

WBC Segmentation using Watershed and Snakes Algorithms for Diagnosis of Malaria

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Abstract— Malaria is a deadly disease caused by parasitic protozoans belonging to Plasmodium type, which is transmitted by an infected female Anopheles Mosquito. Due to sinuous nature of blood cells, it becomes arduous to detect malaria for Haematologists because of minuscule difference in size and geometry of white blood cells and red blood cells. It takes longer to diagnose and the method is susceptible to errors, so to solve these intricate diagnosis, concept of segmentation through active contours and watershed algorithm is proposed in this paper. This paper presents a new concept of detecting malaria on basis of active contours and segmentation of white blood cells from red blood cells. Firstly, on the basis of visage we differentiate WBCs and RBCs using active contours and watershed algorithm. Now, to distinguish between large sized white blood cells and red blood cells, snakes algorithm is used to determine the boundary of cells. This makes the proposed algorithm better in accuracy and time consumption as compared to classification performed by Haematologists.

Key words: WBC Segmentation, Malaria, Watershed and Snakes

I. INTRODUCTION

Malaria is a dangerous disease if not taken seriously in its early stage. When a female Anopheles mosquito bites, she lays parasitic protozoans of Plasmodium type which gets attached on the surface of RBCs. So, to diagnose this disease we need to manipulate the number of infected red blood cells. Due to analogous nature of white blood cells and red blood cells, it becomes little bit difficult to differentiate between them. But, due to some characteristics of both red and white blood cells, segmentation is possible. Red blood cells are devoid of nuclei while white blood cells have nuclei. So, when the blood sample is stained, the pigment sticks on the surface which has nuclei. So, mostly all white blood cells get stained however, in case of red blood cells only the infected ones are stained because the pigment sticks on surface of plasmodium which are attached on infected red blood cells while the non-infected red blood cells are not stained because they are not having nuclei. So, our first objective is to eliminate on the basis of colour. Now, the watershed algorithm is used to identify and label the regions by filling the contours. From this algorithm we can segment small sized and large sized white blood cells. Then small contours are deleted as they are present because of errors in staining. But, our main objective is to distinguish between similar sized stained white blood cells and infected red blood cells. For this, morphological snakes algorithm is used in which snakes are spread on the stained part, we keep on moving towards the boundary as depicted below in the images. Then on the basis of calculated size it is determined whether the cell is infected red blood cell or large sized white blood cell. The paper is organized as follows to present the various process of malaria detection. The introduction and literature is discussed in section I

which consists of segmenting white blood cells from red blood cells and further derivations and images are shown below, which approve the accuracy of the algorithms used. Finally, the experimental result analysis of segmentation of white blood cells is also discussed below and conclusion with future work is shown in section IV.

II. PROPOSED WORK

The segmentation is done with applying colour based threshold followed by watershed algorithm and snakes algorithm.

Active contour algorithm works on the following principle of energy:

$$E_{snake}^* = \int_0^1 E_{snake}(v(s)) ds = \int_0^1 \{ E_{int}(v(s)) + E_{image}(v(s)) + E_{con}(v(s)) \} ds,$$

The steps for performing segmentation are as follows:

1) *Load the image.*

The image is loaded and is converted to grayscale image.

2) *Apply threshold.*

The image of the blood stained slide is stained and the microscope used is brightfield, the malaria infected RBCs and WBCs will be stained with purple colour. The threshold is applied and stained area is obtained from the image.

3) *Compute the exact Euclidean distance from every binary pixel to the nearest zero pixel, then find peaks in this distance map.*

4) *Perform a connected component analysis on the local peaks, using 8-connectivity, and then apply the Watershed algorithm.*

5) *Loop over the unique labels returned by the Watershed algorithm and size based threshold is applied to filter out small stained particles.*

Watershed algorithm gives back contours which are then iterated upon and small contours are removed as they are not area of interest. The contours which are above threshold are the area of interest as they are most probably WBCs, and are stored. Then for each of the contours stored, the next steps are performed.

6) *Apply canny filter to detect edges and then dilate the edges.*

Canny filter helps to redefine the boundary. Canny filter is then applied so as to restrict the boundaries for active algorithm. Active algorithm needs well defined binary boundary for stopping at it, if the boundaries are not properly binarized then the snakes will go out of area of interest.

7) *Initialize the snake at the edge of the nucleus / plasmodium.*

For efficiency purpose, the snakes of active algorithm are initialized at the outer edge ie: with some added offset. The algorithm will not outperform as the worst case scenario for

the snakes is to reach the offset. The difference between offset and actual cell boundary is not that high, so the algorithm is more robust.

III. RESULTS

For deploying the algorithm, a machine with following configuration was used:

Processor:	Intel Core i5-6200 @ 2.30GHz x 2
RAM:	4 GB DD4 Ram
OS:	Linux Mint 18.1 64 bit 4.4.0-53-generic

There is no training time required for the proposed algorithm and the overall time required for segmentation of 61 images is approx. 10 minutes.

The results of the segmentation are as shown below:

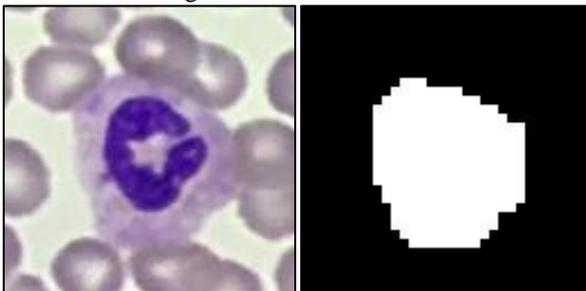


Fig. 1: a) Before

Fig. 1: b) After

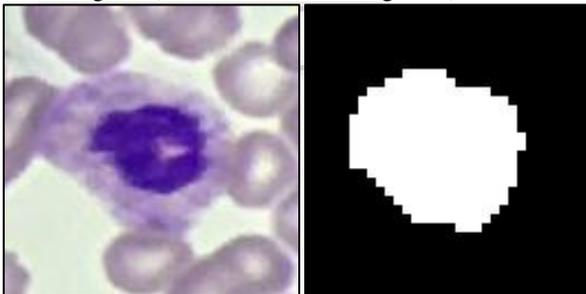


Fig. 2: a) Before

Fig. 2: b) After

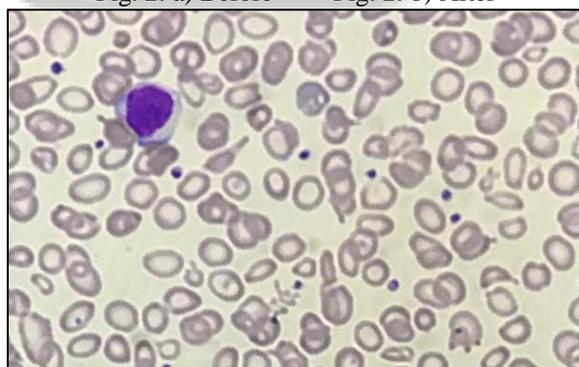


Fig. 3: a) Before Segmentation



Fig. 3: b) After Segmentation

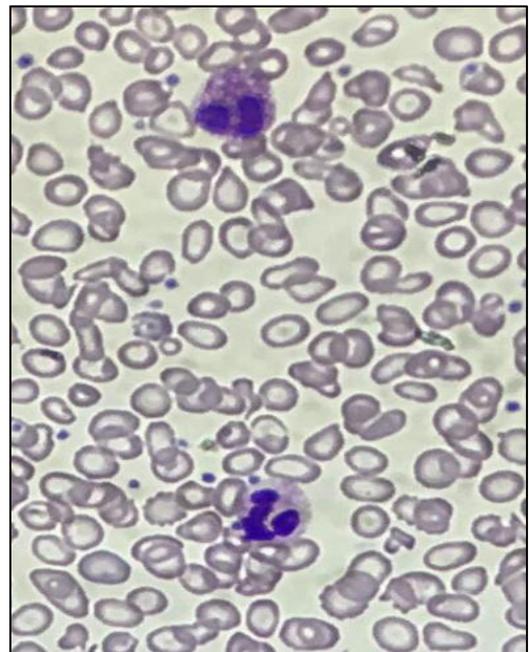


Fig. 4: a) Before Segmentation

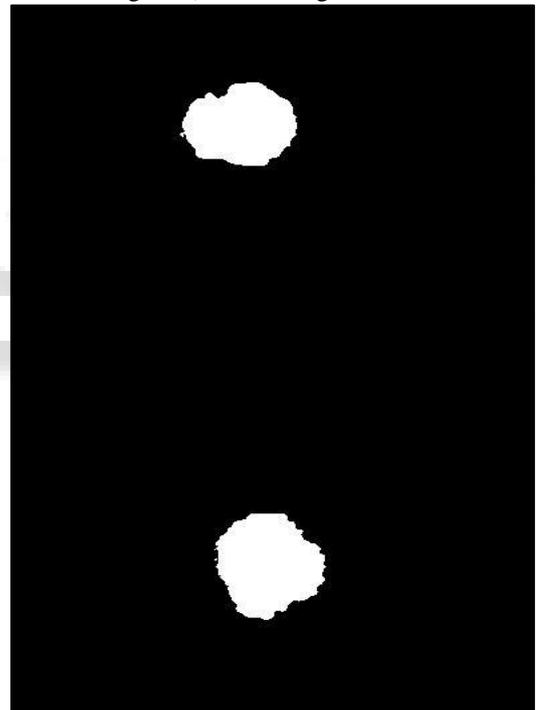


Fig. 4: b) After Segmentation

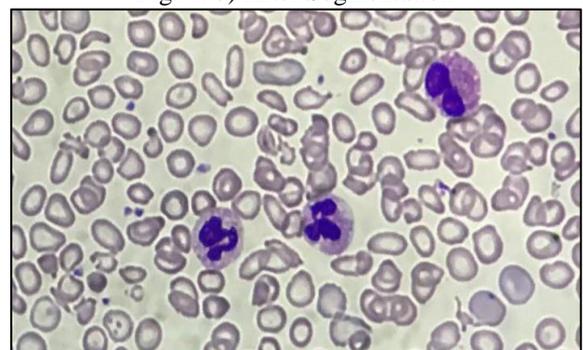


Fig. 5: a) Before Segmentation

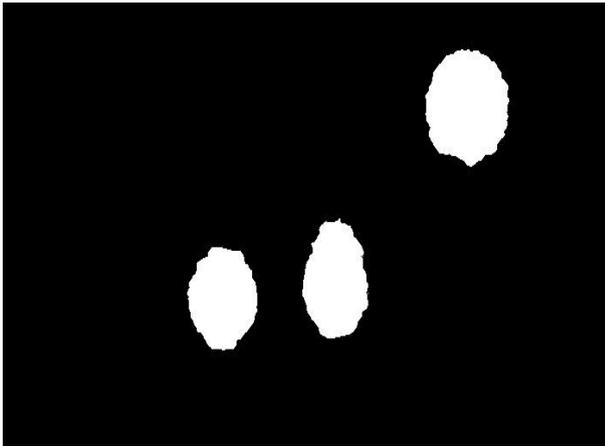


Fig: 5: b) After Segmentation

The time taken for the segmentation of images is as listed below:

Image Number	Time Taken(Seconds)
1	5
2	6
3	15
4	18
5	22

IV. CONCLUSION

This paper demonstrates white blood segmentation using robust and high precision algorithms like watershed and morphological snakes. The output obtained through these algorithms give accuracy up to 75% on a sample dataset.

In future, for better accuracy convolutional neural networks can be deployed.

REFERENCES

- [1] Xiaodong Yang, Houqiang Li, and Xiaobo Zhou, IEEE TRANSACTIONS ON CIRCUITS AND SYSTEMS—I: REGULAR PAPERS, VOL. 53, NO. 11, NOVEMBER 2006, Nuclei Segmentation Using Marker-Controlled Watershed, Tracking Using Mean-Shift, and Kalman Filter in Time-Lapse Microscopy
- [2] J. M. Sharif, M. F. Miswan, M. A. Ngadi, Md Sah Hj Salam, Muhammad Mahadi bin Abdul Jamil 2012 International Conference on Biomedical Engineering (ICoBE), Penang, Malaysia, 27-28 February 2012. Red Blood Cell Segmentation Using Masking and Watershed Algorithm: A Preliminary Study
- [3] Zamani F, Safabakhsh R. Proceeding of 8th IEEE International Conference on Signal Processing. Vol. 2. China: Beijing; 2006. An unsupervised GVF snake approach for white blood cell segmentation based on nucleus.
- [4] Piuri V, Scotti F. Proceeding of IEEE International Conference on Computational Intelligence for Measurement Systems and Applications. United States of America: Boston; 2004. Morphological classification of blood leucocytes by microscope images; pp. 150–4.
- [5] Ritter N, Cooper J. Segmentation and border identification of cells in images of peripheral blood smear slides. Proceedings of the Thirtieth Australasian Conference on Computer Science. 2007;62:161–169.

- [6] Ongun G, Halici U, Leblebicioglu K, Atalay V, Beksac M, Beksac S. Feature extraction and classification of blood cells for an automated differential blood count system. Neural Networks. Proceedings. IJCNN '01. International Joint Conference on. 2001;4:2461–2466.
- [7] Kass M, Witkin A, Terzopoulos D. Snakes: active contour models. Comput Graph Image Process. 1988;1:321–331.
- [8] L. Putzu and C. Di Ruberto, “White blood cells identification and counting from microscopic blood image,” World Academy of Science, Engineering and Technology, vol. 73, pp. 363–370, 2013