Minimax Theory and its Applications
Volume 11 (2026), No. 1, 73 – 80

Development of a MATLAB-Based GUI for Counting Red Blood Cells and White Blood Cells, and Classification of White Blood Cells

Ronald B. Lacaba[1], Gamaliel A. Baldos[2], Roel I. Sabang[3], Jereco Jims J. Agapito[4], Jude Alexes M. Ramas[5]

[1,2,3] Palompon Institute of Technology
[4,5] Eastern Visayas State University Ormoc City Campus

Received 18th September, 2025
Accepted 24th December, 2025
Published 15th February, 2026

Abstract
The Complete Blood Count (CBC) is an essential diagnostic procedure widely employed in clinical laboratories to evaluate overall health and detect conditions such as infections, anemia, and hematologic malignancies. Traditional CBC methods, including manual counting with a hemocytometer and automated analyzers, are either labor-intensive or cost-prohibitive for low-resource settings. This study presents a MATLAB-based diagnostic application designed to detect and classify red blood cells (RBCs) and white blood cells (WBCs), including WBC subtypes, from blood smear images. The system utilizes pre-annotated bounding boxes for cell localization, eliminating the need for complex image segmentation. A user-friendly graphical user interface (GUI) was developed using MATLAB App Designer, allowing real-time display of cell counts and classifications. Clinical validation with licensed medical technologists ensured the morphological accuracy of WBC subtype labels. The system achieved a WBC classification accuracy of 76.92%, an RBC count accuracy of 23.08% (38.46% within a ±2 tolerance), and 100% accuracy in WBC counting. The results demonstrate the tool's effectiveness and practicality for hematological diagnostics in academic and low-resource healthcare environments. Future work includes integrating deep learning techniques for automated classification and batch processing.

Keywords: Complete Blood Count (CBC), MATLAB, Red Blood Cells (RBC), White Blood Cells (WBC), WBC Subtype Classification, Image Processing, Graphical User Interface (GUI).

I. Introduction

The Complete Blood Count (CBC) is a fundamental diagnostic tool routinely utilized in clinical laboratories to evaluate an individual's general health status and to detect a variety of conditions, including anemia, infections, inflammatory diseases, and hematologic malignancies. This test assesses the cellular constituents of blood, including red blood cells (RBCs), white blood cells (WBCs), hemoglobin, hematocrit, and platelet counts, thereby providing a comprehensive overview of hematologic function.

Table 1 presents the standard reference ranges for a Complete Blood Count (CBC) in healthy individuals, with values differentiated for women and men. Red blood cell (RBC) counts typically range from 4 to 5 million per microliter (M/μL) for women and 4.5 to 6.0 M/μL for men, reflecting their role in oxygen transport. White blood cell (WBC) counts, which help fight infection, range from 4.5 to 11 thousand per microliter (K/μL) for both sexes. Platelet counts, essential for blood clotting, range from 150 to 450 K/μL for both women and men. Hematocrit values, indicating the proportion of blood volume occupied by red blood cells, range from 36% to 45% in women and 42% to 50% in men. Hemoglobin levels, which indicate the concentration of the oxygen-carrying protein in red blood cells, generally range from 12 to 15 grams per deciliter (g/dL) in women and 14 to 17 g/dL in men. These standard reference values provide critical information for assessing an individual's general health and identifying potential hematologic abnormalities.

TABLE I: Standard CBC for Healthy Person

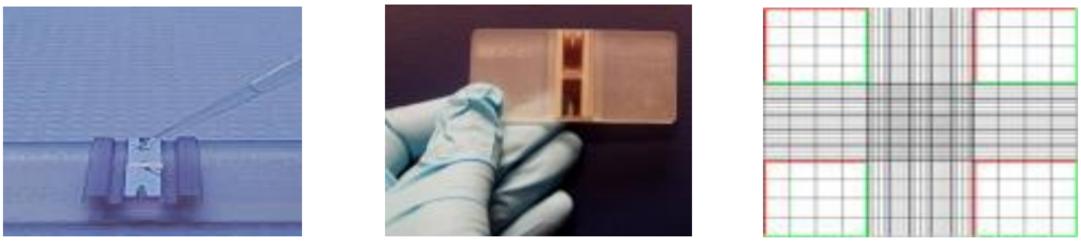
Blood Cell Type	Women	Men	Unit
RBC	4–5	4.5–6.0	M/μL
WBC	4.5–11	4.5–11	K/μL
Platelets	150–450	150–450	K/μL
Hematocrit	36%–45%	42%–50%	%
Hemoglobin	12–15	14–17	gm/100 ml

Units: M = Million; K = Thousand; μL = Microliter; g/dL = Grams per Deciliter.

CONVENTIONAL APPROACH FOR COUNTING RBC AND WBC

Conventional approaches for performing CBCs typically involve manual microscopic techniques or automated hematology analyzers. Manual cell counting, while historically foundational, is time- consuming and requires skilled personnel to ensure accuracy, making it less suitable for high- analysis. On the other hand, automated hematology analyzers offer high-speed and precise analysis but are expensive and necessitate periodic calibration and maintenance, which may be prohibitive in low-resource settings [2].

The conventional method used to count blood cells manually involves the use of a hemocytometer, a device specifically designed for complete blood count analysis. The hemocytometer was invented by Louis-Charles Malassez and consists of a chamber of known dimensions created on a rectangular, thick glass microscope slide. This chamber includes a grid of perpendicular lines etched onto its surface. To perform counting, the user views the hemocytometer through a microscope and manually tallies the blood cells using a hand-held counter. Because the depth of the chamber and the area bounded by the grid lines are predefined, it becomes possible to determine the number of cells within a known volume and thus estimate the overall cell concentration in the fluid being analyzed [4], [5]. The hemocytometer is a precision device commonly used in manual cell counting procedures.



(a) Grid layout (b)Loading chamber (c) Hemocytometer

Fig. 1: Hemocytometer device and its components: (a) Counting grid, (b) loading of sample blood , and (c) External View.

under a microscope. It consists of a thick glass slide with an etched grid of known dimensions and a fixed depth of 0.1 mm when covered with a special cover slip. Figure 1 illustrates the key components of this device: the grid layout (b), the sample loading process (c), and the physical appearance of the hemocytometer (a). The etched grid (b) is typically of the Improved Neubauer type, which contains a central square divided into smaller squares for counting red blood cells (RBCs), and four large corner squares for counting white blood cells (WBCs). To use the device, a diluted blood sample is loaded into the chamber using a pipette (c), allowing the sample to spread evenly across the grid by capillary action. The hemocytometer (a), when observed under a microscope, enables accurate counting of cells within a defined volume. To calculate cell concentrations (either RBC or WBC), the general formula used is:

$$\text{Cell Count} = \frac{N \times D}{A \times d}$$

where:

- N = number of cells counted
- D = dilution factor
- A = area counted (mm2)
- d = depth of chamber (mm)

Given the standardized depth of 0.1 mm, this simplifies further depending on the area counted and the dilution factor used. For RBC counting, cells are typically counted in five small squares (each 0.04 mm2) within the central large square, giving a total area of 0.2 mm2. With a common dilution factor of 200, the RBC count per microliter is calculated using:

$$\text{RBC Count} = \text{Total cells in 5 squares} \times 10{,}000$$

For WBCs, cells are counted in four large corner squares (each 1 mm2), totaling 4 mm2. Using a typical dilution factor of 20, the WBC count is determined by:

$$\text{WBC Count} = \text{Total cells in 4 squares} \times 50$$

These calculations provide the concentration of red and white blood cells per microliter (μL) of blood, which is essential for diagnostic purposes in clinical laboratories.

CONVENTIONAL APPROACH FOR CLASSIFYING WBC

Classifying white blood cells (WBCs) involves manual observation of stained blood smears under a light microscope, a method known as the manual differential count. In this process, a thin blood film is prepared on a microscope slide, allowed to dry, and stained using special dyes such as Wright's stain, Giemsa, or Leishman stain. These stains enhance the contrast between different components of the blood cells, making it easier to differentiate cell types.

A trained medical technologist then examines the smear under oil immersion at high magnification (typically 1000x) and counts 100 WBCs to classify them according to their morphological features. The classification is based on the shape of the nucleus, the presence and color of cytoplasmic granules, the nuclear-to-cytoplasmic ratio, and the overall cell size.

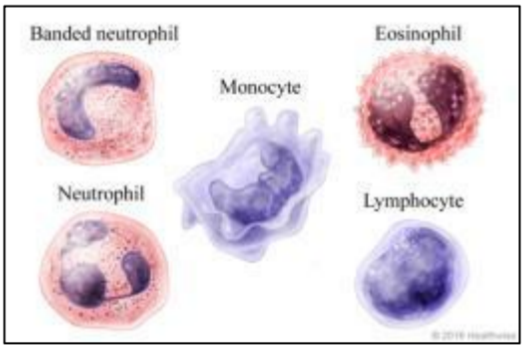


Fig. 2: Types of white blood cells (WBCs) tradi- tionally classified under manual microscopy.

The five main types of WBCs identified are neutrophils, eosinophils, and basophils (collectively known as granulocytes), and lymphocytes and monocytes (known as agranulocytes) as shown in Figure 2. This traditional method, though time-consuming and dependent on the observer's expertise, is still widely used in manual hematology and remains essential in settings where automated analyzers are unavailable or results require verification.

2. Literature Review

Numerous image processing techniques have been developed and employed in the analysis of blood cell images, particularly for tasks such as segmentation, post-processing, and cell counting. In the segmentation phase, methods like the Watershed algorithm are widely used to separate overlapping cells by identifying boundaries between adjacent objects [6]. Although accurate, this technique can be computationally intensive. The Hough Transform is another common method, especially effective for detecting circular shapes such as red blood cells, though it requires more processing time due to its complexity [7]. Simpler alternatives like Otsu thresholding and gray-level thresholding are often employed for efficient image binarization and object-background separation [8]. These methods are frequently enhanced by clustering algorithms such as K-means and Fuzzy C-means, which segment images based on pixel intensity or color similarity, offering a fast and adaptable approach [9]. More advanced algorithms like Angular Ring Ratio (ARR) and hole-filling techniques are also used to resolve issues in overlapping cells and to enhance cell boundary detection [10].

For post-processing, morphological operations such as opening, closing, and dilation are commonly applied to refine the segmentation by removing noise and smoothing object boundaries [11]. Feature extraction then plays a vital role in classification, where characteristics such as shape features (e.g., area, circularity), texture features (e.g., entropy, contrast), and color features (e.g., mean intensity, histogram values) are analyzed [12]. These extracted features are used as input for various classification algorithms, including Support Vector Machines (SVM), K-Nearest Neighbors (KNN), and Artificial Neural Networks (ANN), which have shown high accuracy in distinguishing between different white blood cell types [13]. In addition, techniques like border removal are applied to eliminate peripheral artifacts that might affect analysis results [14].

Regarding cell counting, two main approaches are prevalent. The first is connected component labeling, which identifies and counts individual cells by assigning unique labels to pixel clusters [15]. The second is the Circular Hough Transform, which is particularly effective for detecting and counting red blood cells due to their round shape [16]. These traditional methods form the foundation of many automated diagnostic systems and continue to be refined for use in clinical applications.

This research project demonstrated a modular yet manual approach by utilizing annotation files, thereby eliminating the need to perform segmentation and detection from scratch. A significant strength of the work lies in its integration of a Graphical User Interface (GUI) in MATLAB, addressing not only algorithmic performance but also user accessibility a component often over- looked in academic studies. The system was further enhanced by enabling subtype classification through parsing of WBC subtype annotations (e.g., wbc:lymphocyte), rather than relying on hard- coded labels such as “Neutrophil.” Clinical validation was conducted through consultations with licensed medical technologists to ensure morphological accuracy, addressing a critical gap commonly found in purely algorithmic approaches.

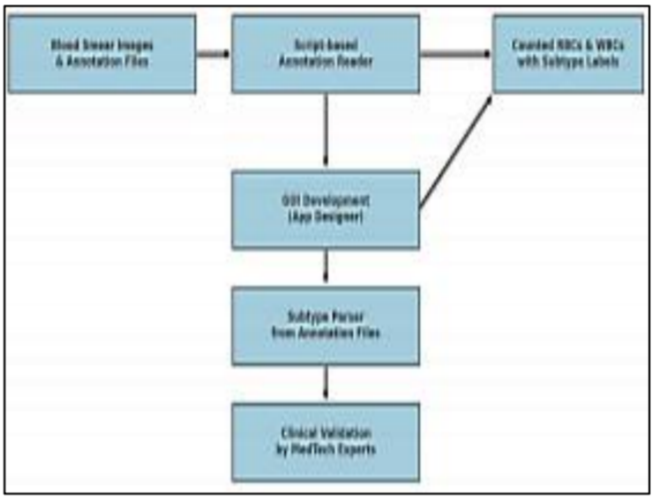


Fig. 3: Block Diagram for the MATLAB-Based Blood Cell Diagnostic Application

tion was conducted through consultations with licensed medical technologists to ensure morphological accuracy, addressing a critical gap commonly found in purely algorithmic approaches.

3. Methodology

This study employed a developmental research design to create a MATLAB-based diagnostic application capable of counting red blood cells (RBCs) and white blood cells (WBCs), and classifying WBC subtypes from blood smear images. The methodology consists of five key phases: data preparation, initial system development, GUI integration, WBC subtype classification, and clinical validation.

A. Data Preparation

The primary dataset consisted of sample microscopic blood smear images paired with corresponding annotation files (.txt format). These annotation files initially included bounding box coordinates for each cell, with generic labels: rbc for red blood cells and wbc for all white blood cells. The annotations were later enhanced to include WBC subtype information, such as wbc:neutrophil, wbc:lymphocyte, and wbc:monocyte.

B. Initial System Development

A MATLAB script-based application was first developed to read and process these annotation files. This version of the system could load images, draw bounding boxes around cells, and count the number of RBCs and WBCs. At this stage, the system did not yet distinguish between WBC subtypes, assigning the label “Neutrophil” to all WBCs by default.

C. Graphical User Interface (GUI) Development

To improve usability and user interaction, the system was transitioned to a GUI-based format using MATLAB App Designer. The GUI allowed users to load any blood smear image, match it with its annotation file, and automatically display the counted cells with labeled bounding boxes—red for RBCs and blue for WBCs. The interface featured image display axes, action buttons (e.g., Load Image, Count Cells, and Classify WBC), and dynamic counters for cell totals.

D. Subtype Classification Mechanism

To enable subtype classification, the format of the annotation files was updated to include WBC subtype labels. The application logic was revised to parse these labels dynamically. The system then displayed the exact subtype label (e.g., “Lympho- cyte,” “Monocyte”) above each detected WBC on the GUI. A helper MATLAB script was developed to simulate varied subtype annotations for testing purposes.

E. Clinical Validation

To ensure the clinical relevance of the application, manual validation of the WBC subtype labels was performed in collaboration with two licensed Medical Technologists. Each annotated image was reviewed to verify the morphological characteristics of the WBCs (nucleus shape, cytoplasmic texture, and cell size). The annotation files were then manually corrected to reflect medically accurate classifications.

F. Limitations and Future Enhancements

Although the system was designed with modular code and functional GUI features, limitations remain in the lack of automated WBC subtype classification through deep learning. While attempts were made to integrate YOLO (You Only Look Once) object detection within MATLAB, practical constraints such as annotation formatting and deep learning toolbox compatibility hindered full implementation. As such, deep learning integration is reserved for future work.

4. Results and Discussion

The developed MATLAB-based diagnostic application successfully detects and classifies blood cells from microscopic images. The project's objective of creating a user-friendly interface that performs RBC and WBC counting and classifies WBC subtypes was achieved through progressive stages of scripting, GUI design, and subtype parsing. This section presents the outcomes of the implementation using multiple sample images and highlights the practical functionality of the system.

Figure 4 shows the overall graphical layout of the MATLAB application developed using App Designer. The user interface is composed of key components such as the image display panel, buttons for loading images and initiating classification, and labels for displaying RBC and WBC counts.

Fig. 4: Design view of the MATLAB GUI for RBC and WBC counting and classification.

Figure 5 demonstrates the detection and classification of a neutrophil. Red bounding boxes denote detected RBCs, while a blue bounding box indicates the identified WBC subtype. The app successfully detected 22 RBCs and 1 WBC, labeled as a neutrophil.

Figure 6 presents another sample output where the app correctly classified a WBC as an eosinophil and counted 25 RBCs. This confirms the parser's capability to distinguish WBC subtypes from the annotation file and display the correct label on the GUI.

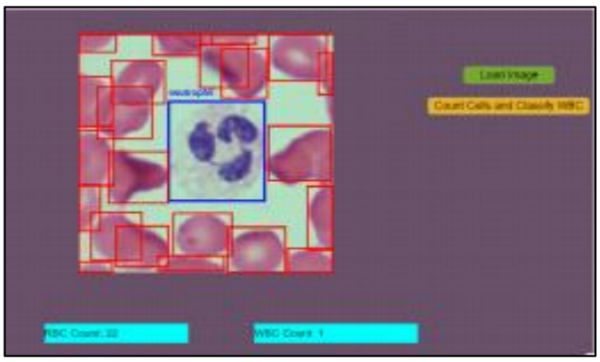


Fig. 5: Neutrophil classification result.

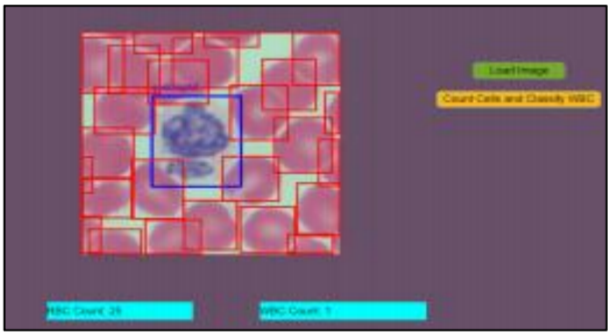


Fig. 6: Eosinophil classification result.

Figure 7 shows the application identifying a monocyte with a surrounding count of 28 RBCs. This scenario further demonstrates the system's robustness in reading varying annotation content and rendering results in real-time.

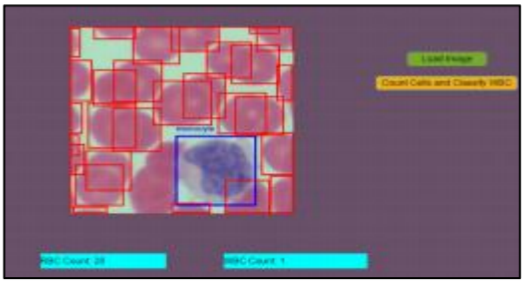


Fig. 7: Monocyte classification result.

Lastly, Figure 8 depicts the classification of a lymphocyte, along with 21 detected RBCs. The labeling mechanism dynamically adjusts to reflect the actual subtype provided in the annotation file.

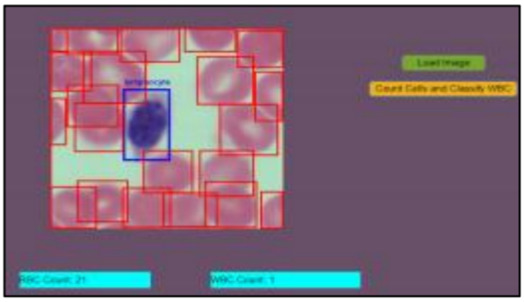


Fig. 8: Lymphocyte classification result.

The system performed as expected, validating its capability to parse annotations, count cells, and classify WBC subtypes accurately. The results support the application's usability and practical relevance in hematological diagnostics, particularly in educational and prototype settings. With its modular structure, the system may be expanded in future versions to incorporate deep learning models for automated classification, batch image processing, and report generation.

SYSTEM ACCURACY EVALUATION

To evaluate the overall performance of the developed MATLAB-based diagnostic system, the researcher assessed three types of predictions: the number of red blood cells (RBCs), the number of white blood cells (WBCs), and the classification of WBC subtypes. Each type of prediction was measured using appropriate accuracy formulas to reflect the system's reliability.

For the classification of WBC subtypes, the researcher compared the actual class labels from the dataset (i.e., Class of WBC) with the system's predictions (i.e., Predicted Class of WBC). Each correct match was counted, and the proportion of correct predictions was computed using the formula:

$$Accuracy_{Class}(\%) = \frac{Number\ of\ Correct\ Class\ Predictions}{Total\ Number\ of\ Predictions} \times 100$$

Using this method, the system achieved a WBC classification accuracy of 76.92% , demonstrating strong performance in identifying neutrophils, lymphocytes, monocytes, and eosinophils from input images.

For the predicted number of RBCs, accuracy was first evaluated using an exact match criterion, where predictions were considered correct only if they matched the actual RBC count exactly. The formula used was:

$$Accuracy_{RBC\ Exact}(\%) = \frac{Number\ of\ Exact\ RBC\ Count\ Matches}{Total\ Number\ of\ Predictions} \times 100$$

Based on this criterion, the system achieved an accuracy of 23.08% . Recognizing that minor counting variations are acceptable in practical applications, the researcher also computed accuracy within a ±2 tolerance range, using the formula:

$$Accuracy_{RBC\ \pm 2}(\%) = \frac{Number\ of\ Predictions\ Within\ \pm 2\ of\ Actual}{Total\ Number\ of\ Predictions} \times 100$$

With this relaxed condition, the RBC count accuracy improved to 38.46% . For the **predicted number of WBCs,** the system's performance was evaluated using an exact match formula similar to that for RBCs:

$$Accuracy_{WBC\ Exact}(\%) = \frac{Number\ of\ Exact\ WBC\ Count\ Matches}{Total\ Number\ of\ Predictions} \times 100$$

The system achieved 100% accuracy in WBC count predictions, indicating that it consistently detected the correct number of white blood cells across all test images.

Conclusion

The Complete Blood Count (CBC) is an essential diagnostic procedure used to assess an individual's health status and identify various hematological conditions. However, conventional methods of blood cell analysis often require either manual counting procedures, which are time-consuming and prone to human error, or automated hematology analyzers, which may be costly and inaccessible in low-resource settings. These challenges emphasize the need for practical and affordable alternatives for blood cell assessment.

A MATLAB-based graphical user interface (GUI) was developed to perform red blood cell (RBC) counting, white blood cell (WBC) counting, and WBC subtype classification from microscopic blood smear images. By utilizing annotation-based localization, the system was able to identify and visualize blood cells without relying on complex image segmentation techniques. The GUI provided an interactive and user-friendly environment for image loading, cell visualization, counting, and classification, making the application suitable for educational and research purposes.

Performance evaluation demonstrated that the system achieved a WBC subtype classification accuracy of 76.92%, an exact RBC counting accuracy of 23.08%, and an improved RBC counting accuracy of 38.46% when a tolerance of ±2 cells was applied. In addition, the application achieved 100% accuracy in WBC counting, indicating reliable detection of white blood cells within the evaluated dataset. These results demonstrate the capability of the developed application to support hematological image analysis and provide meaningful diagnostic information. The developed system achieved its intended objectives and demonstrated the potential of MATLAB-based image processing tools as cost-effective solutions for blood cell analysis. The application also provides a strong foundation for future enhancements involving automated detection, larger datasets, and advanced machine learning or deep learning techniques.

Acknowledgment

We would like to express our sincere gratitude to Dr. Maria Gemel Palconit, our Digital Signal Processing instructor, for her valuable guidance and support throughout this project. Special thanks to the medical technologists Prof. Kristine Lovelle Navarrete and Ruby Jane Agapito for their assistance in validating the classification results. Their contributions were essential to the success of this study.

Future Research Direction

Future researchers may extend this study by evaluating the developed MATLAB-based blood cell diagnostic application using additional performance metrics beyond accuracy, such as precision, recall (sensitivity), specificity, and F1-score, to provide a more comprehensive assessment of the system's performance in detecting, counting, and classifying blood cells. These metrics can offer deeper insights into the model's ability to correctly identify blood cell types, reduce false positives and false negatives, and maintain balanced performance across different WBC subtypes. In addition, future studies may compare the effectiveness of various machine learning and deep learning approaches, including convolutional neural networks (CNNs), YOLO-based object detection models, and transformer-based architectures, to improve classification and counting accuracy. Expanding the dataset to include a larger and more diverse collection of blood smear images, incorporating additional hematological parameters such as platelet detection and abnormal cell identification, and implementing real-time or batch processing capabilities may further enhance the clinical applicability and robustness of the system.

References

1. B. J. Bain, Blood Cells: A Practical Guide, 5th ed. Chich- ester, UK: Wiley-Blackwell, 2015.
2. V. Hoffbrand and P. A. H. Moss, Essential Haematology, 7th ed. Oxford, UK: Wiley-Blackwell, 2016.
3. N. Sharma, A. K. Ray, and S. Sharma, “Segmentation and counting of red blood cells in microscopic images using MATLAB,” Procedia Computer Science, vol. 132, pp. 1423–1431, 2017.
4. J. B. Brown, “History and development of the hemocy- tometer,” Lab Med Journal, vol. 45, no. 3, pp. 117–121, 2014.
5. M. S. Khan and R. Kumar, “Manual cell counting us- ing hemocytometer: A review,” International Journal of Biomedical Sciences, vol. 8, no. 1, pp. 15–20, 2016.
6. J. Illingworth and J. Kittler, ”A survey of the Hough transform,” *Computer Vision, Graphics, and Image Pro- cessing*, vol. 44, no. 1, pp. 87–116, 1988.
7. N. Otsu, ”A Threshold Selection Method from Gray-Level Histograms,” *IEEE Trans. Systems, Man, and Cybernet- ics*, vol. 9, no. 1, pp. 62–66, 1979.
8. Y. D. Zhang et al., ”Exudate detection in color retinal 100 images using automatically selected multiple features,”
9. M. Haralick, ”Statistical and Structural Approaches to Texture,” *Proceedings of the IEEE*, vol. 67, no. 5, pp. 786–804, 1979.
10. C. Cortes and V. Vapnik, ”Support-vector networks,” *Ma- chine Learning*, vol. 20, pp. 273–297, 1995.
11. S. Beucher and F. Meyer,” The Morphological Approach to Segmentation: The Watershed Transformation,” *Math- ematical Morphology in Image Processing*, 1993.
12. R. C. Gonzalez and R. E. Woods, *Digital Image Process-ing*, 4th ed., Pearson, 2018.
13. D. H. Ballard,” Generalizing the Hough Transform to Detect Arbitrary Shapes,” *Pattern Recognition*, vol. 13, no. 2, pp. 111–122, 1981.