AN ACCURATE SEGMENTATION METHOD FOR WHITE BLOOD CELL IMAGES

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Abstract—**This paper describes a part of our research work on an Automated Cell Count project. A major requirement for this project is an efficient method to segment cell images. This work presents an accurate segmentation method for automatic count of white blood cells. First a simple thresholding approach is applied to give initial labels to pixels in the blood cell images. The algorithm is based on priori information about blood smear images. Then the labels are adjusted with a shape detection method based on large regional context information to produce meaningful results. This approach makes use of knowledge of the blood cell structure. The experimental result shows that this method is more powerful than traditional methods that use only local context information. It can perform accurate segmentation of white blood cells even if they have unsharp boundaries.**

1. INTRODUCTION

There are many different classes of white blood cells present in blood smear images. Differential count of these various types of cells gives valuable information and plays an important role in the diagnosis of different diseases. It's a tedious task to count these classes of cells manually. An automatic counter using computer vision helps to perform this medical test rapidly and accurately. The first step of automatic analysis is segmentation of blood cell images, which differentiates meaningful objects from the background. In our case, we are attempting to identify white blood cells with an accurate segmentation method.

This step is crucial because the result is the basis of subsequent analyses. The success of classification depends mainly on the correct segmentation of images. It's also a difficult and challenging problem due to the complex nature of the cells and the uncertainty in the microscopic images. Cells often overlap each other and have variation of different sizes and shapes. The contrast between the cell boundary and the background varies according to illumination inconsistencies.

Many segmentation methods for blood cell images have been proposed. Histogram thresholding, edge detection and region growing methods are often used. Thresholding techniques always can't produce meaningful results since no spatial information is used during the selection of the segmentation thresholds. They are often combined with mathematical morphology operation [1][2][3]. Edge detection methods perform poorly on cell images because not all cell boundaries are sharp, so it's difficult to get all the edge information and locate the cells [4].

Most of these mentioned methods are one-short decision processes and often make wrong crisp decisions. Relaxation methods are proposed to avoid it. A fuzzy patch label relaxation algorithm used patches that provide more useful and meaningful context information than compact local context to obtain better segmentation results [5]. But sometimes the information of a few neighbor patches is still not enough to make correct decisions. For example, too bright illumination often leads to bright gaps inside cytoplasm, and then a part of cytoplasm may be labeled as red blood cell since it is separate from other parts of the cytoplasm and is similar to a red blood cell in position relationship. The neighbor patches play poorly on recovering this mistake. Hence a shape detection method is proposed to provide fast and accurate segmentation by using large regional context information (i.e. a relatively large region containing a whole white blood cell). Since more information is used to help make decisions, the approach is more robust and efficient.

In this paper we present a white blood cell segmentation approach that consists of three steps. First a simple thresholding approach combined with mathematical morphology operation is applied to give initial labels to pixels in the blood cell images. The algorithm is based on priori information about blood smear images derived from a learning process. Next the labels are adjusted with a shape detection method based on large regional context information, which makes use of knowledge of the blood

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cell structure. At last the regions of white blood cells are marked and the shapes of the regions are arranged to form rounded boundaries. The following sections give a detailed explanation of the proposed method along with some experiment results.

2. METHODS

2.1. Initial Segmentation

The goal of initial segmentation is to separate four different regions roughly: background, red cells, cytoplasm and nucleus. Information of colors, brightness and gradients are used in thresholding to create initial labels of the pixels. The bright white or yellow regions correspond to background. The dark regions correspond to nucleus. The regions that have intermediate brightness and small gradients correspond to red cells. Other regions are labeled as cytoplasm temporarily. Most thresholds are derived from priori information of blood smear images. But some sensitive thresholds should be selected automatically to adapt to the illumination variation, which greatly influence the segmentation result.

To select an optimal threshold, we change it from a smaller value to a larger one by a small step and segment the image with it. If the segmentation is correct with this threshold, the edges of the segmented image should have relatively large gradients, which correspond to the real edges of different regions. So we calculate the number of the edge points that have relatively large gradients while the threshold changes, and select the threshold that leads to the largest number of edge points to serve as the optimal threshold.

The regions labeled cytoplasm after thresholding are not real cytoplasm regions. They are repartitioned to three different parts according to their connection status with other components. Regions connected only with red cell regions are relabeled as red cell. Regions connected only with nucleus and regions connected with both are relabeled separately.

Every time the labels of pixels change, the different types of regions are smoothed with mathematical morphology operation to get connected regions and eliminate single points and lines caused by noises.

After initial labeling with thresholding method and morphology operation, the blood smear images are segmented roughly into four regions. Pixels that are sure enough to belong to background or nucleus are determined and other labels of pixels will be adjusted in the following steps.

2.2. Label correction with shape detection

Now the initial nucleus regions along with cytoplasm regions around them make up the initial leukocyte regions. They are not real leukocyte regions since there are many other regions in them such as red cell and stain regions, which may be connected with real leukocyte regions. Some of these false regions can be eliminated by a scan method.

Real leukocyte regions are connected regions with convex shapes. False regions may be connected with them, but there still will have some relatively large gaps between them (Fig.1). So when we scan the images in a certain direction, background regions will be detected between false regions and real regions. Separate regions in this direction can be eliminated. That is, although the false regions are connected with real leukocyte regions somewhere, they are separate in certain directions and can be detected by scanning in these directions.

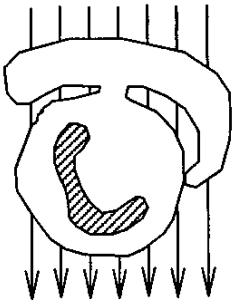


Fig.1 Scan to find separate regions

After the scan process a large region containing several white blood cells have been segmented out. Then we'll give accurate segmentation in smaller regions each containing a single white blood cell.

Nucleus regions are always in the center of the leukocyte. There are many "cytoplasm" regions around them, which may be labeled incorrectly. The real cytoplasm regions can be picked out with a regularity detection method. The distance from a boundary point of the cell to the center point of the nucleus is calculated to serve as the "radius". If a real leukocyte region is missed, a sharp decrease can be detected while we check the radiuses of boundary points in turn. If a false region is added into the leukocyte region, a sharp increase will be detected (Fig.2).

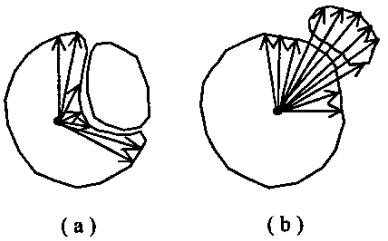


Fig.2 (a) Loss of leukocyte regions leads to sharp decrease of radius. (b) Additional leukocyte regions lead to sharp increase of radius.

These two cases both lead to great variation in radius. So the cytoplasm regions that together form a region with the least variation of the radius should be labeled real leukocyte regions.

2.3. Shape arrangement

Most pixels have been correctly labeled after the previous processes. But the unsharp boundaries between the cells and the background often lead to small regions around the white blood cells, which may be edge regions of the cells and influence the shapes of the cells. The labels of these small regions can be determined according to their positions.

Hough transformation is applied to find a circle in the image of edge points, which corresponds to the rough region of the cell. Small regions over this circle are added to the cell region and the small gaps inside cell regions are filled to form an orbicular shape of the cell (Fig.3).

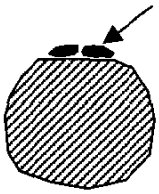


Fig.3 Small regions near the cell are added to the cell region

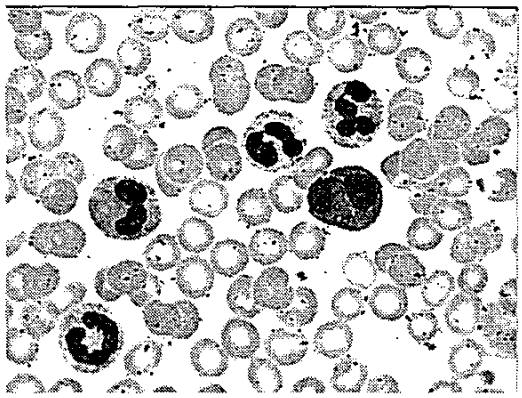
Although we adjust labels of points at every step to avoid making false segmentation, there is no guarantee that the segmentation results are correct all the time. So we identify the regularity of the final boundary of cells by calculating the variation of the radius. Great variation corresponding to an irregular shape means possible incorrect segmentation. The irregular edges are marked to remind users that these edges should be checked manually to avoid mistakes.

3. EXPERIMENTAL RESULTS

The method has been applied to 25 slides and 128 white blood cells have been segmented from background and overlapping red cells successfully. The boundaries of them have been traced out and irregular shapes are marked to avoid mistakes. Fig.4 shows the result of segmentation of one slide with 5 white blood cells in it.

4. CONCLUSION

The proposed shape detection method uses information from a large region that contains a whole white blood cell rather than information from a small local region or a few neighbor patches. Therefore it is powerful to obtain reliable and meaningful segmentation results and trace out accurate boundaries of white blood cells. Although the labels of pixels are adjusted step by step to avoid wrong crisp decisions that are difficult to be reversed, it is not an iterative approach, which makes it faster than most relaxation methods.



(a)

(b)

Fig.4 (a) Original image (b) Final result

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