Volume 2, No. 4, April 2011
Journal of Global Research in Computer Science
RESEARCH PAPER
Available Online at www.jgrcs.info
ISSN-2229-371X

METHOD FOR BLOOD CELL SEGMENTATION

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Abstract*The analysis of blood cells in microscope images can provide useful information concerning the health of patients; however, manual classification of blood cells is time-consuming and susceptible to error due to the different morphological features of the cells. Therefore, a fast and automated method for identifying the different blood cells is required. In this paper, we propose a method to segment nucleus and cytoplasm of white blood cells (WBC). In this work, we segments cell images with varying background and illumination condition is designed. The results of segmentation show the better performance in comparison to the conventional methods. Experimental results suggest that the proposed method performs well in identifying blood cell types regardless of their irregular shapes, sizes, and orientation.* **Key Words** Biomedical Image Processing, White blood cell detection, Segmentation, and feature extraction

INTRODUCTION

Cell segmentation is a challenging problem due to both the complex nature of the cells and the uncertainty present in video microscopy. Manual methods for this purpose are onerous, imprecise and highly subjective, thus requiring automated methods that perform this task in an objective and efficient way.

Biomedical image processing is a major field of research in the current times. Constructing an automated medical diagnosis system that can assist a physician is a significant contribution in this field. Building such an automated system requires confluence of many diversified research activities, of which image processing is a major player. One of the primary tasks of a physician in examining a patient is to conduct a blood test.

Blood carries out many vital functions as it circulates through the body. It transports oxygen from the lungs to other body tissues and carries away carbon dioxide. It carries nutrients from the digestive system to the cells of the body, and carries away wastes for excretion by the kidneys. Blood helps our body fight off infectious agents and inactivates toxins, stops bleeding through its clotting ability, and regulates our body temperature.

Doctors rely on many blood tests to diagnose and monitor diseases. Some tests measure the components of blood itself; others examine substances found in the blood to identify abnormal functioning of various organs. Hence, we here propose system which will assist pathologists to detect blood cell count based on segmentation and help to find out the diseases. This information can be very helpful to a physician who, for example, is trying to identify the cause of a patient's diseases.

Automated detection and classification of white blood cells is a major step in diagnosis of several diseases like Acute Lymphoblastic Leukemia. The traditional procedure requires a haematologist to manually count and classify the cells with the help of a microscope.

In traditional terms, blood cell analysis i.e. complete blood cell count (CBC) is done as a "convention". In which it measures the red blood cells, white blood cells usually assesses the size and shape of red blood cells as per old delayed procedures.

Blood examination provides quantitative information useful for life study and early evaluation of the patient's health status. Traditionally, the haematologist counted the number of white blood cells (WBC) from a slide smeared with peripheral blood or bone marrow, for the purpose of diagnosis and screening. The haematologist would manually count 100 white blood cells with the help of a microscope and then calculate the total occurrence of each type of cell. This is called as differential blood count (DBC). This task is time consuming, complex and tedious [4-6].

Also, the recognition accuracy largely depends on subjective factors like experience and fatigue due to human tiredness. With the increasing demand for more number of such examinations along with the need for quality results, there arose a necessity for the automation of the whole process. This not only reduced the burden on haematologists but also yielded accurate results in significantly short period of time.

An automated diagnosis system will alleviate the workload and the influence of subjective factors [7-8]. Automated detection involves removal of red blood cells and platelets from the background. The main drawback of the existing methods is their inefficiency in handling cell images originating from different sources and environment.

In this paper, we propose a method to segment nucleus and cytoplasm of white blood cells (WBC). WBC composition of the blood provides important information to doctors and plays an important role in the diagnosis of different diseases. We use simple morphological operators and explore the

scale-space properties of a toggle operator to improve the segmentation accuracy. The proposed scheme has been successfully applied to a large number of images, showing promising results for varying cell appearance and image quality, encouraging future works.

REVIEW WORKS

White blood cell segmentation from the cell image background involves subtraction of red blood cells, platelets and other objects mixing in the microscopic images. Illumination inconsistencies and cell occlusion are the main reasons that make cell segmentation challenging [1-2].

Cell classification has widespread interest especially for clinics and laboratories. For example, patient's blood cells counting is use to extract information about other cells that are not normally present in peripheral blood but may be released in certain disease processes by the haematologist [3].

Patient's blood cells counting were performed manually by medical technologists by viewing slide prepared with blood sample of the patient under microscope. A manual count will also give information about other cells that are not normally present in peripheral blood but might be released in certain disease [9].

Unfortunately, the accuracy of cell classification and counting is strongly affected by individual operator's capabilities. In particular, the identification and differential count of blood's cell is a time consuming and repetitive task that can be influenced by operator's accuracy and tiredness [8]. In an effort to overcome the tedious and time-consuming task of human experts in counting white blood cells in bone marrow or peripheral blood, many automated techniques have been proposed[10][11].

Thresholding was one of the earliest methods implemented for image segmentation. The simplicity of implementation and its intuitive properties gave image thresholding a central position in applications of image processing [11, 13]. In the case of cell segmentation, thresholding was followed by morphological operations in most of the cases [12, 14]. Thresholding is computationally cheap and fast.

Region-based approaches work on a certain criterion of homogeneity, usually of same or similar brightness or colour [15, 16]. All the pixels that satisfy the homogeneity criterion were grouped together into a region. These approaches include region splitting and merging approaches [15], seeded region growing approaches [16].

Model based approaches: In this approach, the nucleus and the cytoplasm are extracted by building models. The cell model must include features that discriminate leukocyte regions from others and, intuitively encourage the formation of round, homogeneous regions of certain size [17].

Fuzzy methods have gained sufficient significance in recent times and are now used in major image segmentation techniques. In [18-19], fuzzy technique was used with the aim to allow a good processing of both vagueness and in determination characteristics of images, and the analysis of monochrome instead of colour images.

Jianhua et al. [21] stated that in the case of cell segmentation for blood, edge detection performs poorly on cell images because not all boundaries are sharp and it is difficult to get all edge information and locate cells accurately. They developed an iterative Otsu's approach based on circular histogram for the leukocyte segmentation. Otsu's approach is generalized on the base of least square method.

R. Sukesh Kumar et al. [22] discussed about an approach for colour image segmentation using higher order entropy as a textural feature for determination of thresholds over a two dimensional image histogram. Two basic models for colour images are the RGB (Red, Green, Blue) colour model and the HIS (Hue, intensity, saturation) colour model. Two methods of colour image segmentation used RGB space as the standard processing space. These techniques might be used in blood cell image segmentation. Colour images are very rich source of information, because they provide a better description of a scene as compared to gray scale images. Hence, colour segmentation becomes a very important issue [22].

Colour image segmentation in HIS space requires conversion from RGB space to HIS space since maximum digital colour images are available in RGB format readily for segmentation in RGB space. Two algorithms have been proposed which are Non-Exclusive R, G, B segmentation and Exclusive R, G, B segmentation.

Segmentation of an image into more regions would mean that there are multiple thresholds for the image. Region would be defined as a set of points having intensity values between two consecutive thresholds. This concept of multilevel thresholding has been implemented as an extension of entropy which would yield a set of thresholds instead of the conditional maximum giving a single threshold. The above algorithm has been applied to gray scale and colour images where the regions obtained are filled with different shades depending on the thresholds. The number of thresholds is also optimized [22].

Khoo Boon et al. [23] performed comparisons between nine image segmentation which is gray level thresholding, pattern matching, morphological operators, filtering operators, gradient-in method, edge detection operators, RGB colour thresholding, colour matching and HSL (hue, saturation, lightness) and colour thresholding techniques on RBC and concluded that there is no single method can be considered good for RBC segmentation [23].

PROPOSED METHOD

In blood cell image detection, the task is usually split into two stages; one is image enhancement, for the purpose of reducing noise, and the other is detection of blood cell characteristics. In our proposed stage, image filtering and enhancement is one part of stage and the detection in the later stage. Convolution filtering is often used to reduce the effects of noise in images or to sharpen the detail in blurred images. Counts are calculated by scanning the image and using Edge Detection Algorithm. The original blood image is shown in figure 1.

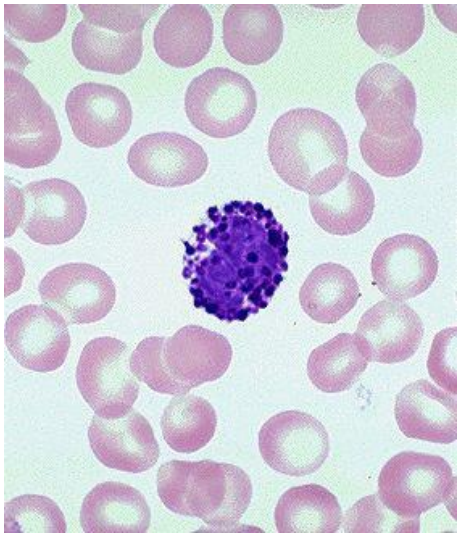


Figure 1 Original Blood Image

Cell segmentation involves removal of background comprising red blood cells, platelets, and other objects from the image acquired. White blood cells, the objects of interest, come as the output of the segmentation process. Accurate segmentation should yield the complete white blood cell, including the cytoplasm and the nucleus. The shape of the nucleus, its texture, area, and the ratio of its content in the cell are some of the features that are required to categorize the cell.

Image segmentation is the most important step and a key technology in image processing, and it will directly affect subsequent processing. With mathematical theories, image segmentation has achieved great progress and a lot of novel segmenting algorithms have been proposed. But most algorithms have their own drawbacks. As for cell images, owing to the complex nature, it still remains a challenging task to segment and count them.

Noise is any undesirable signal. Images are usually degraded by various noises in the signal transmission, coding and decoding processing. The results of image processing such as image segmentation, feature extraction and image recognition will to a great extent depend on the noise removal results. So de-noising an image is of great importance in image processing.

Noise is everywhere and thus we have to learn to live with it. Noise gets introduced into the data via any electrical system used for storage, transmission, and/or processing. In addition, nature will always plays a "noisy" trick or two with the data under observation. When encountering an image corrupted with noise you will want to improve its appearance for a specific application. The techniques applied are application-oriented. Also, the different procedures are related to the types of noise introduced to the image. Some examples of noise are: Gaussian or White, Raleigh, Shot or Impulse, periodic, sinusoidal or coherent, uncorrelated, and granular.

The Gaussian smoothing operator is a 2-D convolution operator that is used to `blur' images and remove detail and noise. It uses a kernel that represents the shape of a Gaussian (`bell-shaped') hump.

The idea of Gaussian smoothing is to use this 2-D distribution as a `point-spread' function, and this is achieved by convolution. Since the image is stored as a collection of discrete pixels we need to produce a discrete approximation to the Gaussian function before we can perform the convolution. In theory, the Gaussian distribution is non-zero everywhere, which would require an infinitely large convolution kernel, but in practice it is effectively zero more than about three standard deviations from the mean, and so we can truncate the kernel at this point. Once we obtain a suitable kernel, then the Gaussian smoothing can be performed using standard convolution methods.

In median filtering, each pixel is determined by the median value of all pixels in a selected neighbourhood (mask, template, and window). The median value m of a population (set of pixels in a neighbourhood) is that value in which half of the population has smaller values than m, and the other half has larger values than m.

This class of filter belongs to the class of edge preserving smoothing filters which are non-linear filters. These filters smooth the data while keeping the small and sharp details.

Median filtering is a simple and very effective noise removal filtering process. Its performance is particularly good for removing shot noise. Shot noise consists of strong spike like isolated values.

In our paper we use Gaussian filer for removing noise, since it produces better results than median filtering.

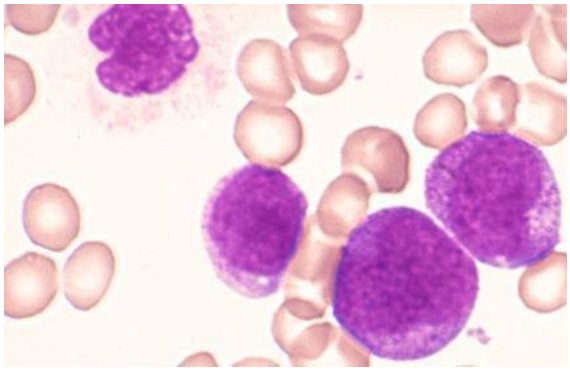
In this paper we propose segmentation scheme for Segmentation of blood cell. We start by identifying the left pixel of the blood image from the image map. We then draw a line vertically from top to bottom identifying the left boundary of the blood cell. We then scan the right side to locate the rightmost pixel on the particular blood cell. After the pixel is located we draw another vertical line from top to bottom passing through the rightmost pixel. This process optimizes the algorithm and increases the processing efficiency. At this stage we try to segment all blood cells that are circular or terminate either on the left base line or the bottom of the image, forming a closed structure. This process removes all noise and discrete objects from the edge map that are inconsequential to the image.

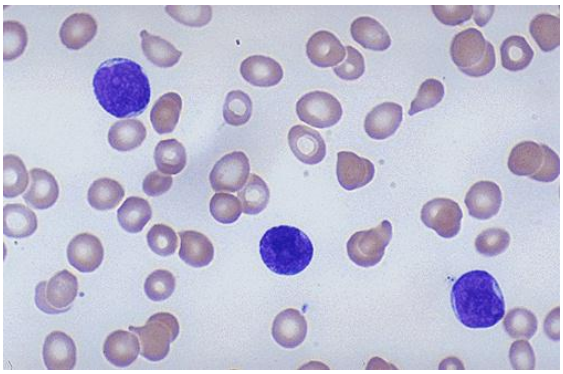
We start by locating all the cells that originates from the top margin line namely the first row of the image. The algorithm travels each individual path and stores them on the plotting list. This list is plotted on another image if the cell is circular or end on the last row of the image or the vertical line representing the left boundary of the cell. After all pixel paths on the first row are traversed the algorithm repeats similar scanning and traversal of all pixel paths from the row that is indicated by dividing the image vertically into segments.

ALGORITHM 1:

Step 1. Scan the image from the Left side of the image to locate the leftmost pixel of the cell region.
Step 2. Draw a vertical line along this pixel from top to bottom representing the Left baseline or boundary.
Step 3. Scan the image from the right side of the image to locate the rightmost pixel of the Cell region.
Step 4. Draw a vertical line along this pixel from top to bottom.
Step 5. Partition the obtained rectangle horizontally into sixteen segments and start with the first row of the first segment.
Step 6. Scan the enclosed rectangle from the right side to left, from the first row of the segment.
Step 7. Obtain a pixel that is black indicating an edge path, traverse the pixel path by considering all the surrounding pixels in a clockwise priority and consider the pixel with the highest priority.
Step 8. The pixels that surrounded the cell pixel, but are of lower priority are stored in a Stack to be used only if the traversal process reaches a dead end.
Step 9. If a dead end is reached, continue with the traversal process.
Step 10. Store the pixels traversed in a Plotting List for plotting.
Step 11. Traversal continues to the next pixel till it reaches the left baseline or the bottom of the image or the start position is reached.
Step 12. If the traversal is terminated, the plotting list is erased and continues from Step7.
else plot pixels from the Plotting List.
Step 13. Continue to Step6 till all blood pixels, indicating an close path, is traversed.
Step 14. Move to the first row of the next segment and continue from Step6 to Step11.
Step 15: Stop

The output of the algorithm is shown in figure 2 below.





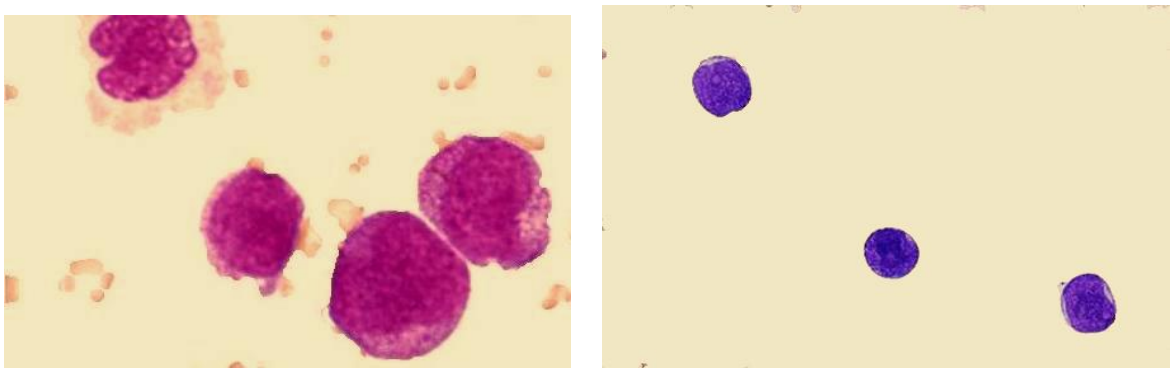


Figure 2 Proposed Algorithm applied on differently stained cell images. The left hand side shows the original images and the right, their corresponding segmented images.

CONCLUSION

The ultimate goal of blood cell segmentation is to extract blood cell's image from complicated background and to segment every cell into morphological components such as nucleus, cytoplasm, holes and some others. The main objective of this study is to develop system on blood cell segmentation. I would like to express my sincere thanks to Pathologists for providing blood cells morphology.

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