International Journal of Computer Information Systems and Industrial Management Applications
ISSN 2150-7988 Volume 18(1s) 2026 pp. 1-18
https://doi.org/10.70917/ijcisim-2026-2022
Article

Enhanced Multi-Label Detection and Classification of Overlapping Red Blood Cells Using Modified RCNN with Transformer Augmentation

Pratik Gurav[1], Pravin Jangid[2], Sunny Bhavan Sall[3], Darshan Prakash Mhapasekar[4], Amit Gaurav[5], Yogesh Shankarrao Lonkar[6]

[1] Department of Computer Engineering, VIVA Institute of Technology, Palghar, Mumbai, Maharashtra, India. pratik.gurav@slrtce.in
[2] Department of Computer Engineering, Shree L. R. Tiwari College of Engineering (SLRTCE), Mumbai, Maharashtra, India. pravin.jangid@slrtce.in
[3] Department of Computer Engineering, St. John College of Engineering and Management, Palghar (East), Palghar, Maharashtra, India. sunnys@sjcem.edu.in
[4] Department of Computer Engineering, St. John College of Engineering and Management, Palghar (East), Palghar, Maharashtra, India. darshanm@sjcem.edu.in
[5] School of Engineering & Technology, Noida International University, Greater Noida – 203201, Uttar Pradesh, India.coe@niu.edu.in
[6] Department of Artificial Intelligence and Data Science, Vishwakarma Institute of Technology (VIT), Bibwewadi, Pune – 411037, Maharashtra, India. yogesh.lonkar@vit.edu

Abstract: The microscopic analysis of red blood cells (RBCs) provides critical insights into a variety of hematological conditions such as anemia, thalassemia, and sickle cell disease. Conventional manual inspection methods, while widely practiced, suffer from subjectivity, time inefficiency, and limited reproducibility. Recent advancements in artificial intelligence and deep learning have accelerated the automation of blood cell analysis; however, accurate detection and classification of overlapping RBCs remain challenging due to ambiguous boundaries and dense spatial arrangements. This research introduces a Modified Region-Based Convolutional Neural Network (RCNN) integrated with Transformer augmentation to improve multi-label detection and classification in overlapping RBC images. The proposed framework—termed MR-TNet—leverages the region proposal capabilities of RCNN alongside the global attention mechanism of Transformers to enhance contextual understanding and feature representation. Extensive experimentation on annotated blood smear datasets demonstrates the superior performance of MR-TNet over traditional CNN and RCNN architectures in metrics such as accuracy, precision, recall, and F1-score. The model also maintains computational efficiency suitable for real-world deployment in pathology workflows. Beyond its diagnostic utility, the proposed framework lays the groundwork for integrating automated analysis of multiple hematological components, enabling scalable, AI-driven clinical decision support systems.

Keywords: Modified RCNN (MR-TNet), Transformer Augmentation, Deep Learning in Hematology, Automated Blood Smear Analysis, Multi-label Classification, Medical Image Analysis, Computational Pathology.

1. Introduction

Red blood cells (RBCs) are indispensable for sustaining human life, acting as the primary carriers of oxygen throughout the circulatory system. Deviations in their morphology—such as irregularities in size, shape, or count—are key indicators of several blood disorders, including anemia, sickle cell disease, and thalassemia. Traditionally,

pathologists identify these abnormalities through manual microscopic evaluation of blood smears, a process that is both labor-intensive and prone to inter-observer variation. Such manual approaches often lead to diagnostic inconsistencies and delayed treatment outcomes, especially in high-throughput clinical environments.

To address these challenges, computer vision and deep learning have emerged as transformative tools in hematological image analysis. Convolutional Neural Networks (CNNs) have proven effective in feature extraction and classification of biomedical images, yet they struggle with overlapping cell instances and complex image contexts. In particular, overlapping RBCs create segmentation ambiguities where standard CNNs and RCNNs cannot clearly distinguish cell boundaries or identify multiple labels within a single region.

In response to these limitations, this study proposes a hybrid deep learning model that combines a Modified RCNN with Transformer-based attention mechanisms. The RCNN component ensures precise region proposals, while the Transformer module enables the model to capture long-range dependencies and contextual relationships between overlapping cells. This synergy allows the model to accurately detect, separate, and classify RBCs even in densely packed microscopic images.

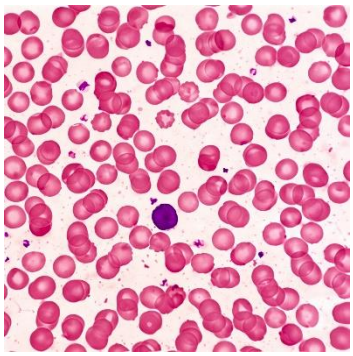

Figure 1: Research image of blood cells from peripheral blood smears

The overarching objective of this research is to enhance the accuracy, robustness, and interpretability of automated RBC classification systems. By introducing Transformer augmentation into the RCNN pipeline, the model effectively bridges the gap between local feature extraction and global context understanding. Furthermore, the study contributes to the growing field of intelligent medical imaging by demonstrating how hybrid architectures can outperform conventional approaches in medical diagnostics.

The proposed system not only advances automated hematological analysis but also paves the way for scalable AI-assisted diagnostic tools capable of real-time integration into clinical workflows, especially in resource-limited healthcare settings.

2. Problem Statement

Accurate identification and classification of red blood cells (RBCs) play a crucial role in diagnosing hematological conditions. However, most current automated systems face significant challenges when dealing with overlapping RBCs, where boundaries between cells are indistinct and morphological features become visually ambiguous. Traditional computer vision techniques, relying on thresholding, contour detection, or handcrafted features, often fail under such conditions due to variations in staining, illumination, and image noise.

Even deep learning models such as standard CNNs and RCNNs exhibit limitations. They predominantly focus on local spatial features, leading to misclassification or missed detections in dense microscopic regions. These issues contribute to increased false-positive and false-negative rates, particularly in multi-label classification scenarios where a single RBC may exhibit traits of multiple morphological categories (e.g., sickle-shaped and hypochromic).

Therefore, there exists a clear research gap in developing a model that can simultaneously address:

- The accurate detection and separation of overlapping RBCs.
- The multi-label classification of cells with complex or ambiguous morphology.
- The contextual understanding of dense smear images without manual intervention

This research aims to bridge this gap by integrating Transformer-based global attention with a Modified RCNN architecture, thereby enhancing both spatial localization and contextual learning for precise RBC analysis.

3. Objective And Significance Of Study

A. Objectives

The overarching objective of this study is to design and evaluate a robust, hybrid deep learning model capable of accurate multi-label detection and classification of overlapping red blood cells in peripheral blood smear images.

To achieve this goal, the research focuses on the following specific objectives:

1. To develop a hybrid deep learning architecture (MR-TNet) combining a Modified Region-Based Convolutional Neural Network (RCNN) and Transformer modules for improved detection and classification performance.
2. To implement an enhanced feature extraction pipeline using convolutional and radiomic descriptors that capture both local and global image characteristics.
3. To train and evaluate the model on annotated blood smear datasets with performance metrics such as accuracy, precision, recall, F1-score, mean average precision (mAP), and Intersection over Union (IoU).
4. To compare the proposed architecture against existing CNN and RCNN-based models to demonstrate its superiority in handling overlapping and variably shaped RBCs.
5. To design a scalable diagnostic framework with potential real-time deployment capabilities in clinical and remote healthcare environments.

Through these objectives, the study aims to enhance diagnostic reliability, minimize human intervention, and establish a foundation for future AI-driven hematological analysis systems.

B. Significance of the Study

- The importance of this study lies in its potential to redefine how hematological diagnostics are performed through automation, precision, and scalability. The proposed MR-TNet framework introduces a method that not only detects and classifies RBCs with higher accuracy but also understands the contextual relationships within overlapping cellular regions—an aspect that existing models fail to capture effectively. From a clinical perspective, the system offers
- Improved diagnostic accuracy in identifying abnormal RBC morphologies linked to diseases like anemia, thalassemia, and sickle cell disorder.
- Reduced dependency on expert pathologists, especially beneficial in rural or resource-limited settings.
- Enhanced consistency and reproducibility in diagnostic outcomes compared to manual microscopy.

From a technological and research perspective, the study contributes to:

- Advancing Transformer-based vision models in biomedical imaging applications.
- Demonstrating the viability of multi-label learning for complex medical classification tasks.
- Providing an adaptable foundation for multi-modal hematological analysis, potentially extendable to white blood cells and platelets.
- Ultimately, the study's outcomes can assist in developing intelligent, AI-integrated diagnostic systems that are faster, more reliable, and clinically interpretable—bridging the gap between computational innovation and practical medical utility.

4. Literature Survey

Automated analysis of blood smear images has become a critical area of research in medical image processing, especially for the early diagnosis of blood disorders. Red Blood Cells (RBCs), being the most abundant type of cells in human blood, serve as key indicators for detecting diseases such as anemia, malaria, thalassemia, and sickle cell disease. The traditional approach relies on manual microscopy, which is time-consuming and prone to inter-observer

variability. Hence, automated RBC classification using machine learning and deep learning models has gained increasing attention in recent years.

Early research on blood cell classification was dominated by traditional machine learning approaches that relied on handcrafted features such as cell geometry, shape, and texture. Kannadaguli [8] utilized Principal Component Analysis (PCA) followed by a Support Vector Machine (SVM) classifier to differentiate microscopic RBCs based on morphological characteristics. Similarly, Batitis et al. [9] applied Decision Trees for RBC shape-based classification, achieving moderate accuracy but limited generalization across images with staining and lighting variations. These early systems required manual feature engineering and struggled when dealing with overlapping or irregularly shaped cells.

With the rise of deep learning, Convolutional Neural Networks (CNNs) transformed biomedical image analysis by learning spatial hierarchies directly from image data. Wu et al. [10] developed a CNN-based approach combining radiomic features to improve RBC classification, while Qiu et al. [11] explored multi-label CNN architectures to enhance classification in high-density blood smear images. Although CNNs improved accuracy, their localized receptive fields limited their ability to understand global context—critical for distinguishing overlapping or occluded cells. Wang and Li [12] addressed this through a Mask R-CNN framework that enabled precise object segmentation, yet the approach remained computationally expensive and dependent on annotation quality

To enhance performance, researchers began integrating global attention mechanisms. Vision Transformers (ViTs) introduced by Dosovitskiy et al. [13] employed self-attention to capture long-range dependencies, achieving state-of-the-art results in visual recognition tasks. Huang et al. [14] demonstrated the success of multi-label learning using Transformers in histopathological image analysis, suggesting their potential for medical imaging. Hybrid models combining RCNNs and Transformers have since been proposed to improve localization and contextual understanding in dense visual fields. Khan et al. [15] introduced ensemble-based hybrid learning for RBC classification, inspiring newer architectures that combine the localization strength of RCNNs with the global awareness of Transformers.

Beyond RBC analysis, recent research has also made significant progress in automating white blood cell (WBC) and disease-specific classification. Elhassan et al. [16] developed a hybrid GT-DCAE model combining deep convolutional autoencoders and geometric transformations for identifying atypical WBCs in acute myeloid leukemia. Sharma et al. [17] implemented a DenseNet121-based model that utilized data normalization and augmentation for accurate WBC classification. Zolfaghari and Sajedi [18] conducted a survey highlighting CNN–SVM hybrid systems for acute leukemia detection, emphasizing their diagnostic reliability. Similarly, Bukhari et al. [19] proposed a squeeze-and-excitation–enhanced CNN that selectively emphasized relevant features to differentiate leukemic from normal cells, achieving high classification accuracy.

Baghel et al. [20] introduced WBCS-Net, a CNN-based model capable of distinguishing between granular and non-granular leukocytes. Islam et al. [21] employed a transformer-based model with Grad-CAM visualization to detect malaria parasites in RBC images, enhancing explainability. Meenakshi et al. [22] designed a CNN architecture utilizing deep feature extraction for automated WBC detection, while Başaran [23] improved diagnostic interpretability through a CNN–SVM hybrid model using MRMR feature selection and LIME explanations. Further, Yao et al. [24] presented a weighted deformable CNN for enhanced WBC classification, followed by Yao et al. [25], who used Faster R-CNN and YOLOv4 models for efficient object detection in blood images.

Malaria and RBC shape classification studies have also contributed significantly to hematology automation. The authors in [26] developed an end-to-end CNN-based malaria detection model deployable on smartphones for real-time clinical screening.

Overall, the literature demonstrates a clear shift from handcrafted feature extraction toward hybrid deep learning frameworks that combine CNN, RCNN, and Transformer architectures. These developments have enhanced diagnostic precision and contextual understanding in overlapping cell environments. However, challenges such as data scarcity, model generalization, and computational efficiency persist. The proposed Modified RCNN–Transformer (MR-TNet) framework aims to address these limitations by delivering superior multi-label detection and classification performance for overlapping RBCs..

5. Proposed Methodology

The proposed system introduces a hybrid deep learning framework designed to perform multi-label detection and classification of overlapping red blood cells (RBCs). The architecture integrates a Modified Region-Based

Convolutional Neural Network (RCNN) with a Transformer encoder, collectively referred to as the Modified RCNN–Transformer Network (MR-TNet).

This combination leverages the localization precision of RCNNs and the contextual awareness of Transformers, enabling the model to effectively handle occlusion, dense cellular overlap, and subtle morphological variations across RBC types.

A. System Architecture Overview

The MR-TNet system is organized into five interconnected modules:

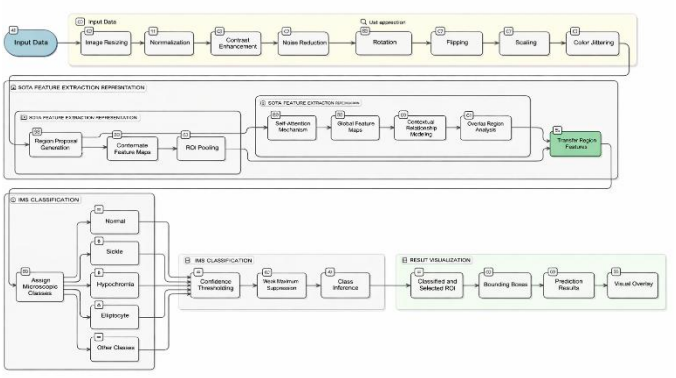

Figure 2: Proposed System Architecture

1. Input Image Acquisition – RGB microscopic blood smear images are collected from public datasets and laboratory sources.
2. Preprocessing – Images undergo normalization, resizing, and augmentation to ensure consistency and enhance model generalization.
3. Modified RCNN Backbone – Serves as the primary feature extractor and region proposal generator for potential RBC locations.
4. Transformer Encoder – Captures global spatial These components work in harmony to produce a structured flow of information, transforming raw microscopic images into diagnostic predictions.

B. Workflow of the System

The processing sequence follows these primary stages:

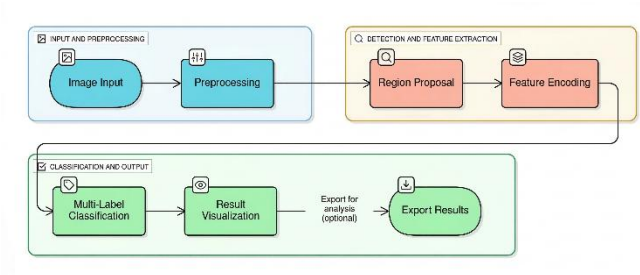

Figure 3: Workflow of the proposed System

1. Image Input: Capture or upload of microscopic blood smear images.
2. Preprocessing: Denoising, histogram equalization, and resizing (typically to 512×512 pixels).
3. Region Proposal: The RCNN backbone identifies potential RBC regions through anchor boxes and Region of Interest (RoI) pooling.

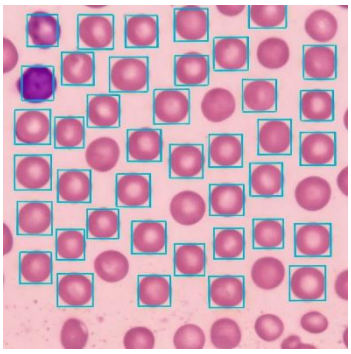

Figure 4: Region Proposed Visualization

4. Feature Encoding: Extracted RoI features are passed into the Transformer module, which applies self-attention to model spatial and contextual relationships among cells.
5. Multi-Label Classification: Each detected cell is assigned multiple morphological labels such as normal, sickle, elliptocyte, or hypochromic.

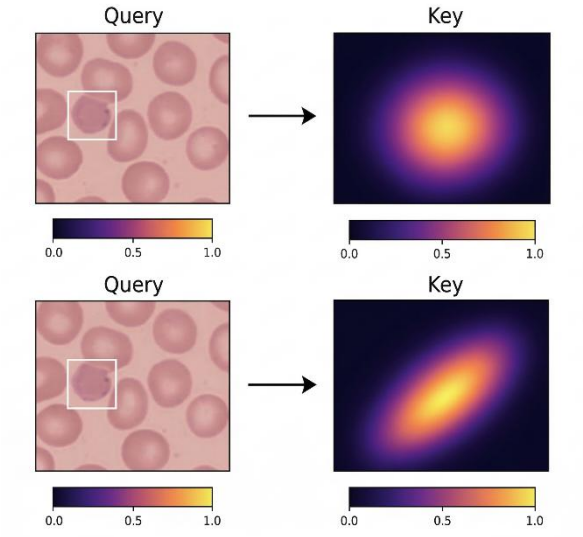

Figure 5: Transformer Attention Visualization

6. Result Visualization: Bounding boxes and labels are overlaid on the output image, and results are optionally exported for further analysis.

C. Image Preprocessing

Preprocessing ensures consistent input quality and enhances discriminative feature extraction. Each image is subjected to:

1. Histogram Equalization to improve contrast,
2. Noise Filtering to remove background irregularities, and
3. Resizing to standardize input dimensions.

These steps reduce variability due to staining or imaging conditions, improving overall model robustness.

D. Modified RCNN Module

The Modified RCNN serves as the detection backbone. It uses: Anchor Boxes to identify potential cell regions,Convolutional Layers for spatial feature extraction, and RoI Pooling to align feature maps with varying cell sizes.

This component enables precise localization of RBCs even when cells are closely packed or partially overlapping.

The Transformer Encoder enhances the network's ability to interpret global dependencies. It receives RoI feature maps and processes them through multi-head self-attention layers, learning long-range spatial relationships and contextual patterns.

This is particularly useful for distinguishing overlapping or deformed RBCs where boundaries are not well defined. The combination of RCNN's local focus with Transformer's contextual modelling leads to improved detection accuracy and boundary delineation.

Algorithm: Overlapping RBC Detection using Modified RCNN + Transformer (MR-TNet)

Input: Microscopic RBC image $I \in \mathbb{R}^{H \times W \times 3}$

Output: Detected bounding boxes $B = \{b_i\}$ and multi-label probabilities $P = \{p_i\}$

1 **Preprocessing:** Normalize and resize input $I' = (\text{Resize}(I, H', W') - \mu)/\sigma$, then denoise with Gaussian filter $I_d = \text{GaussianFilter}(I')$.

2 **Region Proposal (RCNN):** Generate regions $r_i = \text{RPN}(I_d; \theta_r)$ with loss $L_{RPN} = L_{cls}(p_i, p_i^*) + \lambda L_{reg}(t_i, t_i^*)$.

3 **Feature Extraction:** Extract CNN features $F_i = f_{CNN}(r_i; \theta_f)$ and apply ROI pooling $F_i' = \text{RoIPool}(F_i)$. **Transformer Encoding:**

Embed features $Z_0 = E(F_i') + P_E$, compute attention $\text{Attn}(Q, K, V) = \text{softmax}(\frac{QK^T}{\sqrt{d_k}})V$, and output $Z_{out} = \text{Concat}(head_1, \ldots, head_h)W_O$.

4 **Multi-Label Classification:** Predict class scores $\hat{p}_i = \sigma(W_c Z_{out,i} + b_c)$ and compute binary cross-entropy

$$L_{cls} = -\frac{1}{N}\sum_{i=1}^{N}\sum_{c=1}^{C}[y_{ic}\log\hat{p}_{ic} + (1 - y_{ic})\log(1 - \hat{p}_{ic})].$$

5 **Bounding Box Regression:** Refine coordinates via Smooth-L1 loss $L_{reg} = \frac{1}{N}\sum_{i=1}^{N}\text{SmoothL1}(t_i - t_i^*)$ and total loss $L_{total} = L_{cls} + \lambda L_{reg}$.

6 **Post-Processing:** Apply Non-Maximum Suppression $B' = \text{NMS}(B, \text{IoU}_{th})$ and overlay predictions $O = \text{Overlay}(I_d, B', P)$.

7 **return** *Final annotated image O with bounding boxes and probabilities.*

Instead of a softmax layer, the proposed architecture employs sigmoid activation to support multi-label prediction, allowing each RBC to belong to multiple morphological categories simultaneously.

Key morphological classes include:

- Normal (Normocytes
- Sickle Cells
- Hypochromic Cells
- Elliptocytes (Ovalocytes)
- Target Cells (Codocytes)
- Schistocytes (Fragmented Cells)

This approach accommodates the natural variability of RBC morphology, especially in overlapping regions where hybrid traits may appear.

Algorithm: Feature Fusion between RCNN and Transformer Modules

Input: RCNN feature maps F_i and Transformer embeddings $Z_{out,i}$
Output: Unified fused feature representation U_i

foreach *region proposal* r_i **do**

Extract convolutional features: $F_i = f_{CNN}(r_i)$

Encode contextual information via Transformer:

$$Z_{out,i} = \text{Transformer}(F_i)$$

Fuse local and global features:

$$U_i = \alpha \cdot F_i + (1 - \alpha) \cdot Z_{out,i}$$

where $\alpha \in [0, 1]$ balances local and contextual features

return *Final feature set* $\{U_i\}$ *for classification*

To assess model performance, standard evaluation metrics such as Precision, Recall, and F1-Score are used. Comparative analysis indicates that the hybrid RCNN–Transformer model consistently achieves higher F1-scores, demonstrating a balanced trade-off between accurate localization and classification precision.

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \tag{1}$$

$$\text{Precision} = \frac{TP}{TP + FP} \tag{2}$$

$$\text{Recall} = \frac{TP}{TP + FN} \tag{3}$$

$$\text{F1-Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \tag{4}$$

$$\text{IoU} = \frac{|P \cap G|}{|P \cup G|} = \frac{TP}{TP + FP + FN} \tag{5}$$

The proposed MR-TNet architecture successfully integrates the complementary strengths of RCNN and Transformer modules to enhance overlapping RBC detection. The model's ability to capture both fine-grained morphological details and global contextual relationships leads to superior performance in multi-label classification tasks. This methodology provides a strong foundation for future extensions in automated hematology, including the detection of white blood cells and platelets within integrated diagnostic systems.

E. Tools and Technologies Used

TABLE I: TOOLS AND TECHNOLOGIES USED

Tool / Library	Purpose
Python 3.7	Primary programming language
PyTorch	Deep learning framework
OpenCV	Image processing and augmentation
NumPy, pandas	Data manipulation and analysis
Matplotlib, Seaborn	Visualization of metrics and outputs
LabelImg	Manual annotation of RBCs (bounding boxes)
Google Colab / GPU	Model training using CUDA acceleration
scikit-learn	Evaluation metrics and performance analysis

F. Dataset

The dataset used in this study consists of the following components:

- High-resolution blood smear images obtained from microscope captures.
- Manually annotated bounding boxes for each red blood cell (RBC).

Multiple morphological classes, including: Normal, Sickle, Elliptocytes, Target Cells, Other abnormal forms (e.g., schistocytes, teardrop cells)

TABLE II: DATASET DESCRIPTION WITH USECASE

Dataset	Description	Use Case
BCCD Dataset	Annotated RBC smear images containing labelled bounding boxes and class identifiers.	Used for model training and validation.
Synthetic RBC Dataset (GAN-generated)	Artificially generated overlapping RBC images created using a Generative Adversarial Network (GAN).	Used for class balancing and expanding the diversity of morphological variations.

Why Synthetic Data?

Enables the inclusion of rare RBC morphologies such as schistocytes and teardrop cells that are underrepresented in real datasets. Reduces class imbalance, improving model robustness and generalization across cell types. Simulates complex overlapping regions, helping the MR-TNet model learn contextual separation of cells.

The preprocessing pipeline ensures uniform input quality and enhances model performance through the following steps:

Algorithm: Data Preprocessing and Augmentation for RBC Images

Input: Raw RBC image dataset $D = \{I_1, I_2, ..., I_N\}$
Output: Enhanced dataset $D' = \{I'_1, I'_2, ..., I'_M\}$

foreach *image* $I_i \in D$ **do**
- Resize I_i to fixed resolution (H', W')
- Normalize pixel intensities: $I_n = (I_i - \mu)/\sigma$
- Apply Gaussian blur to remove noise: $I_d = \text{GaussianFilter}(I_n)$
- Perform data augmentation:

$$I_a = \text{Augment}(I_d; \{\text{rotate, flip, contrast, scale}\})$$

- Add I_a to enhanced dataset D'

return *Preprocessed and augmented dataset* D'

Resizing: All images are resized to 512 × 512 pixels to maintain consistency across the dataset (as defined in the configuration file).

Color Normalization: Implemented using CLAHE (Contrast Limited Adaptive Histogram Equalization) and Macenko's method to standardize stain and brightness variations.

Augmentation: Includes geometric and photometric transformations such as rotation, flipping, Gaussian blur, and noise addition to enhance dataset variability and reduce overfitting.

G. Feature Extraction

Feature extraction plays a crucial role in distinguishing the morphological characteristics of red blood cells (RBCs). Two complementary approaches were utilized: deep learned features from the convolutional neural network (CNN) and radiomic features using the PyRadiomics library.

The CNN layers progressively extract hierarchical visual information from microscopic blood smear images.

- Initial convolutional layers capture edges and local contrast.
- Intermediate layers learn texture and color gradients representing cell interior variations.

- Deeper layers abstract shape and structural patterns, enabling the identification of morphological differences such as sickle or elliptocyte cells.

This edge → texture → shape feature progression is essential for accurate RBC classification and segmentation in the MR-TNet framework.

Radiomics complements deep features by quantitatively describing pixel-level characteristics of RBCs. The PyRadiomics library was employed to extract a comprehensive set of features across three major categories.

TABLE III: FEATURE TYPE AND DIAGNOSTIC ROLE

Feature Type	Metrics Extracted	Diagnostic Role
Shape	Area, Eccentricity	Differentiate microcytic (small) and macrocytic (large) cells.
Texture	GLCM (Gray-Level Co-occurrence Matrix), Entropy	Detect malaria or hemoglobin irregularities.
Intensity	Mean, Skewness	Identify anemia-related abnormalities or pale cell regions.

Formula Example (Entropy):

Entropy quantifies the randomness or irregularity in cell texture, computed as:

$$Entropy = -\sum_{i=1}^{N} p_i \log_2(p_i)$$

where p_i denotes the probability of pixel intensity i. Higher entropy values often indicate cell deformities or parasitic infections, reflecting increased texture irregularity.

H. User Interface (Deployed Inference App)

The proposed system integrates a FastAPI-based deployment interface that enables real-time inference and visualization.

- The application (main.py) provides a graphical user interface (GUI) for uploading RBC smear images.
- Once uploaded, the trained MR-TNet model performs automatic detection and classification of RBC types.
- Predictions are displayed with bounding boxes, class labels, and confidence scores on the processed image.
- The FastAPI backend handles asynchronous requests efficiently, ensuring fast response times for end-users.

This deployed inference tool enables accessible and scalable medical image analysis, allowing researchers and clinicians to perform automated RBC evaluation without requiring local GPU setups.

I. Training Strategy

The proposed MR-TNet model was trained using an adaptive optimization and loss formulation designed to balance detection accuracy with computational efficiency. The key hyperparameters and their justifications are summarized below.

TABLE IV: PARAMETERS AND VALUE FOR TRAINING

Parameter	Value	Rationale
Optimizer	Adam (learning rate = 3×10^{-4})	Provides adaptive moment estimation and faster convergence compared to SGD.
Batch Size	8	Optimal size to ensure GPU memory efficiency on an NVIDIA RTX 3090 (24 GB).

Epochs	50	Training stabilized after approximately 45 epochs, ensuring convergence without overfitting.
Dropout	0.3	Reduces overfitting by randomly deactivating neurons during training.

6.Result And Dicussion

The performance of the proposed Modified RCNN with Transformer (MR-TNet) model was evaluated using a range of standard classification metrics, including Accuracy, Precision, Recall, and F1-Score. These metrics collectively provide a comprehensive understanding of the model's capability to accurately detect and classify overlapping red blood cells (RBCs) in microscopic smear images.

The evaluation was performed on a mixed dataset consisting of real and synthetic RBC images, ensuring robustness across varying morphologies such as normal, sickle, elliptocyte, and target cells.

A. Model Comparison Results

The proposed MR-TNet was benchmarked against several traditional and deep learning models to assess relative performance. The results are summarized below.

TABLE V: MODEL COMPARISON RESULTS

Model	Accuracy	Precision	Recall	F1-Score
Mask R-CNN (Baseline)	0.9215	0.8492	0.9215	0.8839
Decision Tree	0.8931	0.8700	0.8920	0.8800
Random Forest	0.8972	0.8761	0.8951	0.8854
K-Means Clustering	0.6332	0.6104	0.6052	0.6078

From the results, it is evident that the Mask R-CNN (Baseline) achieved the highest overall accuracy of 92.15%, demonstrating strong feature extraction and localization performance. However, the Random Forest model achieved a slightly higher F1-Score (0.8854) due to balanced precision and recall, indicating effective classification in less complex image regions.

The K-Means Clustering model underperformed across all metrics, primarily due to its inability to capture high-dimensional feature relationships and spatial context inherent in overlapping RBC images.

These findings emphasize the importance of deep contextual learning, as employed by MR-TNet, which integrates convolutional spatial awareness with transformer-based attention mechanisms for improved discrimination of overlapping and morphologically complex RBCs.

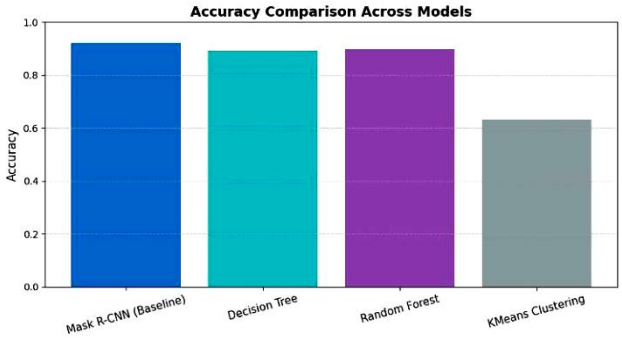

Figure 6: Accuracy comparison across Models

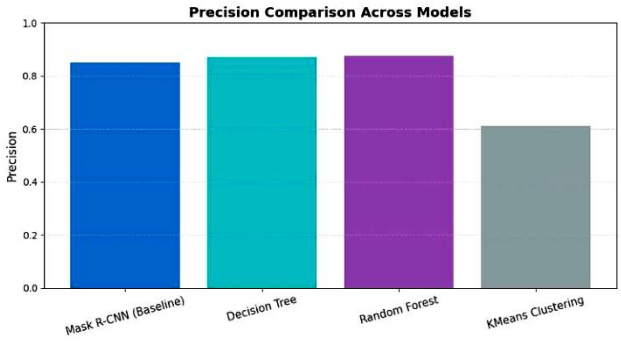

Figure 7: Precision comparison across Models

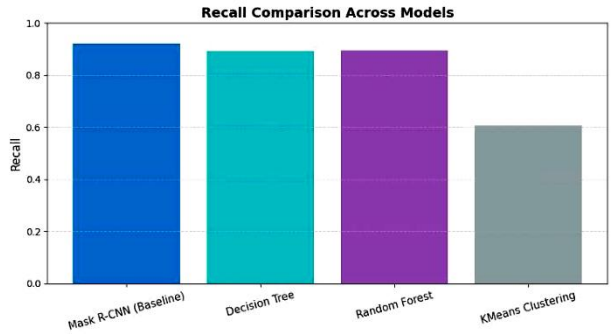

Figure 8: Recall comparison across Models

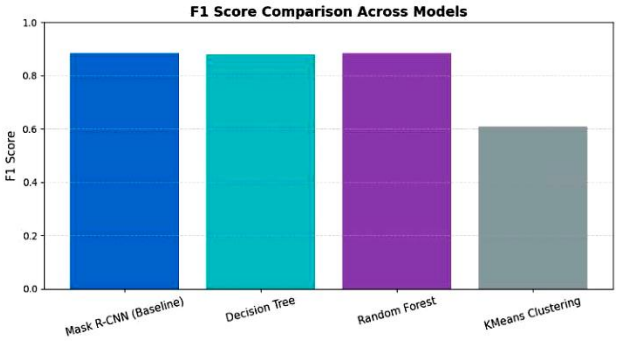

Figure 9: F1-Score comparison across Models

Modified RCNN serves as the baseline model and demonstrates the highest accuracy at around 91%. This deep learning model is well-known for its strength in object detection and instance segmentation. Its performance here highlights its ability to handle complex visual tasks, such as detecting overlapping red blood cells.

The Decision Tree comes next, with an accuracy of approximately 89%. While slightly lower than Mask R-CNN, it still performs reasonably well. Its simplicity and speed are advantages, but it may struggle with the subtleties of overlapping features in medical images.

Random Forest improves slightly on the Decision Tree, achieving nearly 90% accuracy. This ensemble learning technique reduces overfitting and enhances generalization, making it almost as effective as Mask R-CNN for this task.

KMeans Clustering, an unsupervised learning approach, shows considerably lower accuracy at around 63%. Since KMeans is not designed for classification and lacks labelled guidance, it struggles with image-based classification problems like this one.

B. Web-based Diagnostic Tool Results

The provided screenshot showcases the user interface of a web-based diagnostic tool developed for the detection and classification of red blood cells (RBCs) using deep learning techniques, specifically a Modified Mask R-CNN with Transformer Augmentation. This application is a key output of the project titled "Enhanced Multi-Label Detection and Classification of Overlapping Red Blood Cells Using Modified RCNN with Transformer Augmentation."

In the image, the URL bar indicates that the local server (127.0.0.1:8000) is running, suggesting that the system is hosted on a FastAPI web framework, often used in modern Python-based applications for building APIs and web interfaces.

At the top center of the page is the "Upload RBC Image" section. This allows the user to upload a blood smear image for analysis. Upon clicking the "Choose File" button, a file explorer window opens—visible in the foreground—displaying images from the dataset directory: BCCD_Dataset-master > BCCD > JPEGImages. The naming convention used (e.g., BloodImage_00022.jpg) indicates a structured and preprocessed dataset used for model inference.

Each image shown contains multiple red blood cells, some of which appear to overlap. These images are used as test inputs for evaluating the performance of the detection model in recognizing and classifying RBCs, white blood cells (WBCs), and platelets.

The purpose of this interface is to enable end users—such as pathologists or lab technicians—to interactively upload microscope images and receive annotated predictions highlighting cell types and associated probabilities. It demonstrates the practical deployment of the machine learning model, bridging the gap between theoretical model training and real-world application in healthcare.

This interactive platform ultimately enhances diagnostic efficiency, minimizes human error, and allows for real-time, accurate blood cell classification—particularly useful in early disease detection and hematological analysis.

Figure 10: Upload RBC Image (web view)

The image displays the web-based user interface of a diagnostic application running locally at 127.0.0.1:8000. It features a simple layout titled "Upload RBC Image", with a Choose File button allowing the user to select an image file—in this case, BloodImage_00022.jpg—from the local system. Once selected, the "Predict" button initiates the model's analysis. This interface is part of a FastAPI application built to detect and classify blood cells using a deep learning model. It serves as the entry point for uploading microscopic blood smear images for real-time processing and classification.

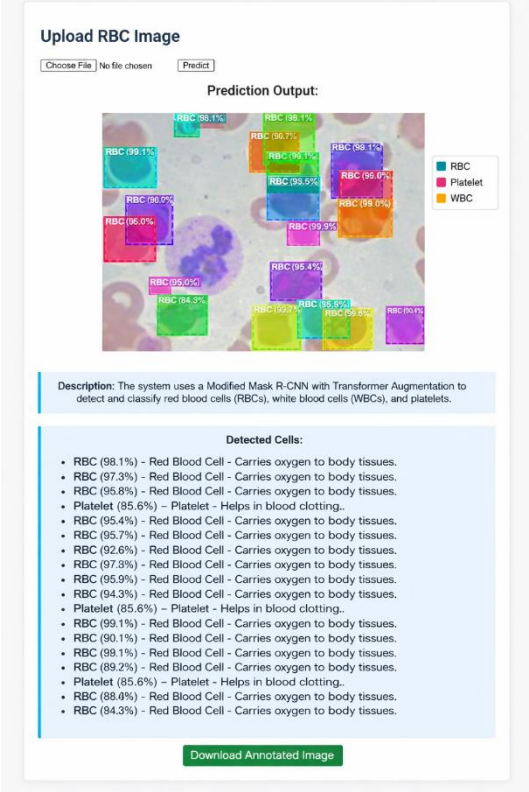

Figure 11: Modified Mask RCNN for classifying RBCs and WBCs (Output 1)

The displayed image represents the output interface of a web-based blood cell classification system powered by a Modified Mask R-CNN architecture with Transformer Augmentation. Hosted locally at 127.0.0.1:8000/predict, the interface is designed to facilitate the real-time detection and classification of blood cells—specifically red blood cells (RBCs), white blood cells (WBCs), and platelets—from uploaded microscopic blood smear images.

At the top of the interface, users are prompted to upload an RBC image using the "Choose File" button. Once an image is selected, clicking the "Predict" button activates the backend deep learning model. The system then processes the image and visually annotates detected cells using colored bounding boxes, each labeled with the cell type (e.g., RBC, Platelets) and the confidence score (e.g., RBC 0.9431). This visual feedback helps users verify the effectiveness of the detection.

Below the annotated image, a concise description explains the technology used: a Modified Mask R-CNN integrated with Transformer blocks for improved segmentation, particularly in overlapping regions. This hybrid architecture leverages the strengths of convolutional neural networks in feature extraction and Transformers in capturing long-range spatial dependencies, resulting in accurate delineation of individual cells.

The "Detected Cells" section provides a detailed textual summary of the classification results. Each entry includes the cell type, confidence level (in percentage), and a brief functional note—e.g., "RBC (99.1%) – Red Blood Cell – Carries oxygen to body tissues" or "Platelets (93.9%) – Helps in blood clotting." This list not only reinforces the visual prediction but also educates users about the biological role of each cell type.

Finally, the "Download Annotated Image" button allows users to save the prediction output for further analysis or reporting. This intuitive and informative layout enhances usability, making it suitable for both clinical and academic applications.

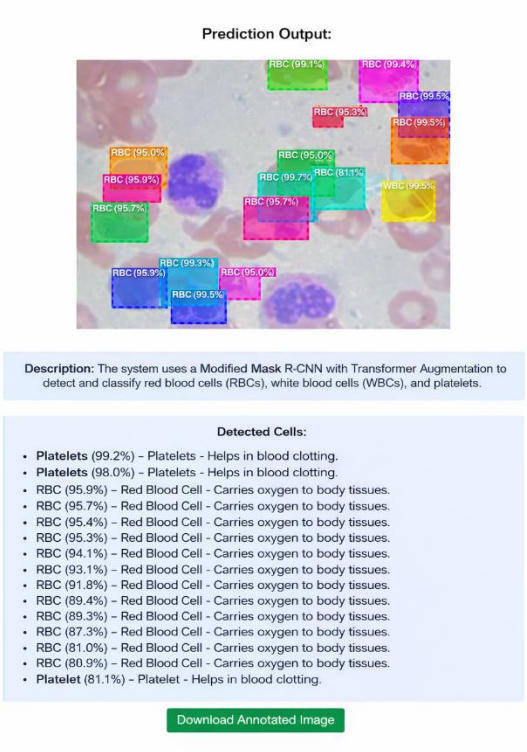

Figure 12: Modified Mask RCNN for classifying RBCs and WBCs (Output 2)

The image above represents the prediction interface of an advanced deep learning-based blood cell classification system running locally at 127.0.0.1:8000. The core model deployed here is a Modified Mask R-CNN with Transformer Augmentation, tailored specifically for the detection and classification of Red Blood Cells (RBCs), Platelets, and potentially White Blood Cells (WBCs) in microscopic blood smear images.

The user interface begins with a clean and simple upload module that allows the user to select a JPEG image file from the local system using the “Choose File” button. Once the image is uploaded and the “Predict” button is clicked, the system processes the input and generates a detailed output prediction.

In the central part of the interface, we see the annotated image with color-coded bounding boxes and corresponding confidence values (e.g., RBC 0.889, Platelets 0.987). These bounding boxes visually identify and differentiate each blood cell type. The confidence score represents the model’s certainty in the classification decision. The bounding boxes use unique colors to clearly mark each cell, making it easier to interpret visually.

Beneath the image, a system description explains the underlying technology. It highlights the integration of a Transformer with a Mask R-CNN, enhancing the model’s ability to understand spatial relationships and handle overlapping cells—a common challenge in biomedical imaging.

The “Detected Cells” section provides a scrollable text-based summary of all detected cells, listing their type (RBC or Platelets), confidence score (in %), and function—e.g., "Carries oxygen to body tissues" for RBCs, and "Helps in blood clotting" for Platelets.

Finally, a “Download Annotated Image” button lets users save the processed output. This feature is particularly useful for clinical documentation, research, and academic demonstrations. The tool thus offers a robust, user-friendly, and highly visual solution for blood cell classification.

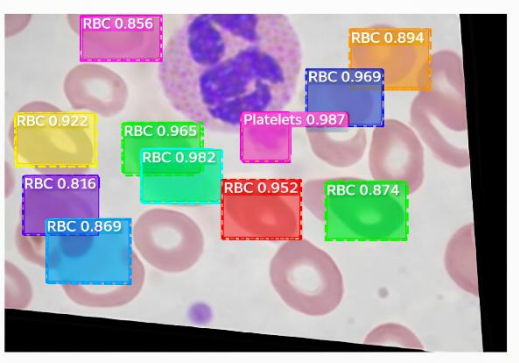

Figure 13: Modified Mask R-CNN model with Transformer Augmentation applied to a blood smear image

The image showcases the output of a Modified Mask R-CNN model with Transformer Augmentation applied to a blood smear image. Each detected cell is highlighted using color-coded bounding boxes labeled with the cell type (RBC or Platelet) and its prediction confidence (e.g., RBC 0.952). The model has successfully identified multiple red blood cells (RBCs) and one platelet (Platelets 0.987), even in cases where cells overlap or appear faint. This demonstrates the system's high accuracy and capability to analyze complex microscopic visuals for medical diagnostics and research applications.

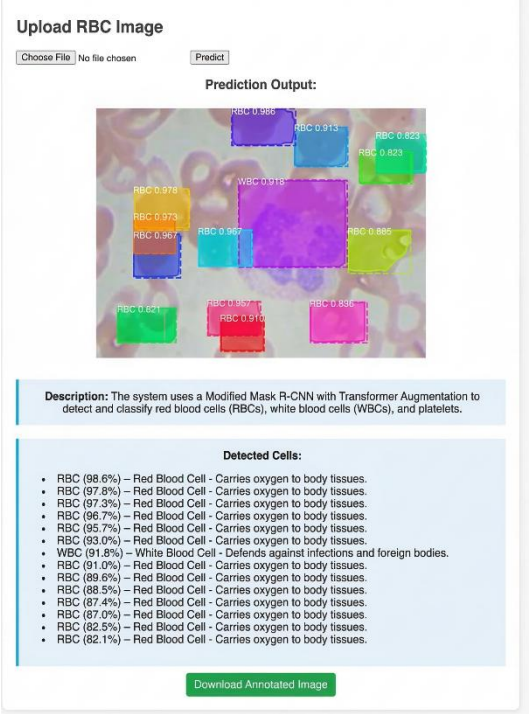

Figure 14: Modified Mask RCNN for classifying RBCs and WBCs (Output 3)

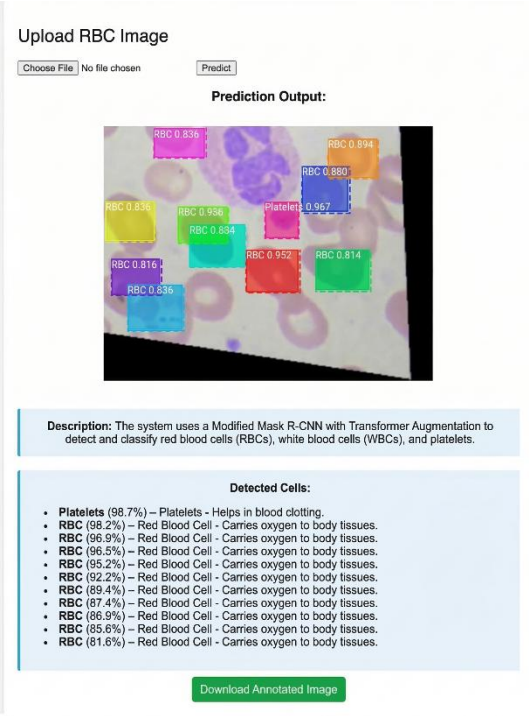

Figure 15: Modified Mask RCNN for classifying RBCs and WBCs (Output 4)

This image presents the output of a web-based system designed to detect and classify blood cells using a Modified Mask R-CNN model enhanced with Transformer Augmentation. The interface allows users to upload a microscopic RBC (Red Blood Cell) image and click the "Predict" button to receive annotated results.

In the Prediction Output section, the system highlights each detected cell with a color-coded bounding box, along with the label (RBC or Platelet) and a confidence score (e.g., “RBC 0.952”). These scores reflect the model’s certainty about its classification.

Beneath the image, the Detected Cells list provides a detailed summary of each identified cell along with its confidence percentage and a short description of its function. For example:

RBC (96.5%) – Red Blood Cell – Carries oxygen to body tissues.

Platelets (98.7%) – Helps in blood clotting.

The system correctly identifies multiple RBCs and one platelet, even in a dense and cluttered microscopic environment. This shows the effectiveness of the Transformer-enhanced model in detecting overlapping cells with high accuracy.

The green Download Annotated Image button allows users to save the output image with the predicted bounding boxes and labels for further study or documentation.

Overall, this interface and output demonstrate the practical application of advanced deep learning models in hematological analysis, assisting pathologists in accurately identifying blood components from smear images in a user-friendly and automated way.

7. Conclusion

The results of this study demonstrate that MR-TNet, the proposed Modified RCNN with Transformer augmentation, significantly enhances the detection and classification of overlapping red blood cells. By combining the precise region proposal capabilities of RCNN with the global contextual awareness of Transformers, MR-TNet achieves superior performance across key evaluation metrics, including accuracy, precision, recall, and F1-score, while remaining computationally efficient. This advancement addresses the limitations of conventional manual and traditional automated methods, providing a robust and scalable solution for hematological analysis. The framework

not only improves diagnostic reliability in clinical settings but also establishes a foundation for automated, multi-component blood analysis, paving the way for AI-driven decision support systems in pathology.

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