



A REVIEW PAPER ON AN EFFICIENT METHOD FOR DETECTION AND CLUSTERING OF RED BLOOD CELLS IN DIGITAL IMAGES IN SICKLE CELL ANEMIA DIAGNOSIS

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ABSTRACT

There is group of blood disorders that causes red blood cells to become misshapen and break down. Sickle Cell Anemia is one of them. It requires consistent lab tests or imaging. In this paper, we propose image processing technique for analysis of red blood cells in blood smear samples of Sickle cell disease. It draws the contour plot for each cell to highly visualize the difference between Normal and Sickle cell. First, algorithm locates the point of interest and then shape adjustment algorithms are applied to get the best fit. This method examines each cell from cluster of several cells without any human interaction.

Keywords: cell contours, circumference fitting, level set, concave points, ellipse fitting, sickle cell.

I. INTRODUCTION

Cell morphology is the branch of biology that deals with structure of an organism or one of its parts irrespective of its function. Blood disorders can cause morphological changes in blood cells. Therefore blood morphology examination is a fundamental step in diagnosis of most common disorder, Anemia. Anemia causes due to insufficient number of circulating erythrocytes (Red Blood Cells). This happens when person's body does not able to produce enough healthy cells, destroys too many of them or may produce abnormal hemoglobin molecules. An abnormal hemoglobin molecule leads to structural changes in healthy erythrocytes, so they are not able to carry adequate oxygen and carbon dioxide to and from the tissues.

Normal erythrocytes are shaped like discs, biconcave with centers partly scooped out. They are soft and flexible so easily moves through very small blood vessels delivering oxygen through person's body. But in case of sickle cell anemia, erythrocytes become rigid, sticky and crescent shaped. Such cells can get stuck in small blood vessels which block the blood flow and oxygen through them. It causes pain, jaundice, shortness of breath, dizziness, Headaches etc.

Generally, the diagnosis of sickle cell anemia is done by retrieving information derived from a visual assessment of blood samples which gives an idea about the variations in size, shape and estimates of hemoglobin contents. These blood samples for microscopy analysis are prepared using dragging technique. Using this technique, more



cell groups are apparent in the samples due to the spreading process. The experiments did not consider cells that were overlapped during sample preparation because determining the cell types is quite difficult by considering only part of the cell contour. Therefore the sample preparation process can affect the quantity of overlapping erythrocytes in the images studied. Thus, the simple blood test is a tiresome and error-prone process which should be replaced by an effective, advanced and accurate technique to successfully diagnose the sickle cell disease. One such method can be prepared by using Image processing technique.

II. LITERATURE REVIEW

In the literatures, several techniques have been proposed to analyze erythrocytes and cell clusters in blood smear sample.

Xin Qi et al. [1], proposed a two-step algorithm that can separate touching cells in hematoxylin-stained breast tissue microarrays specimens. In the first step, the geometric centers of cells (seeds) are detected by using this single-pass with mean shift voting approach rather than iterative voting which gives efficient computation. Then the contour of each cell is obtained by segmentation process, performed using level set algorithm based on an interactive model. The whole disc is separated into connected components so that algorithm can run in parallel in multiple cores and then final segmentation is done by assembling all connected components. The algorithm was implemented using graphic processing units (GPU) which speed ups the entire segmentation procedure.

To detect an individual cells present in cell cluster, Nguyen et al. [2], proposed an approach based on natural feature of the cell. As the red blood cell is disc like structure, central point of cell has different value than background. Boundary-covering degree is applied to select potential central point. Single cell extraction is employed in order to estimate the average size of cell. Finally, by using clumped cell splitting algorithm, overlapping cells are divided into individual cell. Also this method is able to detect other distorted structures in blood smear image.

Most of these techniques are not applicable to relatively elliptically shaped cells.

In Shashi Bala et al. [3], sickle cell anemia detected and counted; an image processing techniques applied on RBC cell to count the normal and abnormal cells using Watershed Segmentation. Form factor is calculated for each cell to differentiate between normal and abnormal cell. Also contour plot of RBC cell drawn to highly visualize the RBC cell and Sickle cell.

Xiangzhi Bai et al. [4] implemented an algorithm which includes two parts: contour pre-processing and ellipse processing. The purpose of contour pre-processing is to smooth fluctuations of the contour, find concave points of the contour and divide the contour into different segments via the concave points. The purpose of ellipse processing is to process the different segments of the contour into possible single cells by using the properties of the fitted ellipses. Because concave points divide the whole contour of touching cells into different segments and different segments of one single cell have similar properties, the ellipse processing can separate the touching cells through ellipse fitting. This paper demonstrates a new way of using ellipse fitting to split the binary contour of touching cells.

S. Kothari et al. [5], presents a novel, fast and semi-automatic method for accurate cell cluster segmentation and cell counting of digital tissue image samples. Cluster segmentation is done in three steps. The first step involves pre-processing required to obtain the appropriate nuclei cluster boundary image from the RGB tissue samples.

The second step involves concavity detection at the edge of a cluster to find the points of overlap between two nuclei. The third step involves segmentation at these concavities by using an ellipse-fitting technique. Once the clusters are segmented, individual nuclei are counted to give the cell count.

Mojtaba Taherisadr et al.[6], extracts several features relating to shape, internal central pallor configuration of red cells and their circularity and elongation have been extracted and with the help of decision logic all those various types of red blood cells were classified into 12 categories.

J. Huang [7] used a method based on the theory of mathematical morphology combined with watershed algorithm. It uses two basic mathematical morphology operations: corrosion and expansion. The algorithm firstly use four neighborhood and eight neighborhood structures of overlapping cell image elements and morphologic in order to reduce the distortion of the red blood cells. By using continuous corrosion, separated cells are obtained which are thinner as compared their original size. Therefore to recover the separated cell diagram, expansion operation is performed which draws the divided line of overlapping area.

Gady Agam et al. [8], proposed a concept of k-curvature for determining point of interest. The first step in the proposed approach is improvement of sampled images by filtering additive random noise and increasing the effective sampling resolution. Then the chromosome contours are obtained and interesting points are detected on them. Each hypothesis checks several concurrent possible separation lines. Since the proposed approach is not connected tightly to chromosomes, it can be adopted for other applications where separation between overlapping objects is needed as in case of our study.

Manuel Gonzalez-Hidalgo et al. [9], proposed a method for the analysis of the shape of erythrocytes in peripheral blood smear samples of sickle cell disease, which uses ellipse adjustments and an algorithm based on concept of k-curvature for detecting notable points.

III. PROPOSED METHODOLOGY

In proposed work, detection process is applied on digital images of peripheral blood smear samples. Overall process of proposed system is shown in fig.1.

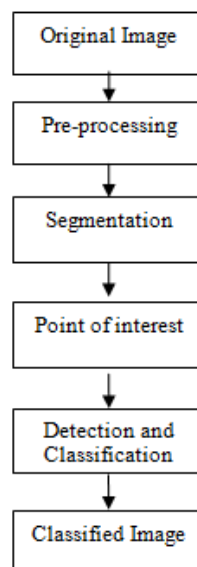


Fig. 1 Flowchart of proposed system



Image segmentation is used for blood cell identification within an image. Before that, preprocessing is done for removal of noise and to transform an image as necessity for further processing. Segmentation method detects the counters of separate and overlapped cells within an image. Level set method with automatic initialization based on grayscale intensities can eliminate the internal holes. These holes are due to composition of erythrocytes and more frequent at the center in normal erythrocytes.

After the cluster contours have been obtained, the algorithms used for concave point detection and for detecting each object in clusters are applied. Points of interest are located using concave point detection and then quantity of cells in cluster is determined. For detection of overlapping circular objects, we can use circumference adjustment algorithm. However, for overlapping elliptical objects, we propose the use of an ellipse adjustment algorithm.

Once the perfect adjustment is done, cells are marked with two different colors to classify them as either normal or sickle cell.

3.1 Locating points of interest

The cluster contour obtained by level set method contains number of overlapping cells, so first we have to locate the initial points where adjustment algorithms are going to be applied. Proposed work uses concave point algorithm which is based on previous k-curvature method [8] to locate the points of interest in a digital image of blood smear sample. K-curvature is found by taking difference between k-slope at that pixel and k-slope of its k^{th} left neighbor. Where, k-slope at contour pixel is defined as the slope of line connecting that pixel to its k^{th} right neighbor.

Proposed Algorithm for Locating Points of Interest:

1. Evaluate contour slope by connecting each pixel with its right neighbor; take its derivative with respect to length in x and y direction to get curvature function.
2. Take product of absolute values of curvatures in both directions.
3. Convert the values in binary form which generates small point sequences that corresponds to contour; take middle point of these sequences as point of interest.
4. Take neighbors of middle point which are at k^{th} position to the right and left, form a line joining them and take its midpoint.
5. If midpoint lies in interior part of contour, the point of interest exists on convex part of contour, but otherwise on concave. Use concave points of interest.

At the end of this algorithm, we get adjacent concave points. Pairs of adjacent concave points divide contours forming number of arcs.

3.2 Circumference Adjustment

As the normal erythrocytes are circular shaped, circumference adjustment is used to analyze circular objects in digital image. During this adjustment, after the concave points have been detected, the arches are taken between the pairs of concave adjacent points and the circumference is found with the best fit to this arch.

Proposed Algorithm for Circumference Adjustment

1. Take arc between pairs of adjacent concave points.
2. Find its radius.
3. Find circumference with best fit to that arc.



3.3 Ellipse Adjustment

Due to lack of oxygen carrying capacity, erythrocytes start elongating. So an ellipse can be used to represent a sickle cell. This ellipse is adjusted according to the adjacent concave points. An ellipse is obtained by performing a least square adjustment of an arc formed due to adjacent concave points. We can use parametric model of least square adjustment that relates the data obtained to the data predictors using one or more coefficients of the model. Several ellipses are found for same object. The best fit is selected based on percentage of object occlusion.

IV. CONCLUSION

The paper proposes an image processing technique for detecting and contour marking of both normal and sickle shaped blood cells. The proposed method will detect all the cells within blood cell samples in very short time. Cells are going to classify according to their rate of change of shape. For proper visualization of classification, contours will be marked with different colors.

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