AUTOMATIC SEGMENTATION AND CLASSIFICATION OF PAP SMEAR CELLS

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Abstract—

Cytologic screening has been widely used for detecting the cervical cancers. Most of the Woman's of the world were affected by the cervical cancer in their different age groups. So, Most of the Researchers, Pathologists and also more number of collegiate have been invented more number of solutions to identify this cancer from the test images of pap smear screening test. But their results were represented only that the women are affected or not affected by the cancer with less accuracy. According to the Existing report, I proposed to identify the cancer from the pap smear cells with high accuracy. The proposed work is based on segmentation, feature extraction and classification process. Test results shows that area value based classification of the normal and abnormal cell. The proposed system provides a feasible and effective tool in evaluating cytologic specimens.

Keywords — cervical cancer; segmentation; nuclei detection; feature extraction; classification;

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I. INTRODUCTION

Cytology evaluation is a safe, efficient, and well established technique for the diagnoses of many diseases. The most famous success in cytology is its ability to reduce the mortality and morbidity of cervical cancer through mass screening. It was reported that the invasive cancer incidence decreased by 47.8% after national screening from 1995 to 2006 in Taiwan [1]. Edge detection is the process of locating these edges. While simple kernel based edge detectors, such as Canny's edge detector [2], have shown good performance, their lack of edge notion, i.e., built-in knowledge of what constitutes good edges, limits their ability to exploit local edge continuity information to reduce fragmented edges in noisy environments [3].

Gradient vector field was used for building 3D model [4]. Xiaowei Chen presented an automated segmentation, classification, and tracking of cancer.

cell nuclei in time-lapse microscopy [5]. Enlargement and deformation of cell nuclei are two major criteria to recognize the abnormal cells in Pap smear exam. Recently, automatic cell nuclei segmentation has been made much more attraction and also provided one of the most interesting topics in cytological image analysis. The inherent problems due to the video microscopy and the smear make this work a challenge. We attempt to identify and label those abnormal cells with enlarged and deformed nuclei in order to simplify the recognition process as screening purpose.[6]

Commercial devices that use these technologies can be divided into the following categories based on their approaches: 1) improved slide preparation to reduce sampling error, e.g., thin-layered liquid based preparation (Thin Prep, Sure Path, Tri path) [7], [8]; 2) reduced workload and screening error as in the auto screening system (Thin Prep Imaging System, Cyto, Boxborough, MA; FocalPoint System, Tripath Imaging, Burlington, NC); 3) improved laboratory quality control like rescreening (Papnet) [9]; and 4) enhanced quality assurance, such as the proficiency test [10]. However, most of these devices do not assist objective diagnosis by providing the calculable variables that would eliminate interpretation errors and inter observer discrepancy [11]. In addition, they are not applicable to the general cytological laboratory because of high cost and technical or linguistic gaps[12].

Mathematical morphology is a new mathematical theory which can be used to process and analyze the images [13]. It provides an alternative approach to image processing based on shape concept stemmed from set theory [14], not on traditional mathematical modeling and analysis. In the mathematical morphology theory, images are treated as sets, and morphological transformations which derived from Minkowski addition and subtraction are defined to extract features in images [15].

METHODOLOGY

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

FLOW CHART

The following Flow chart that represent the work flow of how to detect the cervical cancer by using Pap Smear cell.

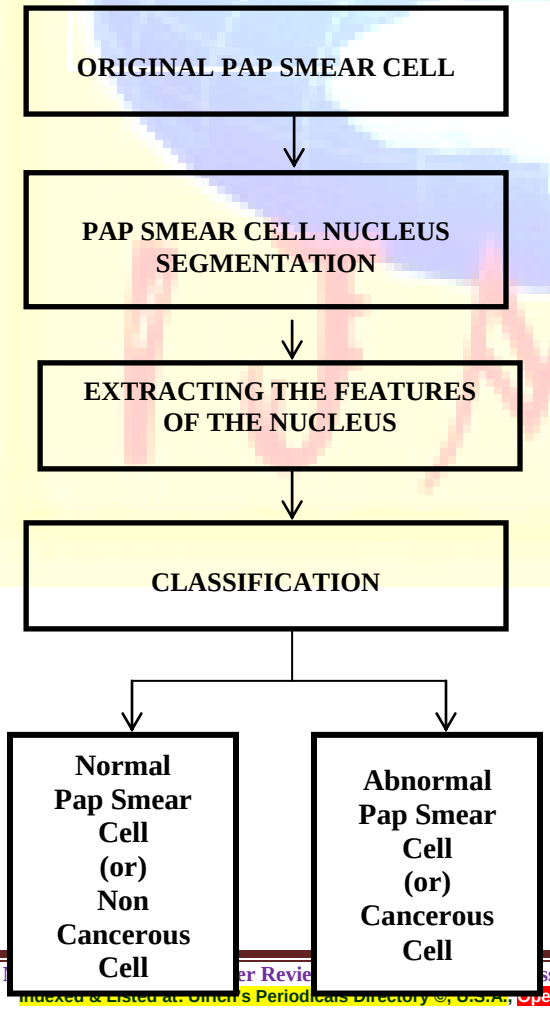


Fig.1. FLOW CHART

1. NUCLEUS SEGMENTATION

Original thinprep cervical cell color Image, if it is a normal, bright or dark image,first it was converted into respective Red,Green and Blue plane Image.

Then Each R, G and Bplane cell imagewas first locallythresholded byusing given equations 1,2 &3.that is the mean value of the original input image was multiplying with the factorsα,β &γ, by adjusting the value of this factors we got somewhat segmentationof the nucleus. So Cytoplasmic regions were removed by performinga Morphological closing of the image using a structuringelement smaller than the smallest nucleus,and nuclear inhomogeneity was correctedby an Morphological opening of similar size. The resultingsegmented image for the respective R,G and B plane were used for identifying the nucleus with more details than the original image and it is given in equations 4,5& 6.

$$MI_R = Mean\ (I_R) \times \alpha \quad (1)$$

$$MI_G = Mean\ (I_G) \times \beta \quad (2)$$

$$MI_B = Mean\ (I_B) \times \gamma \quad (3)$$

$$SI_R = ((TI_R \bullet MC_R) \circ MO_R) \quad (4)$$

$$SI_G = ((TI_G \bullet MC_G) \circ MO_G) \quad (5)$$

$$SI_B = ((TI_B \bullet MC_B) \circ MO_B) \quad (6)$$

Where SI_R, SI_G, $SI_B$is the resulting segmented image for the respective R,G and B plane. TI_R, TI_G, $TI_B$is the thresholded imagefor the respective R,G and B plane,MC_R, MC_G,MC_B, MO_R,,MO_G, MO_B are structuring elements for the respective R,G and B plane. The symbols● and odenote morphological closing and opening, respectively.

Then by combining R, G and B Channel Segmented image SI_R, SI_G, SI_Bwe get the segmented cervical cell image is equation 7.

$$SI_{RGB} = ((TI_{RGB} \bullet MC_{RGB}) \circ MO_{RGB}) \quad (7)$$

whereSI_{RGB} is the resulting segmented color image,I_{RGB} is the original thinprep Image, $TI_{RGB}$is the thresholded image, MC_{RGB} andMO_{RGB} arestructuring elements. The symbols● and odenote morphological closing and opening, respectively.

2. 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, perimeter, pixels 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 pap smear cell.

3. CLASSIFICATION

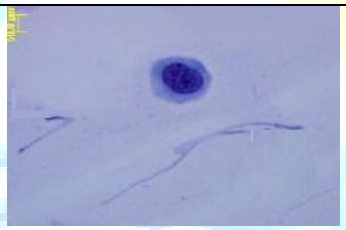
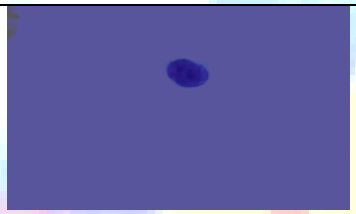
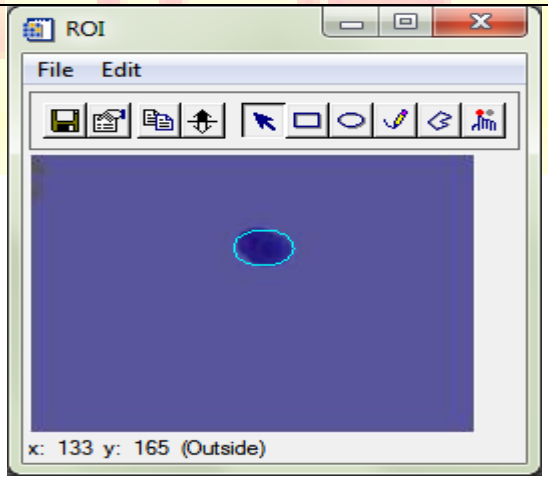
After the features of the nucleus were extracted then it is further move into the classification process.

In this classification process is mainly focused on main feature of the nucleus like area value. By using this value we can identifying the given cell is affected or not affected by a cancer based on normal or abnormal growth of the nucleus.

II. 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 Table.1.and the results are classified based on the Table.2.

TABLE 1. CANCER RESULTS OF THE PAP SMEAR CELL

S.No	Image Names & Important Factors	Images & Resulting Factors
		Figure
a)	Input Image	
b)	Segmentation	
	α	0.57
	β	0.52
	γ	0.77
c)	Feature Extraction Process - ROI Window & Nucleus Selection	

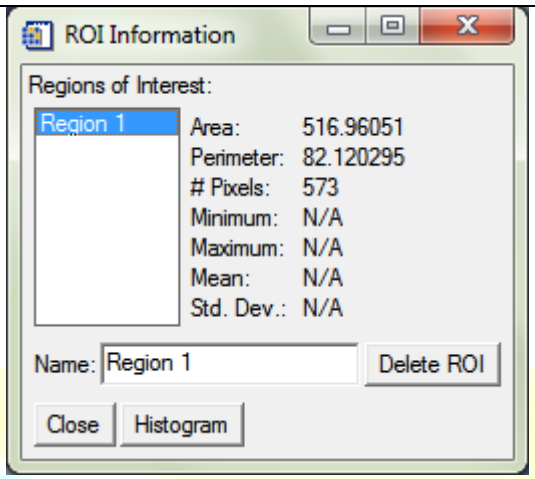
	ROI Information	
d)	**Classification**	
	Area	**516.96051**
	Result	**Abnormal Cell**

TABLE 2. NORMAL CELL AND CANCEROUS CELL AREA RANGE CLASSIFICATION TABLE

S.No	Cell	Area Range
1	Normal Pap Smear Cell	below 201
2	Abnormal Pap Smear Cell (or) Cancer Cell	above 200

Basically, how was the cancer might detected means, Mainly it depends upon decreased or increased area value of the region of interest (ROI) that is nucleus.

Then how can I found the ranges of the area value of the nucleus, purely it was fully based on the results of tested more than 200 number of Pap Smear Cells samples.

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 the feature like area value of the region of interest for finding the given cell is normal or abnormal. Hence the resultants reports will be very useful to the pathologists for their further reference.

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