CANCER CELL PREDICTION IN BLOOD SAMPLES

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ABSTRACT—Cancer is the malignant neoplasm involves abnormal cell growth with potential to invade or spread to the other parts of body. Cancer diagonosis requires examination of tissue sample by traditional method which is time consuming.In this paper, we present a new hybrid and semi-automated cell segmentation algorithm. It consist of cell profile generation , cell nuclei isolation, & cell cytoplasm separation. We apply watershed transformation on tissue in combined with histogram based global approach like Histogram stretching and Histogram Equilization.The experimental results demonstrate the cytological evaluation of cells in blood samples.

Keywords— Cell segmentation, Watershed transformation,Global histogram, cytopathalogy.

I. INTRODUCTION

Cancer is a class of diseases characrerised by out of control cell growth.Their are over 100 different types of cancer and each is classified by the type of cell that is initially affected.Cancer harms the body when damaged cells devide uncontrollabely two form lumps or masses of tissue called tumors. Tumers can grow and interface with the digestive,nervous and circulatory sestems,and they can realese hormones that alter the body function. there are two types of tumors that are benign tumor and malignant tumor. benign tumors are not malignant that is they are not harmful whereas malignant tumors are harmful.

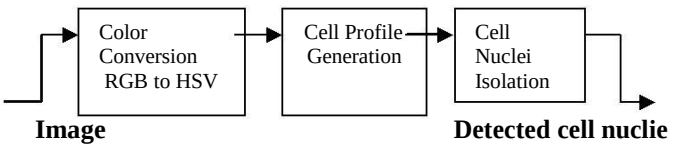
In examining of precancerous changes in the functioning or texture of an organs, cytopathological tests are regularly used to detect abnormalities in the acquired cells.To detect abnormalities in size and shape of the nucleus,Segmentation of the nucleus from the cell background is performed manually or by semiautomated methods. Precise evaluation of abnormalities in the nuclei of cells is quite complicated even though some automated test procedures have been advanced.Hence, manual evaluation is still practice, although it is a time-consuming process. separating foreground objects from background objects is the main aim of segmentation. When the foreground and background objects are detected, the boundary between them can be reached by techniques which depends on either the global difference between foreground and background objects, such as intensity histogram thresholding or intensity-based clustering.Using only one approach for cell segmentation may not provide acceptable results in real applications.To avoid these, we proposed a new hybrid method to perform cell segmentation. To segment an image, we generate a “cell profile”, using watershed-based k-means clustering.This cell profile is a separation of the cell that is the nuclei and cytoplasm from the image background. Then we detect cell nuclei using global histogram thresholding. Next, we use watershed-based clustering, to combine cytoplasm in cell profiles

with individual cells. With this semi-automatic algorithm, we are able to reckon both boundaries between cells and boundaries between nucleus and cytoplasm within the same cell.

In present paper, we proposed a new semi-automated cell segmentation algorithm. The technique is then followed by histogram based global approach with local watershed segmentation. Accurate representation of cell nuclear structure can be obtained by using these techniques. The principles that are used in this paper are based on image processing tools such as image enhance- ment which includes filter & noise removal and image segmentation. The time factor was taken into account to discover the abnormality issue in target images. Image quality and accuracy is the core factor of this research. Our proposed technique gives very promising results comparing with other used techniques.

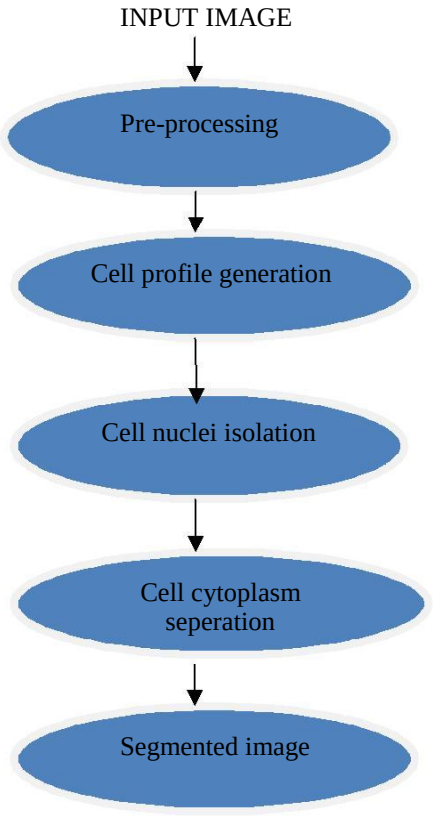
II. OVERVIEW OF PROPOSED SCHEME

In our proposed approach we first take an input image of blood sample The original image is generally in the Red-Green-Blue (RGB) color space. This original image of blood sample is then converted to High Saturation Value (HSV) color space.RGB image to HSV image is then next followed by cell segmentation which is performed by watershed algorithm. Cell profile is generated using k-mean clustering. It separates nuclei and cytoplasm from image background. Then, cell nuclei is detected using global histogram thresholding which then followed by nuclei labeling. In next section, cell cytoplasm is extracted by using watershed segmentation. After this, nuclei-oriented clustering is done. Boundary formation between nucleus and cytoplasm in each cell is generated. Steps will be described in detail in the following sections:



III. METHODOLOGY

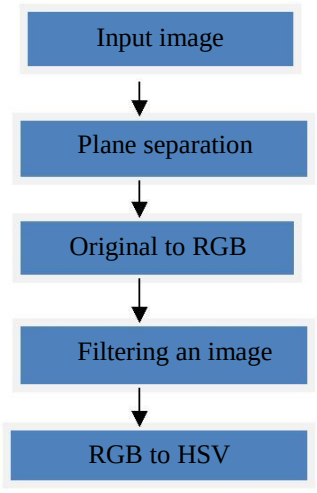
In this, we describe the algorithm for Cell Segmentation.



Basically, methodology is the systematic , theoretical analysis of the methods applied to the field of study. In this an images are categorized in three parts that are cell ,mask and label. I is used to represent an images of cell which may be a gray-level images or a RGB color images. M is used to represent a mask images. A mask images is simply an image where some of the pixel intensity values are zero, and others are non-zero. L is used to represent a label images which are used to generate a boundaries in the final segmentation result. Methodology are followed by five steps that are

1. Pre-processing.
2. Generation of cell profile.
3. Cell nuclei isolation.
4. Cell cytoplasm separation.
5. Post-processing.

1. Pre-processing :



The main aim of pre-processing is to generate an suitable image for subsequent steps. In pre-processing first an original image is converted into a RGB (Red-Green-Blue) color space. However, RGB color space is not favourable for image processing. Because in RGB color space the intensity information is spreaded in all three dimensions. So, the RGB image is converted into a HSV (Hue-Saturatoin-Value) color space to re-generate the intensity information to one dimension that is in only V dimension. The main task in pre-processing is to transformed RGB image IRGB to HSV image IHSV, and the IV component IHSV is used for watershade segmentation.

To convert RGB to HSV image we are using median filter. Median filtering is a nonlinear method used to remove noise from images. It is widely used as it is very effective at removing noise while preserving edges. It is particularly effective at removing 'salt and pepper' type noise. The median filter works by moving through the image pixel by pixel, replacing each value with the median value of neighbouring pixels. The pattern of neighbours is called the "window", which slides, pixel by pixel over the entire image 2 pixel, image. The median is calculated by first sorting all the pixel values from the window into numerical order, and then replacing the pixel being considered with the middle (median) pixel value. This is used for the watershed segmentation

2. Generation of cell profile :

Cell profile generation is followed by three steps-

Watershed segmentation.
K-means clustering.
Generation of cell profile based on K-means clustering

2.1 Watershed Segmentation

The watershed transformation takes its origin from the topographic interpritation of the gray scale image. The watershed are the zones dividing adjacent catchments basins. In numerical implementation of the watershed algorithm the original image is transformed. IV which is generated from step one is given as the input to this step. By filtering an IV component of IHSV we get a gradient magnitude image i.e. IVGM .

2.2 K –means clustering

K- means clustering is a method of vector quantization , that is popular for cluster analysis.K- means clustering aims to partition n observations into k cluster in which each observation belongs to the cluster with the nearest mean. K-means clustering uses a median in each dimension instead of mean. To produce cell profile, K-means clustering is used for collecting regions belonging to cell. For K-means clustering there are two important parameters are needed and that are : the number of clusters and the every small part is generated by watershed segmentation i.e the feature vector of each sample. In our method the number of cluster is set to 3. If the cluster number is set as 2,few region known as cytoplasm region will be clustered into the background cluster.

2.3 Generation of cell profile

After completion of k-means method this step produce a three unidentified clusters of the region Which implies that we don't know which one is the cell cluster and which one is the background cluster.From the image IV,it can be

seen that the nuclei region of the image have the lowest brightness while the background region of the image have a higher brightness . It can also observed that the cytoplasm region of the image have the intensities between the background region and nuclei region. So the clusters having the lowest and second lowest i.e an average intensity are known as the " cell cluster". To separate the cell content i.e nuclei and cytoplasm the corresponding regions or parts are combine to generate the cell profile mask MCELL and the corresponding cell profile image IV-CELL from the IV component of IHSV .

3. Cell nuclei isolation:

The main aim of cell nuclei isolation is to separate a nuclei of the cell from cell profile image IV-CELL which is the result of the step2.

3.1 Histogram Transform

Histogram transformed is the method in image processing of contrast adjustment using an images histogram . This method generally increases the global contrast of many images , especially when the image is represented by close contrast values. In histogram equalization intensities are better distributed. This allows for areas of local contrast to gain a higher contrast. This method is useful in images with backgrounds and foregrounds that both bright or both dark.

Due to low contrast between the nuclei and cytoplasm it is difficult to separate a nuclei from cytoplasm . Hence, a histogram equalization and histogram stretching is used to increase the contrast between the nuclei and cytoplasm and further improve the effect of histogram thresholding. Histogram stretching and histogram equalization are performed on the image IV-CELL independently , which further produce the histogram stretching result IV-CELL-HS and the histogram equalization result I V-CELL-HE . Then the equation is given by-

IA1 = IV-CELL-HS + IV-CELL-HE

IA 2 = IA 1 - IV-CELL-HE

IA 3 = IA 1 + IA 2

The resulting image I A3 has a wider intensity than an original image I CELL.

3.2 Histogram thresholding based on intensity stretched images

The threshold for nuclei isolation is obtained by otsu's method. Ostu's method is used to performed clustering based image thresholding or a reduction of gray level to binary level. To minimize the difference between two cluster we use ostu's method that find the single threshold i.e the difference between the nuclei and cluster .

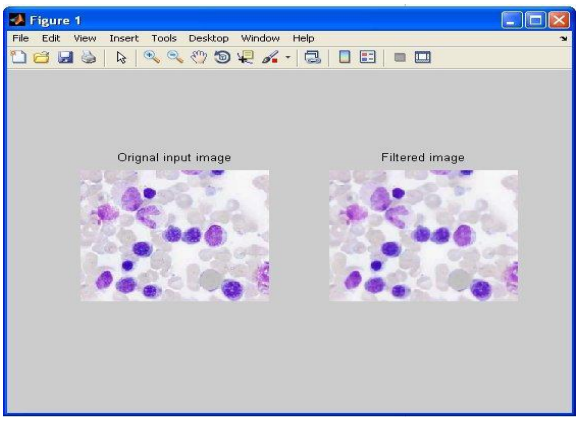
3.3 Labeling of nuclei based on histogram

Based on image IA3 we perform a global histogram thresholding to obtain a mask Mn .

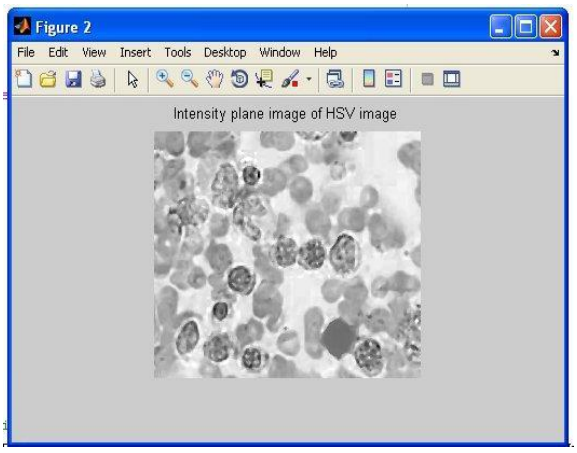
IV.RESULT AND OBSERVATION

The proposed techniques has been applied on tissue samples. Following results are obtained:

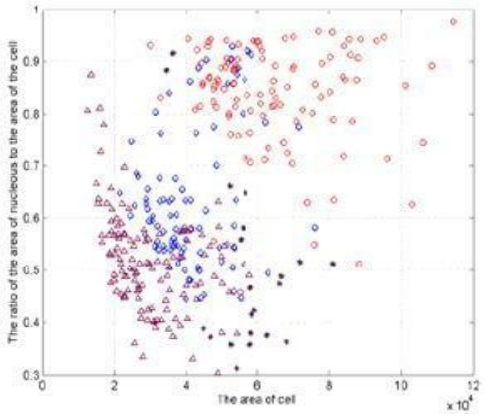
A.Different Position of cancer cells



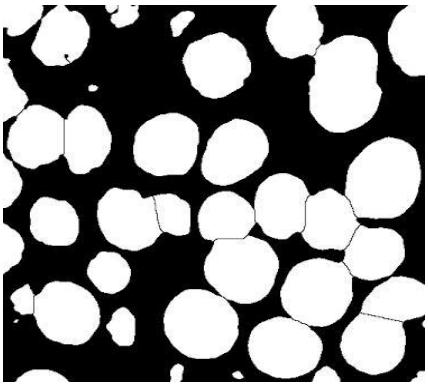
B. HSV Image



C.The distribution of cell locations in the plane formed by 2 geometrical features.



D. Segmented image



V.CONCLUSION

Thus, cancer cells are detected using the new hybrid and semi-automated cell segmentation algorithm. The proposed technique is efficient for segmentation principle. The time factor was taken into account to discover the abnormality issue in the target images. Image quality and accuracy are the core factors of this research.

VI.REFERENCES

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