Chapter 17
Automatic White Blood Cells Counting Using OPENCV

Prabhakar Telagarapu
https://orcid.org/0000-0003-3287-6325
GMR Institute of Technology, India

Babji Prasad Chapa
GMR Institute of Technology, India

Sahithi Reddy Pullanagari
University of Sydney, Australia

ABSTRACT

Counting the number of white blood cells (WBCs) is a crucial procedure in medical laboratories for diagnosing various diseases. However, manual counting can be time-consuming and susceptible to errors. To overcome this, a research study has proposed an automated approach for WBC counting in sampled images using OpenCV, an open-source computer vision library. The authors developed an algorithm that segments the WBCs from the background by utilizing preprocessing techniques, followed by edge detection (canny edge detection) to identify the cells' boundaries. The number of cells is counted by implementing a simple circular Hough transform method. For this, the authors approached and collected datasets from ALL-IDB team for sampled images to test the proposed method. The proposed method has achieved high accuracy rates and outperformed manual counting in terms of speed and efficiency. The developed approach has the potential to be integrated into existing medical laboratory workflows, automating the WBC counting process and improving the diagnosis and treatment of various diseases.

1. INTRODUCTION

Reddy, V. H. (2014) proposed blood plays a major role in the human body. Noor, A. M., et.al (2020) developed blood is a complex fluid that contains various types of cells. Poomcokrak, J., & Neatpisarnvanit, C. (2008) presented and Hiremath, P. S., et.al., (2010) described white blood cells are comprised of monocytes, lymphocytes, neutrophils, eosinophils, basophils, and macrophages, each with different properties and functions. Anisha, P. R., Reddy, et.al (2022) performed comparison to white blood cells.

DOI: 10.4018/979-8-3693-5893-1.ch017

Allugunti, V. R. (2019) characterized these cells circulate through the body via the arteries and veins. Yao, X., et.al (2021) lack a nucleus and are small and thin in the center, giving them a distinctive appearance like red doughnuts. Parrino, V., et al., (2018) feature nuclei that stain a dark purple hue. Anisha, P. R., Reddy, et al., (2015) proposed the nuclei of many white blood cells are segmented, which means they are split into two or more smaller parts that are still connected. This segmented nucleus appearance is like twisting a long balloon to create a sculpture. Larsson, A., Smekal, D., & Lipcsey, M. (2019) identify and count a specific type of white blood cell. Deng, Y., & Li, H. (2023) focuse on identifying and quantifying the number of these specific blood cells. Reddy, C. K. K., et.al (2015) detailed the process of categorizing white blood cells from an image of a blood smear taken from the periphery of the body involves using the histogram of oriented gradient feature that depicts the shapes of nuclei. From this paper the blood cells will be classified by using the method of histogram of oriented gradient feature (HODF). Tessema, A. W., et.al (2021) described the extraction of specified blood cells before counting. Luo, J., et.al (2020) described in the medical field many bloods related deceases are being discovered nowadays. So, the curing methods must be also increased. By detection and counting of blood cells many deceases like leukemia, Hemophilia. This helps to fast recovery of the decease. This is one of the most useful concepts of Telemedicine system. Lee, S. J., et.al (2022) suggested an advanced neural network design aimed at precisely identifying. We evaluated our model using the publicly available BCCD dataset. Blood smear images often suffer from low resolution, resulting in blurry and overlapping blood cells. Their focuses on delving deeply into the factors influencing their accuracy and experimental findings demonstrate that our models achieve precise recognition of blood cells under conditions where cell overlap is minimal.

Kouzehkanan, Z. M., et.al (2022) introduces The Raabin-WBC dataset is a freely accessible compilation of normal peripheral white blood cell images, totaling around 40,000 images with accompanying color spots. Cao, H., et.al (2018) explored Utilizing the accurate algorithm is developed for segmenting peripheral blood leukocytes. Tomari, R., et.al (2014) proposed Geometrical properties of the RBCs are then extracted to gather information about them.Farhan, A., et.al (2022) introduced Open Blood Flow is a software package crafted to precisely measure flow velocity of blood and cell count in zebrafish. Developed using the Python programming language renowned for its effectiveness in tackling biological challenges. Li, H., et.al (2020). performed to precisely segment adhesive WBCs in the extracted results, we introduce a third class dedicated to cell borders, alongside the foreground and background classes.

Liu, Y., et.al (2016) tackles There are two primary challenges in segmentation: locating white blood cells (WBCs) and segmenting sub-images. Lopez-Puigdollers, D., et.al (2019) delve into the potential of local image descriptors, known for their simplicity and resilience against background interference in various visual tasks without needing explicit segmentation. This approach holds significance in expert and intelligent systems as it is problem-agnostic and general, eliminating the need for human experts to provide precise visual signs.

Doering, E., et.al (2020) unlike many current techniques that rely on specific feature knowledge or require extensive preprocessing, our method streamlines tasks like counting infected cells, which can be quite manual for trained professionals. Such manual processes can lead to diagnostic and treatment delays, potentially causing severe consequences. This integrated approach aims to automate the detection and counting process, minimizing the time from infection to diagnosis and ultimately improving patient. López Flórez, S., et.al (2023) demonstrated improved performance metrics and contrasted its performance with the existing segmentation-based U-Net and OpenCV models. Their findings indicate that the proposed YOLOv5 model effectively recognizes and counts the various types of cells found in laboratory settings.