Review on Automatic Detection and Quantification of WBCs and RBCs

Pravin S.Bhusare[1], Shri.Sanjeev D.Bhosale[2]
[1]*PG Student, Department of E&TC Engg., Shree Tuljabhavani College of Engg.Tuljapur*
[2]*Professor & Head, Department of E&TC Engg., Shree Tuljabhavani College of Engg.Tuljapur*

***Abstract*- Segmentation and counting of blood cells are considered as an important step that helps to extract features to diagnose some specific diseases like malaria or leukemia. The manual counting of white blood cells (WBCs) and red blood cells (RBCs) in microscopic images is an extremely tedious, time consuming, and inaccurate process. Automatic analysis will allow hematologist experts to perform faster and more accurately. The proposed method uses an iterative structured circle detection algorithm for the segmentation and counting of WBCs and RBCs. The separation of WBCs from RBCs was achieved by thresholding, and specific preprocessing steps were developed for each cell type. Counting was performed for each image using the proposed method based on modified circle detection, which automatically counted the cells. Several modifications were made to the basic (RCD) algorithm to solve the initialization problem, detecting irregular circles (cells), selecting the optimal circle from the candidate circles, determining the number of iterations in a fully dynamic way to enhance algorithm detection, and running time. The validation method used to determine segmentation accuracy was a quantitative analysis that included Precision, Recall, and F-measurement tests.**

***Index Terms*- material modified circle detection , RCD algorithm.**

1.INTRODUCTION

The analysis of microscopy images is extremely important in both the medical and the computer science fields. Many research problems are related to the analysis of microscopy images, such as complete blood count (CBC) tests [1] and the analysis of blood smears, which is considered the first step in detecting and diagnosing malaria, leukemia, and anemia. Additionally, during a complete physical exam a series of tests are performed. One of these tests is the CBC, which is used to evaluate the composition and concentration of all cellular blood components. The CBC determines red blood cell (RBC) counts, white blood cell (WBC) counts, platelet counts, hemoglobin (HB) measurements, and mean red blood cell volumes [2].

CBC tests and the analysis of blood smear images help to evaluate, diagnose, and monitor various health conditions, such as anemia, leukemia, infections, and allergic conditions [3]. For blood disorders, such as anemia, which is based on HB level, the production and destruction of red blood cells are evaluated. In red blood cell disorder such as anemia, other red cell indices such as (mean cell volume) MCV, mean cell hemoglobin (MCH), mean corpuscular hemoglobin concentration (MCHC), RBC, and red blood cell distribution width (RDW or RCDW) are evaluated to narrow down on the causes of anemia. If the red cell indices are suggested of iron deficiency anemia (IDA), further tests to confirm the IDA will be done. In normal blood, red blood cell (RBC) counts range from 4.2 to 5.9 million cells per square centimeter. High RBC counts can be indicative of serious medical conditions, such as heart, lung, or kidney disease. Primary or secondary polycythemia in polycythemia HB is also raised; a bone marrow disorder also causes high RBC counts [2]. Normal WBC counts range from 4,500 to 10,000 WBCs per microliter of blood [4]. High WBC counts (above 30000 cells per microliter) indicate an infection, systemic illness, inflammation, allergy, leukemia, or burn-induced tissue injury. If leukemia is suspected, analysis of blood smear is done to look for morphology of the leukemic cells and followed by bone marrow examinations [2–4]. For platelets, which are small blood cell fragments that assist in blood clotting, normal counts range from 150,000 to 450,000 platelets per microliter. In patients with low platelet count such as in patients with dengue infection, their platelet count is monitored closely

and the value is within critical level, the patient might need platelet transfusion [2]. Generally, any abnormal blood smear reading indicates an infection or disease.

Malaria and Babesia are parasites that infect RBCs; the analysis of thin blood smear remains the gold standard for diagnosis in such disease [5]. Microscopy images are also still used for early diagnosis, analysis, and count of some blood disorder such as sickle cell anemia and leukemia, before confirming it with other laboratory tests. However, manual or visual quantification of parasitemia in thin blood films and WBCs in leukemia is an extremely tedious, subjective, and time-consuming task with a high probability of counting error [6, 7]. An accurate segmentation and counting mechanism that gathers information about the distribution of microscopic particles may help diagnose abnormalities during clinical analysis. Our objective in this paper is to develop and validate an algorithm that segments and automatically counts red and white blood cells in microscopy images. The ground truth of the images was determined by experts. For the evaluation, quantitative analyses were performed on the segmentation results based on the ground truth, and the -measure method was used to confirm accuracy. In the following sections of this paper, we will summarize related work on the segmentation and counting of RBCs and WBCs (Section 2), present the methodology used (Section 3), discuss the results and experiments (Section 4), and review the conclusions.

2. LITERATURE REVIEW

Many researchers have investigated blood cell segmentation and counting. Some researchers [5, 8–10] used morphological operations and thresholding to do the segmentation and counting. Berge et al. [5] presented an approach based on a morphological method and iterative threshold techniques. Segmentation was performed on red blood cells, which included clumped cells, and boundary curvatures were used to construct a Delaunay triangulation. They used real microscopy images prepared in the laboratory, and the ground truth was determined by a laboratory expert. A 2.8% difference was calculated between the manual and automatic counting of red blood cells. Their method tolerated a degree of overlapping, but in cases with a high degree of overlapping cells, the cells were unable to be detected. Additionally, the iterative threshold method was unable to detect faint red cells. Damahe et al. [8] used the S and V image components of a HSV color model with Zack's thresholding technique for cell segmentation. Thresholding combined with a sequential edge-linking algorithm was used to increase segmentation accuracy. The experimental dataset and blood cell images were collected from the Dhruv Pathology Lab and the CDC-DPDx, respectively, and the ground truth was determined by experts. The dataset size was limited. Several RBCs that were detected possessed holes. Additional preprocessing steps should have been implemented to increase the accuracy. Panchbhai and Vishal [9] proposed an automated analysis that counted red blood cells and detected malaria parasites in thin blood smear samples. The green color layer was processed to count all of the RBCs; segmentation was performed on the infected RBCs using Otsu thresholding. A histogram was used to determine the optimal threshold. CDC datasets were used for the experimental part, and the ground truth was determined by a pathology expert who compared their results with the manual counts. However, because the detection algorithm used morphology and thresholding, their method was unable to detect clumped and overlapping cells. Khan et al. [10] proposed a method to count WBCs, RBCs, and platelets. Several preprocessing steps were performed before converting the image to binary. Segmentation and cell counting were performed based on the optimal threshold value, which was determined from a histogram. They achieved 95% accuracy with their proposed method compared to manual counting and a hematology analyzer. However, this method is unable to detect overlapping cells. When using iterative thresholds, the probability of losing useful information from the image is high; this decreases the accuracy of segmentation.

Nguyen et al. [11] used distance transform to solve the overlapping cells problem; they proposed a method that concentrated on clumped cells. First, they assigned central points based on a distance transform. The optimal center points were selected by checking the degree of boundary covering the center point, and the average size of a cell was estimated by the extraction of a single cell. Then an algorithm was developed that used a single cell mask to split the

cells. Their dataset ground truth was labeled by experts, and the accuracy of the proposed method using -measurements was 93.5% and 82%. Clumped cells were tolerated, but the cells had to be regularly shaped and focused at a high magnification. Not all blood cells have regular cell shapes, and this is especially true if the blood cells are diseased. Therefore, cell detection methods should be able to detect irregular cells. Additionally, because of noise the performance of their method was not good.

Rhodes and Bai [12] presented a circle detection method using specific properties of Gabor wavelet filter to detect the image features such as circularity. It is able to extract radius wraps around the origin and the plane wave radiates from the center of the filter. They test their proposed method on synthetic images and real microscopic images, which allow a certain degree of overlapping cells. The results were 91.3% and 87% of the cells detected in the two microscopic test images.

Since blood cells are approximately circular shape, circle detection algorithms can still handle the challenge of blood cells detection. Hough Transform is considered as one of the most known algorithms for line and circle detection. It was developed by Richard Duda and Peter Hart in 1972 [13]; they called it as a generalized Hough Transform after the related 1962 patent of Paul Hough [13]. Hough Transforms maps every edge pixel into parameter space and use conventional HT to detect lines, circles, or any other parametric shape. In this paper, we concentrate on circle detection algorithms. There are many techniques used for circle detection. Many HT-based algorithms that detect circles were developed using different methods. Yip et al. [14] reduced the accumulator array to enhance computation time and improve memory consumption. Other methods use pixel gradient information [15, 16] to reduce computation time and the accumulator array. Ho and Chen used the geometric properties of circles to improve performance [17]. Xu et al. [18, 19] developed the randomized Hough Transform (RHT), which randomly selects three noncollinear edge pixels , maps them into parameter space, and requires less computation time and memory storage compared with Standard HT methods. A simple voting strategy in the accumulator is used to collect evidence and determine the existence of a circle. Chung and Huang [13] presented a method that can substitute various shape detection algorithms. This method enhanced the speed of the original algorithm. They applied their method in RHT and randomized circle detection (RCD) algorithms to detect lines, circles, and ellipses. Their method presented good results when compared with original methods.

Chiu et al. [20] presented a fast randomized Hough Transform method for detecting circles, to improve RHT which is less efficient in complex images due to its probability usage problem. They pick one random edge pixel from the image, and it is considered as a seed point. Then, a checking method was developed to observe if this selected seed point is lying on a true circle or otherwise. The checking criterion is based on finding two other points whose distances are the same from the selected seed point by using a window centered by the selected seed point. This method enhanced the probability to find relevant points on a true circle. They have proven that using one random selected point's probability is sufficient in comparison to three random selected points [13–19].

Chen and Chung [21] presented a circular algorithm called RCD. They claimed that RCD outperformed other most efficient Hough Transform based algorithms [13–19]. Regardless of accumulator usage as in [13–19], RCD works by randomly selecting four edge pixels from the whole image. Then, these pixels are examined if they are noncollinear and it will proceed to form a candidate circle. RCD determines that circle is a possible circle based on distance criteria. After finding its center and radius, it checks the number of pixels lying on the boundary of this possible circle. This checking criterion is performed by calculating the distance between all edge pixels in the image and the boundary of this possible circle. If this distance is lesser than a fixed threshold value, then it will be considered as a boundary of this possible circle. Finally, another fixed threshold value has also been used to decide a true circle or otherwise based on number of edge pixels lying on a possible circle's boundary. Other related issues on RCD are less efficient when dealing with huge image size consisting of a high number of edge pixels. RCD also requires four selected edge pixels randomly from the whole image, which causes low probability forming a true circle. Furthermore, RCD has a drawback in terms of its fixed number of iterations in which it is highly correlated to the image texture. In addition,

RCD acquires many parameters and threshold values to be predefined and it ignores irregular circles.

Since the Hough Transform presented a good performance in different fields, many researchers [22–25] used Hough transform method for detecting circle when performing RBC's and WBC's calculation task in the microscopic images. Mahmood et al. [22] applied Hough transform method for counting the RBC's and WBC's for the microscopic images. In the first step, they converted the source image to color space model and performed color segmentation process of red and white cells based on feature lightness over the channel ranging between 130–150 and 80–100, respectively. Then, the second step begins with applying some morphological operators which are followed by applying Canny operator for edge detection process. Lastly, they performed cell detection and counting using Circular Hough Transform. The dataset was composed of 108 images from the "Acute Lymphoblastic Leukemia Image Database for Image Processing" database that was established and maintained by Labati et al. [26]. Depending on the processing and type of cells being analyzed, they achieved an accuracy ranging from 64% to 87%. The Hough Transform consumed memory storage and required a long computation time to determine a large range of accepted radii. Additionally, the ability to tolerate a high degree of overlapping and irregular cells was limited; therefore, accuracy was not high.

Mahmood and Mansor [23] examined 10 image samples of normal blood cells; image transformed to the HSV color space, and then Saturation or "S" channel was selected to proceed with image analysis. Morphological operators and thresholding method were used over S channel for cell segmentation. They used Circular Hough Transform to investigate the circularity feature of the red blood cells in order to perform detection and counting. Their proposed method achieved approximately 96% of accuracy rate in comparison to manual counting. Extracting and counting normal cells are simple tasks if the detected cells are normal cells and consist of small number of overlapping cells with regular shape. For this kind of easy case, the idea of using Hough Transform can be very helpful because it can produce a good performance.

With similar inspiration to [23], Venkatalakshmi and Thilagavathi [24] have also applied circular Hough Transform method to count the RBCs from microscopic images after performing preprocessing steps such as HSV transformation, S channel extraction, histogram thresholding morphological operations, XOR logical operation, and Canny edge detection. However, again, this proposed idea is less tolerant to any overlapping cells or irregular cells' shape. Later, Maitra et al. [25] presented a composition method to extract red cell from five microscopic images; these steps include spatial smoothing and filtering, adaptive histogram equalization, and edge detection. Similar to [23, 24], they used basic Circular Hough Transform to detect the red cells based on prior information such as size and shape features. Those methods [23–25] employ classic Hough Transform method to detect the blood cells which inherits some drawbacks, for example, required more computation, high memory consumption, and less ability in detecting overlapping cells or irregular cells.

Finally, Cuevas et al. [27] presented a method which is not Hough Transform based to detect white blood cells. They used a combination of circle detection with electromagnetism-like optimization from the edge map image. This method tolerated noise. In blood smear images, the number of white cells was small compared with the number of red cells; therefore, small degree of overlapping white cells can be detected with their method. However, they did not test the method on clumping cells. Their results were compared with other methods, and their method demonstrated good accuracy.

3. CONCLUSION

This paper proposed a method to automate the segmentation and counting of red and white blood cells using iterative structured circle detection algorithm. Several improvements were made to the RCD algorithm, including an initialization step to find 8-neighbor connected component. Additionally, the proposed model features an enhanced probability of selecting the correct circle from four candidate circles, the capability to detect irregular cells, the use of dynamic number of iterations, and improved detection of overlapping cells. The proposed method performed the segmentation and counting of WBCs and RBCs well when results were compared with the ground truth, which was determined by experts. The

following segmentation and counting accuracies were achieved using the proposed method: PR = 89.7%, RC = 98.4%, and -measure = 93.9% for WBC and PR = 95.3%, RC = 97.5%, and -measure = 96.4% for RBCs.

REFERENCES

[1] M. Habibzadeh, A. Krzyzak, and T. Fevens, "Application of pattern recognition techniques for the analysis of thin blood smears images," Journal of Medical Informatics & Technologies, vol. 18, 2011.View at Google Scholar

[2] M. M. Osman, "Normal reference value of blood cell count, red, white and platelet of Khartoum North Area," Al Neelain Medical Journal, vol. 3, no. 8, 2013. View at Google Scholar

[3] (NIH) National Institutes of Health, "A service of the U.S National Library of Medicine, "http://www.nlm.nih.gov/medlineplus/ency/article/003642.htm.

[4] http://www.buzzle.com/articles/high-white-blood-cell-count.html.

[5] H. Berge, D. Taylor, S. Krishnan, and T. S. Douglas, "Improved red blood cell counting in thin blood smears," in Proceedings of the 8th IEEE International Symposium on Biomedical Imaging: From Nano to Macro (ISBI '11), pp. 204–207, Chicago, Ill, USA, April 2011. View at Publisher • View at Google Scholar • View at Scopus

[6] S. S. Savkare and S. P. Narote, "Automatic classification of normal and infected blood cells for parasitemia detection," International Journal of Computer Science and Network Security, vol. 11, no. 2, pp. 94–97, 2011. View at Google Scholar

[7] J. M. Sharif, M. F. Miswan, M. A. Ngadi, S. Hj, and M. Mahadi, "Red blood cell segmentation using masking and watershed algorithm: a preliminary study," in Proceedings of the International Conference on Biomedical Engineering (ICoBE '12), pp. 258–262, Penang, Malaysia, February 2012. View at Publisher • View at Google Scholar

[8] L. B. Damahe, P. G. Student, R. G. College, and R. G. C. Engg, "Segmentation based approach to detect parasites and RBCs in blood cell images," International Journal of Computer Science and Applications, vol. 4, no. 2, 2011. View at Google Scholar

[9] L. B. D. Panchbhai and V. Vishal, "RBCs and parasites segmentation from thin smear blood cell images," International Journal of Image, Graphics and Signal Processing, vol. 10, no. 10, pp. 54–60, 2012. View at Google Scholar

[10] S. Khan, A. Khan, and A. Naseem, "An accurate and cost effective approach to blood cell count,"International Journal of Computer Applications, vol. 50, no. 1, pp. 18–24, 2012. View at Google Scholar

[11] N. Nguyen, A. Duong, and H. Vu, "Cell splitting with high degree of overlapping in peripheral blood smear," International Journal of Computer Theory and Engineering, vol. 3, no. 3, pp. 473–478, 2011.View at Google Scholar

[12] A. Rhodes and L. Bai, "Circle detection using a gabor annulus," in Procedings of the British Machine Vision Conference, pp. 108.1–108.11, September 2011. View at Publisher • View at Google Scholar

[13] K.-L. Chung and Y.-H. Huang, "A pruning-and-voting strategy to speed up the detection for lines, circles, and ellipses," Journal of Information Science and Engineering, vol. 24, no. 2, pp. 503–520, 2008.View at Google Scholar • View at Scopus

[14] R. K. K. Yip, P. K.-S. Tam, and D. N. K. Leung, "Modification of Hough transform for circles and ellipses detection using a 2-dimensional array," Pattern Recognition, vol. 25, no. 9, pp. 1007–1022, 1992. View at Publisher • View at Google Scholar • View at Scopus

[15] E. P. Lyvers and O. R. Mitchell, "Precision edge contrast and orientation estimation," IEEE Transactions on Pattern Analysis and Machine Intelligence, vol. 10, no. 6, pp. 927–937, 1988. View at Publisher • View at Google Scholar • View at Scopus

[16] C.-T. Ho and L.-H. Chen, "A fast ellipse/circle detector using geometric symmetry," Pattern Recognition, vol. 28, no. 1, pp. 117–124, 1995. View at Publisher • View at Google Scholar • View at Scopus

[17] C.-T. Ho and L.-H. Chen, "A high-speed algorithm for elliptical object detection," IEEE Transactions on Image Processing, vol. 5, no. 3, pp. 547–550, 1996. View at Publisher • View at Google Scholar •View at Scopus

[18] L. Xu, E. Oja, and P. Kultanen, "A new curve detection method: randomized Hough transform (RHT)," Pattern Recognition Letters, vol. 11, no. 5, pp. 331–338, 1990. View at Google Scholar • View at Scopus

[19] L. Xu and E. Oja, "Randomized Hough transform (RHT): basic mechanisms, algorithms, and computational complexities," CVGIP: Image Understanding, vol. 57, no. 2, pp. 131–154, 1993. View at Publisher • View at Google Scholar • View at Scopus

[20] S.-H. Chiu, J.-J. Liaw, and K.-H. Lin, "A fast randomized Hough transform for circle/circular arc recognition," International Journal of Pattern Recognition and Artificial Intelligence, vol. 24, no. 3, pp. 457–474, 2010. View at Publisher • View at Google Scholar • View at Scopus

[21] T.-C. Chen and K.-L. Chung, "An efficient randomized algorithm for detecting circles," Computer Vision and Image Understanding, vol. 83, no. 2, pp. 172–191, 2001. View at Publisher • View at Google Scholar • View at Scopus

[22] N. H. Mahmood, P. C. Lim, S. M. Mazalan, and M. A. A. Razak, "Blood cells extraction using color based segmentation technique," International Journal of Life Sciences Biotechnology and Pharma Research, vol. 2, no. 2, 2013. View at Google Scholar

[23] N. H. Mahmood and M. A. Mansor, "Red blood cells estimation using Hough transform technique,"Signal & Image Processing, vol. 3, no. 2, pp. 53–64, 2012. View at Google Scholar

[24] B. Venkatalakshmi and K. Thilagavathi, "Automatic red blood cell counting using Hough transform," in Proceedings of the IEEE Conference on Information and Communication Technologies (ICT '13), pp. 267–271, JeJu Island, Korea, April 2013. View at Publisher • View at Google Scholar

[25] M. Maitra, R. K. Gupta, and M. Mukherjee, "Detection and counting of red blood cells in blood cell images using Hough transform," International Journal of Computer Applications, vol. 53, no. 16, pp. 18–22, 2012. View at Google Scholar

[26] R. D. Labati, V. Piuri, and F. Scotti, "All-IDB: the acute lymphoblastic leukemia image database for image processing," in Proceedings of the 18th IEEE International Conference on Image Processing (ICIP '11), pp. 2045–2048, Brussels, Belgium, September 2011. View at Publisher • View at Google Scholar • View at Scopus

[27] E. Cuevas, D. Oliva, M. Díaz, D. Zaldivar, M. Pérez-cisneros, and G. Pajares, "White blood cell segmentation by circle detection using electromagnetism-likeoptimization,"Computational and Mathematical Methods in Medicine, vol. 2013, Article ID 395071, 15 pages, 2013. View at Publisher •View at Google Scholar

[28] L. Putzu and C. di Ruberto, "White blood cells identification and counting from microscopic blood image," World Academy of Science, Engineering and Technology, vol. 7, no. 1, pp. 363–370, 2013. View at Google Scholar