DETECTION OF CANCER CELL IN BLOOD SAMPLES USING AN EFFECTIVE ALGORITHM

[1]Ms. Sneha Dhakne, [2]Ms. Kumudini K. Borkute, [3]Ms. Priyanka Ikhar
Department of Electronics Engineering
Rajiv Gandhi College of Engineering and Research,Nagpur.
Maharashtra

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 consists of cell profile generation cell nuclei isolation, & cell cytoplasm separation. It consist of preprocessing stage for image conversion followed by watershed transformation on tissue in combined with histogram based global approach like Histogram stretching and Histogram Equalization It also includes K-mean clustering algorithm to determine boundary conditions. The [performance parameters like speedup factor and PSNR gives the efficient evaluation of algorithm. The experimental results demonstrate the cytological evaluation of cells in blood samples.

Keywords- Cell segmentation, Watershed transformation, Global histogram, cytopathalogy, clustering .

I. INTRODUCTION

Cancer is the second leading cause of death worldwide in which greater than 90% of deaths in cancer patients are ascribed to metastasis. Cancer is considered a localized disease in its early stage; however, it has often become systemic by the time a patient becomes indicative and the disease is detected by the currently available imaging technology such as traditional radiography (X-ray), magnetic resonance imaging (MRI), computed tomography (CT), positron emission tomography (PET), or ultrasound. There is growing evidence that cancer cells are shed from the primary tumor into the circulation prior to the presentation of clinical symptoms.

In diagnosis of a variety of precancerous lesions, cytopathological tests are consistently used to detect abnormalities in the acquired cells. Segmentation of the nucleus from the cell background is performed, either manually or by using a semi automated methods, to detect abnormalities in size and shape of the nucleus. Although some automated test procedures have been developed over the past few decades, accurate evaluation of abnormalities in the nuclei of cells is quite difficult.

In examining of precancerous changes in the functioning or texture of organs, cytopathological tests are regularly used to detect abnormalities in the acquired cells. For detecting the abnormalities in size and shape of the nucleus segmentation technique was used. Segmentation of the nucleus from the cell background is performed manually or by semiautomated methods. But the effective evaluation of abnormalities in the nuclei of cells is quite complex even though some automated test procedures available in advance. Hence, manual evaluation is still practice, which is a time-consuming process. The separation of foreground

objects from background objects is the main aim of segmentation. When the foreground and background objects from cell nuclei 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.

Cancer a term used for diseases in which abnormal cells divide without control and are able to attack other tissues. Cancer cells can spread to other parts of the body through the blood and lymph systems. Cancer is not just one disease but many diseases. There are more than 100 different types of cancer. Most cancers are named for the organ or type of cell in which they start for example, cancer that begins in the colon is called colon cancer; cancer that begins in melanocytes of the skin is called melanoma. All cancers begin in cells, the body's basic unit of life. To understand cancer, it's helpful to know what happens when normal cells turn out to be cancer cells. The body is made up of many types of cells. These cells grow and divide in a controlled way to produce more cells as they are needed to keep the body healthy. When cells become old or spoiled, they die and are replaced with new cells. However, sometimes this orderly process goes wrong. The genetic material (DNA) of a cell can become damaged or changed, producing mutations that affect normal cell growth and division

Cancer is a class of diseases characterized by out of control cell growth. There 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 divide hysterically two form lumps or masses of tissue called tumors. Tumers can grow and interface with the digestive, nervous and circulatory systems and they can release hormones that alter the body function. There are two types of tumors classified as benign tumor and malignant tumor. benign tumors are not malignant that is they are not harmful whereas malignant tumors are harmful.

Using only one approach for cell segmentation may not provide adequate 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 background of an image followed by detection of 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.

This paper is systematized as follows: in the first part, we introduce our proposed cell segmentation method. In the second part, we describe our new hybrid method in detail.

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 by using preprocessing stage. .RGB image to HSV image is then next followed by cell segmentation follows the separation of foreground objects from background object which is performed by watershed algorithm. Steps will be described in detail in the following sections.
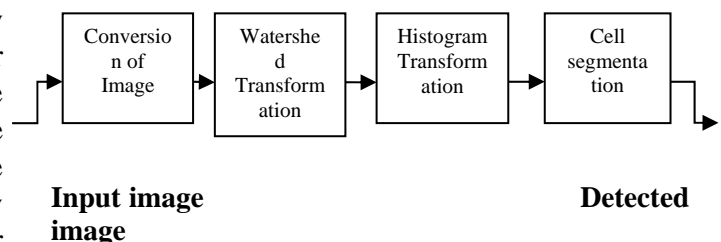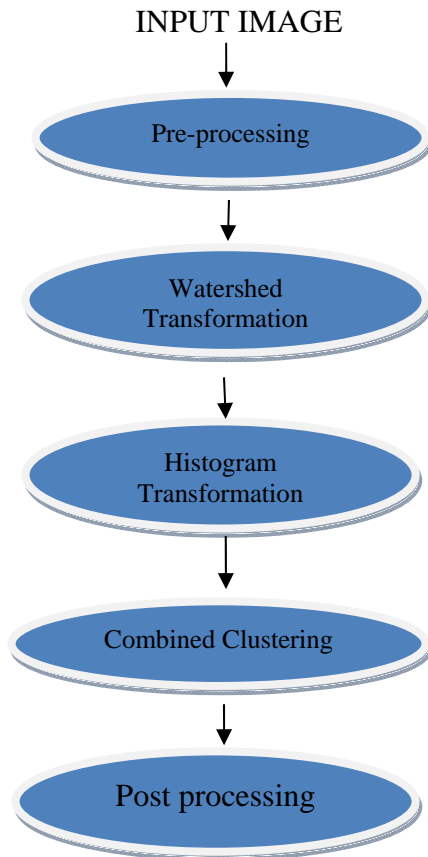

Input image   **Detected image**

Figure 1.   Overview of the proposed scheme.

III. METHODOLOGY

In this, there is description of the boundary formation.

INPUT IMAGE

Pre-processing

Watershed Transformation

Histogram Transformation

Combined Clustering

Post processing

Basically, methodology is the efficient, theoretical analysis of the methods applied to the field of study. The images are categorize in three parts which is called as cell, mask and label. I is used to represent an images of cell nuclei 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.

A. Development Environment

In this paper we are considering two algorithms; such as Watershed algorithm and Combine clustering along with filtering for determination of cell. The various output parameters are detected. The various steps are-
   i. Preprocessing stage for image conversion.
   ii. Segmentation of cell nuclei
   iii. Representation of Output parameters.

B. Pre-processing

Input image

Plane separation

Original to RGB

Filtering an image

RGB to HSV
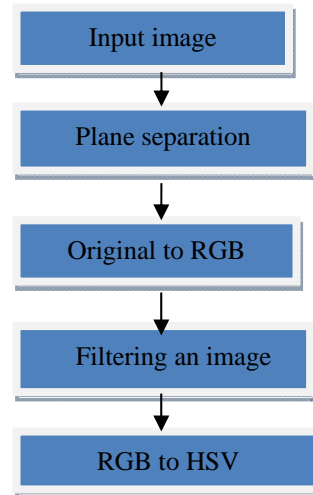
The main aim of pre-processing is to generate an suitable image for subsequent steps. In pre-processing first an original image is converted into a RGB (Red-Green-Blue) color space. However, RGB color space is not favorable for image processing. Because in RGB color space the intensity information is speeded in all three dimensions. So, the RGB image is converted into a HSV color space to re-generate the intensity information to one dimension. The main task in pre-processing is to transformed RGB image to HSV image.

To convert RGB to HSV image we are using median filter. 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.

C. Watershed Transformation

The watershed transformation takes its origin from the topographic interpretation of the gray scale image. The watersheds are the zones dividing adjacent catchments basins. In numerical implementation of the watershed algorithm the original image is transformed which is generated from step one and is given as the input to this step.

D. Histogram Transformation:

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.

Histogram transformation uses K-mean clustering method. K- means clustering is a method 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. K-means clustering is used for collecting regions belonging to cell.

E. Segmentation:

Segmenting the nucleus and cytoplasm is a very difficult task, as the images show heterogeneous staining and high-cell population. As described above edge detection and histogram transformation have been combined to extract the nucleus and cytoplasm of cells. These technique of segmentation is applied as the images shows uniform backgrounds and high contrast that appropriately defines the objects of interest.

F. Combined clustering:

Clustering refers to grouping together data objects so that objects within a cluster are similar to one another, while objects in different clusters are dissimilar. In combined clustering, two images are combined , first one is the segmented image and second one is the clustered image.

After combining both the images an image known as clustered image is obtained.

G. Post processing:

The objective of post-processing is to form both boundaries between different cells and the boundary between nucleus and cytoplasm within each cell. Formation and maintenance of boundaries between neighboring groups of cells must often be kept to distinct groups of cells with different functions.
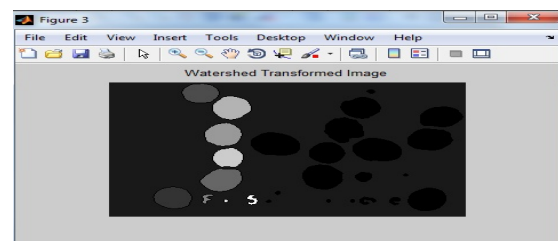
IV RESULT

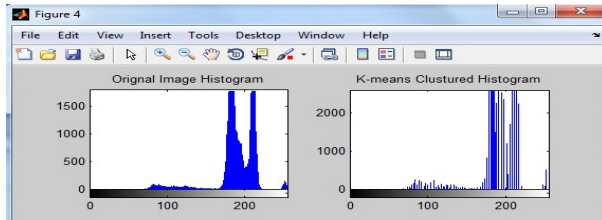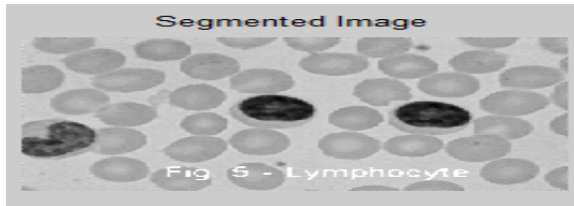### A) Different Positions cancer cells in Blood Samples
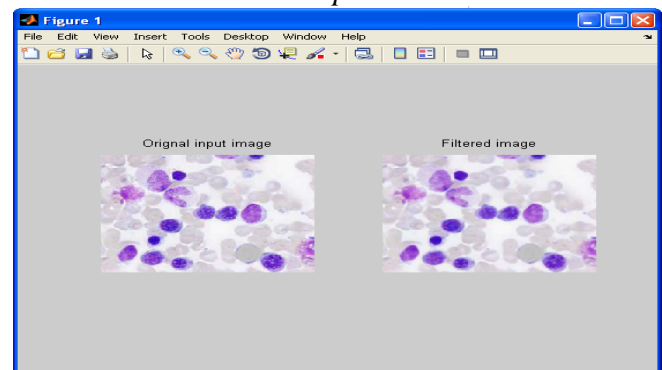
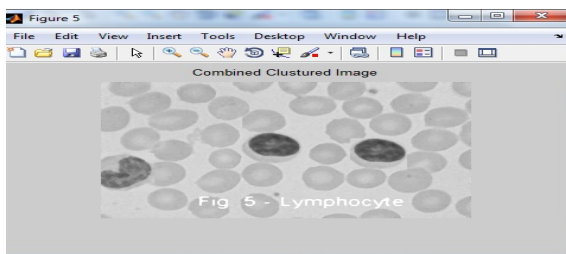### B. HSV Image
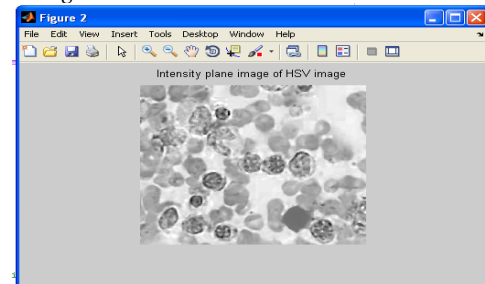
D. Watershed image

E. Histogram image

F. Segmented image

G. Combined clustering 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 FUTURE WORK

We are approaches towards the determining output parameters as a PSNR and Speedup factor.

REFERENCES

[1] H.T. Madhloom, S.A. Kareem, H. Ariffin, A.A. Zaidan, H.O. Alanazi, B.B. Zaidan, "An automated white blood cell nucleus localization and segmentation using image arithmetic and automatic threshold", Journal of Applied Sciences, Vol. 10, pp 959-966, 2010.

[2] P. Quelhas, M. Marcuzzo, A.M. Mendoca, A. Campilho, "Cell Nuclei and cytoplasm joint segmentation using the sliding band filter", IEEE Transactions on Medical Imaging, Vol. 29, No. 8, pp1463-1473, 2010.

[3] A. Jain, "Data clustering: 50 years beyond k-means," Pattern Recognition Letters, vol. 31, no. 8, pp. 651 – 666, June 2010.

[4] W. Zhao, H. Ma, Q. He, "Parallel K-Means Clustering Based on MapReduce," in: Cloud Computing, vol. 5931, pp. 674-679, 2009.

[5] W. D. Arthur, S. Vassilvitskii, "K-means++: the Advantages of careful seeding," in Proc. 2007 Symposium on Discrete Algorithms, pp.1027-1035.

[6] R. Ghafar, N. A.Mat Isa, U.K. Ngah, M.Y. Mashor, N.H.Othman. "Segmentation of Stretched Pap Smear Cytology Images Using Clustering Algorithm", Proceedings of World Congress on Medical Physics and Biomedical Engineering (WC2003), Paper No. 2356. Vol. 4, 2003.

[7] P. Soile, "Morphological image analysis, principles and applications", Springer, Berlin, 2003

[8] L. Olivier, E. Elmoataz, C. Hubert, G. Gilles, L. Michel, E. Hubert, R. Marinette, "Segmentation of cytological images using color and mathematical morphology",Acta Stereologica, Vol. 18 , No. 1, 1999

[9] Matlab user manual – Image processing toolbox, MathWorks, Natick, 1999.

[10] T. Wagner, "Texture analysis" (in Jahne, B., Haussecker, H., and Geisser P., (Eds.), Handbook of Computer Vision and Application), Academic Press, pp. 275-309, 1999

[11] D. Lowe, "Object recognition from local scaleinvariant features," in ICCV, 1999, pp. 1150–1157.

[12] V. Vapnik, "Statistical Learning Theory", Wiley, N.Y., 1998.

[13] Y.J. Zhang "A survey on evaluation methods for image segmentation", Pattern Recognition 29 (8) (1996) 1335 - 1340

[14] W. Wolberg, W. N. Street, O. L. Mangasarian, "Machine learning to diagnose breast cancer from image-processed features", Rep. of Uni. Wisconsin, 1994 .