between [122-150] & [151 – 200] and cancerous cell ranges between [80-100] & [51 – 100] – [12] and also these results were used only for the particular cell was affected or not affected by the cancer, but my new research will be very useful to the pathologist for not only to identify the malignancy but also to classify the given cell into which stage of the malignancy by using the mean and area value of the table 3. But the table results were only applicable for single cervical cell, that was present in an image not for multiple number of cervical cell image.

Table.2 : Classification Results:

S.No	Region	Mean Value	Cancerous Cell Range (Mean below 100)	Non Cancerous Cell Range (Mean above 100)
1	Region 1	66.2580	Cancerous Cell	
2	Region 2	80.6872	Cancerous Cell	
3	Region 3	106.952		Non Cancerous Cell

IV.CONCLUSION

This work shows that the many number of image processing techniques like segmentation, feature extraction and classification used for finding the details of the region of interest from the initial cervical cell image have seen by us very clearly with more accuracy than the original image. And also extracting some of the features like mean of the region of interest for finding the given cell is normal or abnormal.

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