Convex Hull Based Detection of Overlapping Red Blood Cells in Peripheral Blood Smear Images

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Abstract— **The Segmentation of Red Blood Cells (RBCs) in blood smear images to obtain their count is often the first step in the diagnosis of various pathological conditions. Although several procedures have been devised for this task, a majority of them suffer from performance degradation due to the overlapping of cells. Various researches have been carried out to split these overlapping cells. The proposed paper aims at suggesting two algorithms to find the concavity points in the overlapping RBCs' contours. In the first approach, the dip points are obtained by analyzing the concave regions, obtained by finding out the Euclidean distance of all points in the overlapping cell to their convex hull. In the second approach, dip point identification is based only on the convex hull of the overlapping cell. The contours of the concave regions are analyzed from the perspective of the centroid. These two strategies were compared with the approach used in an earlier work, which also addressed the splitting of overlapping RBCs, by identifying the dip points using curve fitting and smoothing of the contours. The two approaches proposed in this paper are quite efficient in terms of accuracy and the time taken to achieve results. The specificity of the first approach was 90% and that of the second approach was 94%, meaning that the two new methods are far more advanced than the earlier work for which the specificity was only 75%.**

Keywords— **Segmentation, convex hull, clumped RBCs, dip points.**

I. Introduction

The usual diagnostic approach in the study of blood disorders is to examine the blood film and obtain a total blood count. Obtaining the differential count of Red Blood Cells (RBCs) is vital in order to obtain the total blood count, RBCs in normal peripheral blood are circular and fairly uniform in size. They have a zone of central pallor about one third the size of the RBC. Though most of the RBCs are singular, few of them are found to be overlapping or clumped in groups. Various researches are carried out in splitting of overlapping cells. If intensity based segmentation was done. Overlapping objects may not be split [1] [2]. Hence a marker controlled watershed Transform may be used which split overlapping cells for which the regional minima were clearly identified [3]. Gametocytes touching RBCs were defected using distance transform of RBCs [4]. Various researches were carried out in segmentation using level set methods to detect overlapping objects. The contour of each cell is obtained using a level set algorithm based on an interactive model [5]. A shape-based approach is proposed to do curve evolution for the segmentation of medical images containing known object types [6]. A study to cluster the nuclei seen in confocal microscopy images was done using a clump-splitting algorithm

One recent common method used for segmenting overlapping or clumped cells is by doing their concavity analysis. A novel nonparametric concavity point analysis-based method for splitting clumps of convex objects in binary images is presented in [7]. The method is based on finding concavity point-pairs by using a variable- size rectangular window. Results obtained with images that have clumps of biological cells show that the method gives accurate results.

In peripheral blood smear images two or three RBCs overlap in various forms resulting into one or more concavities. In some of the overlapping cells, the gradient values in the overlapped region do not show remarkable difference compared to the other areas of the cell. Hence splitting them according to the concavity and convexity of the overlapped cells is more appropriate.

In one of the earlier works of the primary author, Watershed Transform was used to split such overlapping RBCs [8]. The Watershed Transform was able to split almost all the overlapping RBCs except for a few whose regional minima were not clearly identified. Such overlapped cells were split by obtaining dip points using concavity analysis [8]. The proposed work aims at suggesting two more algorithms to find the concavity points in the overlapping RBCs' contours. The first method obtains the dip points by finding out the Euclidean distance of all points in the contour of the overlapping cell to the centroid of the object. In the second approach, the dip points are identified by using the distance transform of all pixels within the convex hull of the overlapping cell. The work also compares both the approaches with the earlier work of the author, which uses

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curve fitting and smoothing of the contours in order to find the dip points.

The paper is organized with Methodology in Section II, Results and Findings in Section III and Conclusion in Section IV of the paper.

II. Methodology

A. Image Acquisition

The Images for the study were obtained using a digital camera attached to a compound microscope. These images are TIFF images of resolution 1024 x 1024. 150 such images have been used for the study.

B. First Approach

In the first approach, the convex hull of the overlapping cell is obtained. It is understood that the dip points may be found in the region where any two points in the convex hull are far apart. This is shown in Fig. 1. Therefore the Euclidean distance of all the points in the border of the overlapping cell between these two points to the centroid of the cell are computed. It is found that the point which has the minimum distance from the centroid is the dip point.

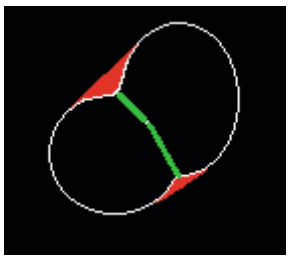

Fig. 1 Dip Points by First Approach

C. Second Approach

In the second approach, the Distance Transform of the region within the convex hull of the overlapping cell is obtained, resulting in the distance of the various pixels in the overlapping cell to the border of the convex hull. The points having minimum distance are marked, which are none other than the dip points of the overlapping cell.

III. Results and Findings

A prototype application was developed for testing the algorithms of both the approaches discussed. The input for the application was peripheral blood smear images. The overlapping cells that were not split by the Watershed Transform were identified as in [8]. The overlapping cells identified were tested for splitting by both the approaches. The step-by-step results are shown in Table 1. The results of these two approaches were compared with the results in [8]. It is seen that the approach in [8] used curve fitting and smoothing, which is a time consuming process. This was rectified in our approaches and hence the methods were made quite simple.

Table 1

1 Dip Point		**2 Dip Points**		**3 Dip Points**	
App 1	App 2	App 1	App 2	App 1	App 2
 Contour	 Contour	 Contour	 Contour	 Contour	 Contour
 Centroid	 Mask	 Centroid	 Mask	 Centroid	 Mask
 Convex Hull Pts	 Dist. Transfm	 Convex Hull Pts	 Dist. Transfm	 Convex Hull Pts	 Dist. Transfm
 1 Dip Point	 Concave Regions	 2 Dip Points	 Concave Regions	 3 Dip Points	 Concave Regions
 Split Cells	 1 Dip Point	 Split Cells	 2 Dip Points	 Split Cells	 3Dip Points

IV. Conclusion

The two approaches proposed in this paper are quite efficient in terms of accuracy and the time taken to achieve results. The specificity of the first approach was 90% and that of the second approach was 94%, meaning that the two new methods are for more advanced than the earlier work for which the specificity was only 75%.

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