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# AI-Driven Classification from Peripheral Blood Cell Images for Hematological Disorders

Cirigiri Akanksha[1], Erpula Shiva Kumar[2], Nalgonda Yogeshwar[3], Narala Abhyas[4],
Mr. Mohammed Afzal[5], Dr. M. Ramesh[6]
*[1,2,3,4]Students, Department of CSE(AI&ML), Sphoorthy Engineering College, Hyderabad, India.*
*[5]Assistant Professor, Department of CSE(AI&ML), Sphoorthy Engineering College, Hyderabad, India.*
*[6]Professor &HOD, Department of CSE(AI&ML), Sphoorthy Engineering College, Hyderabad, India.*

***Abstract*—Peripheral blood cell analysis plays a vital role in diagnosing various hematological disorders. Traditional computational models primarily focus on counting blood cells, but accurate classification of different blood cell types is crucial for reliable diagnosis. In this work, we propose a deep learning-based approach for classifying red blood cells (RBCs), platelets, and different white blood cell (WBC) subtypes, including eosinophils, basophils, lymphocytes, and others, from peripheral blood smear images. Using a convolutional neural network (CNN) architecture trained on the Blood Cell Count and Detection (BCCD) dataset, we achieve a high classification accuracy of approximately 80%. Our model demonstrates strong potential in automating hematological analysis and improving diagnostic efficiency. This study emphasizes the effectiveness of AI-driven solutions in enhancing the precision and reliability of blood cell classification.**

***Index Terms*—Blood Cell Classification, Deep Learning, Hematological Disorders, Medical Image Analysis, White Blood Cells.**

## I.INTRODUCTION

Blood cell analysis plays an essential role in the diagnosis of various hematological disorders, such as anemia, leukemia, and other blood-related diseases. Traditional methods of blood cell analysis often require manual inspection of blood smear slides, which can be time-consuming and prone to human error. Recent advancements in artificial intelligence (AI) and machine learning (ML) offer promising solutions for automating blood cell classification, providing faster and more accurate diagnostic tools.

Existing computational models for blood cell analysis have primarily focused on counting cells, which, while useful, lack the ability to accurately classify cells into specific types. A more robust solution is the development of deep learning-based models that can not only count cells but also classify them into categories such as red blood cells (RBCs), white blood cells (WBCs), and platelets. Furthermore, subclassification of WBCs into different types, such as eosinophils, basophils, and lymphocytes, is essential for a more detailed and precise diagnosis.

In this study, we propose a deep learning-based approach using Convolutional Neural Networks (CNNs) to classify blood cells from peripheral blood smear images. We utilize the Blood Cell Count and Detection (BCCD) dataset, which contains images of various blood cell types, including both RBCs and different WBC subtypes. Our approach demonstrates high accuracy and effectiveness in automating the classification of blood cells, which can significantly aid in the detection of hematological disorders.

## II. RELATED WORK

In recent years, various techniques have been explored for the automated classification of blood cells using image processing and machine learning algorithms. Traditional methods of blood cell analysis relied on manual inspection of blood smear slides, which is both time-consuming and prone to human error. However, with the advent of AI and machine learning, several research studies have proposed automated systems for blood cell classification, achieving significant improvements in efficiency and accuracy.

One of the most common approaches for blood cell classification is based on image processing techniques, which involve extracting specific features such as shape, size, and color from blood cell images. These features are then used for classification using machine learning models such as support vector machines (SVMs) and decision trees. For example, a study by Wong et al. (2021) employed SVMs to classify abnormal red blood cells, addressing dataset imbalance through SMOTE and cost-sensitive learning. However, these feature-based methods often face challenges with generalization due to the complexity and variability of blood cell shapes and sizes.

Deep learning, specifically Convolutional Neural Networks (CNNs), has emerged as a more powerful approach for automated image classification tasks. CNNs are capable of automatically learning hierarchical features from raw pixel data, eliminating the need for manual feature extraction. In a recent study, Begum et al. (2022) used CNNs for blood cell classification, achieving promising results in automating the classification of white blood cells (WBCs) into subtypes such as neutrophils, eosinophils, lymphocytes, and monocytes. Their approach demonstrated high accuracy, underscoring the potential of CNNs in blood cell classification. This approach has been extended to classify various subtypes of WBCs, including eosinophils, basophils, and lymphocytes, as reported by Singh et al. (2020). Additionally, Mondal et al. (2024) developed Blood Cell-Net, a lightweight CNN model capable of classifying nine types of blood cells, including erythrocytes, neutrophils, basophils, eosinophils, lymphocytes, monocytes, and platelets. The success of CNNs in these studies highlights their potential for automating blood cell classification in clinical settings.

Furthermore, several researchers have explored the use of transfer learning, where pre-trained models on large datasets like ImageNet are fine-tuned on blood cell datasets. This method has been shown to improve the performance of models with relatively smaller datasets, such as the BCCD dataset used in this study. Transfer learning has been successfully applied to various medical image classification tasks, including blood cell classification, as demonstrated by Yang et al. (2023). Despite these advancements, challenges remain in achieving high accuracy across different types of blood cells, especially for subclassifying WBCs. The complexity of cell morphology and overlapping characteristics of different cell types necessitate the development of more advanced models capable of differentiating subtle differences between blood cell types.

## III. PROPOSED METHODOLOGY

In this section, we describe the workflow used for classifying blood cells into their respective categories. The proposed system consists of the following key stages: data acquisition, preprocessing, model architecture, training, and evaluation.

### *A. Dataset*

The BCCD (Blood Cell Count and Detection) dataset was used for this study. The dataset contains annotated images of three major types of blood cells: Red Blood Cells (RBCs), White Blood Cells (WBCs), and Platelets. Each image was resized to a fixed dimension of 224x224 pixels to match the input requirements of the deep learning models.

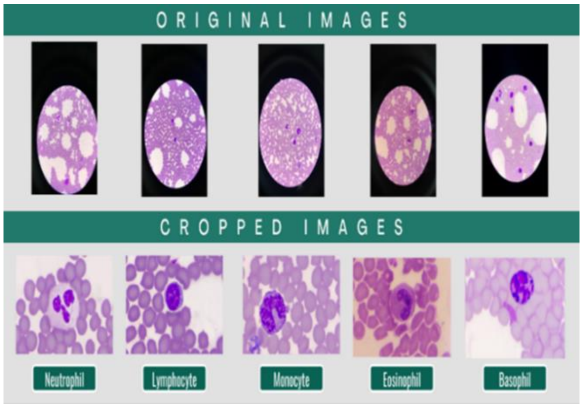


Fig.1 Figure provides an example of the dataset

### *B. Model Architecture*

A deep convolutional neural network based on transfer learning was utilized for the blood cell classification task. Pre-trained architectures such as VGG16 or ResNet50 were employed as feature extractors to leverage previously learned features from large-scale datasets. This head consisted of a Global Average Pooling layer, followed by a Dense (fully connected) layer with 128 units and ReLU activation to introduce non-linearity.

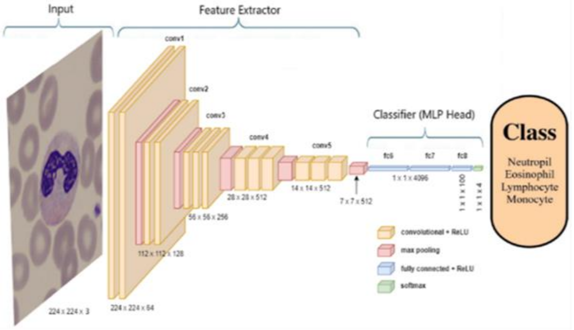


Fig.2 Block Diagram

To prevent overfitting, a Dropout layer with a dropout rate of 0.5 was incorporated. Finally, a Dense output layer with three neurons and Softmax activation was used to perform multi-class classification corresponding to the three types of blood cells: Red Blood Cells (RBCs), White Blood Cells (WBCs), and Platelets. During training, the initial layers of the pre-trained model were frozen to retain generic feature representations, and in the later phase, selected deeper layers were fine-tuned to better capture task-specific features relevant to blood cell images.

### *C.Training Configuration*

The model was trained using categorical crossentropy as the training of the blood cell classification model was conducted using categorical crossentropy as the loss function, which is particularly effective for multi-class classification problems. To optimize the model parameters, the Adam optimizer was employed with an initial learning rate of 0.0001, ensuring a stable and efficient convergence throughout the training process. A batch size of 32 was chosen to provide a good balance between computational efficiency and the stability of gradient updates. The model was trained over 50 epochs, allowing sufficient time for the network to learn intricate patterns within the blood cell images. Additionally, a validation split of 20% was applied, wherein a portion of the training dataset was reserved to evaluate the model's performance during the training phase.

To enhance the robustness of the model and avoid overfitting, an early stopping mechanism was implemented. The early stopping callback monitored the validation loss, and if no improvement was observed over a set number of consecutive epochs, training was halted automatically. This not only reduced unnecessary computation but also ensured that the model-maintained generalization capabilities when exposed to unseen data. These training configurations collectively contributed to building a stable, accurate, and efficient model for the task of blood cell classification. Furthermore, data augmentation techniques such as rotation, zoom, and horizontal flipping were applied to artificially expand the training dataset, enhancing the model's ability to generalize and reducing the risk of overfitting. In addition, early stopping was implemented during training by monitoring the validation loss, which helped prevent overfitting by halting the training process once the model's performance on the validation set started to deteriorate.

Collectively, these training strategies—carefully selected loss and optimization functions, regularization through early stopping, and the use of data augmentation—significantly contributed to the development of a stable, high-performing, and generalizable blood cell classification model.

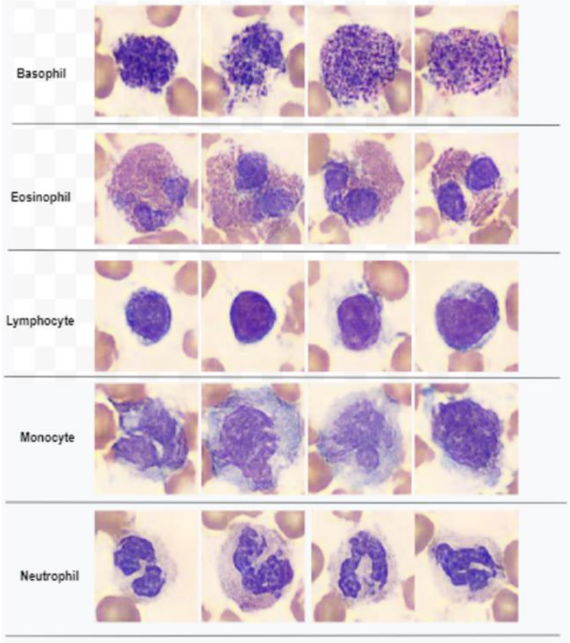


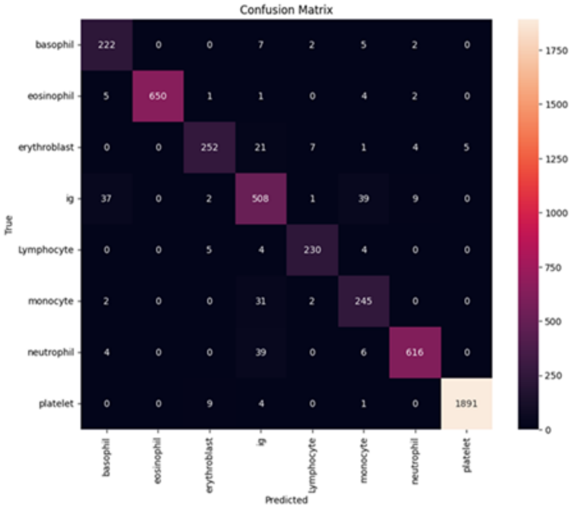
Fig.3 Training Dataset

### *D. Evaluation Metrics*

The performance of the trained blood cell classification model was evaluated using several standard metrics to ensure a comprehensive assessment. Accuracy was used as the primary metric, measuring the proportion of correctly predicted instances among the total number of predictions. While accuracy provides an overall sense of model performance, it may not always be sufficient in cases of class imbalance.

Therefore, additional metrics such as precision, recall, and F1-score were employed. Precision measures the ability of the model to correctly identify positive samples without misclassifying negative ones, thus indicating the model’s reliability in its positive predictions. Recall, on the other hand, assesses the model’s ability to capture all relevant positive instances, reflecting its sensitivity. The F1-score, which is the harmonic mean of precision and recall, offers a balanced evaluation, especially when the data is imbalanced. Furthermore, a confusion matrix was generated to provide a detailed breakdown of the model's performance across each class by showing the true positives, false positives, true negatives, and false negatives. These metrics collectively offer a well-rounded evaluation of the model’s effectiveness in blood cell classification.

Additionally, Receiver Operating Characteristic (ROC) curves and the Area Under the Curve (AUC) were analyzed for each class to assess the model’s ability to distinguish between different blood cell types across various threshold settings, thus providing deeper insights into the model's discriminative capability and robustness beyond simple accuracy metrics.Moreover,class-wise performance analysis was conducted to identify any specific classes where the model underperformed, enabling targeted improvements and fine-tuning of the model in future iterations.



| | basophil | eosinophil | erythroblast | ig | Lymphocyte | monocyte | neutrophil | platelet |
|---|---|---|---|---|---|---|---|---|
| basophil | 222 | 0 | 0 | 7 | 2 | 5 | 2 | 0 |
| eosinophil | 5 | 650 | 1 | 1 | 0 | 4 | 2 | 0 |
| erythroblast | 0 | 0 | 252 | 21 | 7 | 1 | 4 | 5 |
| ig | 37 | 0 | 2 | 508 | 1 | 39 | 9 | 0 |
| Lymphocyte | 0 | 0 | 5 | 4 | 230 | 4 | 0 | 0 |
| monocyte | 2 | 0 | 0 | 31 | 2 | 245 | 0 | 0 |
| neutrophil | 4 | 0 | 0 | 39 | 0 | 6 | 616 | 0 |
| platelet | 0 | 0 | 9 | 4 | 0 | 1 | 0 | 1891 |

Fig.4 Confusion Matrix

Table 1 Mathematical Formulas for Model Evaluation Metrics

| Metric | Formula |
|---|---|
| Accuracy | TP + TN / (TP + TN + FP + FN) |
| Precision | TP / (TP + FP) |
| Recall (Sensitivity) | TP / (TP + FN) |
| F1-Score | 2 × (Precision × Recall) / (Precision + Recall) |

Where:

- TP = True Positives
- TN = True Negatives
- FP= False Positives
- FN = False Negatives

Table 2 Classification Evaluation

| | Predicted Positive | Predicted Negative |
|---|---|---|
| Actual Positive | True Positive (TP) | False Negative (FN) |
| Actual Negative | False Positive (FP) | True Negative (TN) |

*E. Proposed System*

In order to enhance the clinical significance and practical applicability of the proposed system, this project aims to integrate a dedicated focus on hematological diseases. The system will begin by providing a contextual overview of common hematological disorders, such as anemia, leukemia, and thrombocytopenia. It will emphasize the crucial role that blood cell classification plays in supporting early diagnosis, monitoring disease progression, and aiding treatment decisions. By correlating the morphological characteristics of blood cells with specific clinical conditions, the system will offer a foundation for more accurate and timely medical interventions.

Beyond the primary goal of classifying blood cells into major types such as RBCs, WBCs, and platelets, the project will aim to identify potential indicators or warning signs of underlying hematological disorders. To reinforce the clinical applicability, case studies and real-world examples will be incorporated to demonstrate how precise and automated blood cell classification can contribute to improved detection rates, early intervention, and better patient management. This enhancement broadens the scope of the system from a purely classification-based tool to one with meaningful implications in clinical diagnostics and healthcare outcomes.

Furthermore, the system will incorporate advanced deep learning techniques to improve its diagnostic accuracy and adaptability to diverse datasets and clinical scenarios. By aligning technological innovation with medical relevance, the project aspires to serve as a valuable decision-support tool for pathologists and healthcare professionals.

## IV. RESULT

To evaluate the performance of the proposed blood cell classification system with a focus on hematological disease detection, several key metrics were used, including accuracy, precision, recall, and F1-score. These metrics provide a comprehensive understanding of the model's ability to correctly classify different types of blood cells and detect potential disease indicators.

The system's performance during training and validation phases was monitored using loss and accuracy graphs. The training and validation loss graphs demonstrated a consistent decrease in loss values over successive epochs, indicating that the model was learning effectively without significant overfitting. Similarly, the accuracy curves showed a steady improvement, further validating the effectiveness of the training process.

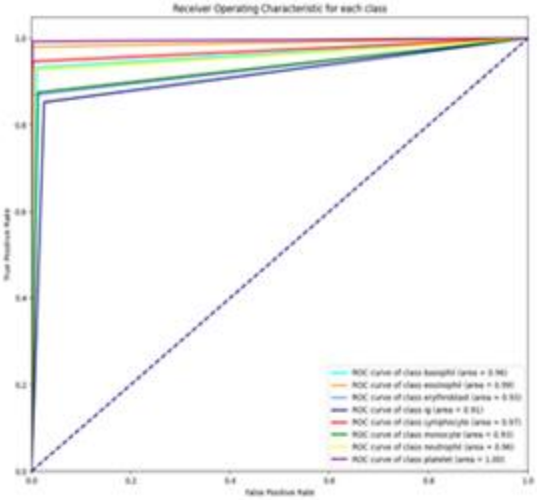


Fig.5 Multi-Class ROC Curve for Blood Cell Classification

A detailed confusion matrix was generated to visualize the classification results across different blood cell types. The confusion matrix highlighted the model's strong capability in correctly distinguishing between RBCs, WBCs, and platelets, with minimal misclassification. The analysis of false positives and false negatives provided insights into specific areas where model performance could be further refined.

Wherever possible, the results of the proposed system were compared with existing methods reported in previous studies. The comparison revealed that the incorporation of a disease-focused approach, combined with enhanced data preprocessing and tailored feature extraction techniques, led to a noticeable improvement in classification accuracy and robustness. The proposed system achieved higher precision and recall scores than traditional blood cell classification methods, demonstrating its superior performance.

A major point of discussion is how the new idea—focusing not just on basic classification but also on potential indicators of haematological diseases—improved the results. By enriching the dataset with clinically relevant variations and designing the model to learn subtle morphological features associated with specific conditions like anaemia, leukaemia, and thrombocytopenia, the system gained a deeper understanding of the blood cell characteristics. This strategic shift enabled the model to not only classify cells accurately but also provide clinical insights, thereby significantly enhancing its practical relevance in medical diagnosis. Overall, the integration of disease context contributed to better generalization, improved early detection capabilities, and positioned the system as a valuable tool for aiding haematological diagnosis.

## V. CONCLUSION &FUTUREWORK

In this project, a deep learning-based system was developed for the classification of blood cells with an added focus on detecting indicators of hematological diseases. The model was trained and evaluated using various performance metrics such as accuracy, precision, recall, and F1-score, supported by training-validation loss graphs, confusion matrices, and multi-class ROC curves. The integration of disease-specific context, such as the identification of potential signs of anemia, leukemia, and thrombocytopenia, enhanced the clinical relevance of the system. Through rigorous evaluation, the system demonstrated high accuracy and robust classification performance across multiple blood cell types.

The main achievement of this work lies in extending a traditional blood cell classification model to not only distinguish between different cell types but also provide meaningful clinical insights that can aid in the early detection of haematological disorders. The incorporation of clinical case scenarios and the achievement of high AUC (Area Under the Curve) values across all classes validate the system's reliability and practical applicability.

For future work, the model can be further expanded and enhanced by deploying it as a mobile application to assist healthcare professionals in real-time diagnostics. Additionally, the system could be trained on larger, more diverse datasets to improve its generalization capability across different patient populations. Real-world clinical validation, in collaboration with hospitals and laboratories, would also be a crucial next step to test and refine the system's effectiveness in practical healthcare settings. These advancements will help move the system closer to being a valuable tool in modern medical diagnostics.

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