

A Cloud-Enabled Deep Learning Framework for Real-Time Red Blood Cell Infection Diagnosis

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ABSTRACT

Red blood cell (RBC) infections, such as malaria and sickle cell disease, remain serious public health concerns, particularly in regions with limited diagnostic resources. Conventional diagnostic techniques, including manual microscopic examination and biochemical testing, are time-consuming, subjective, and reliant on expert interpretation, often resulting in delayed or inconsistent diagnoses. To address these limitations, this study proposes an artificial intelligence-based framework for automated detection and classification of RBC infections using image analysis. Initially, traditional machine learning models such as Decision Tree Classifier (DTC) and Extra Trees Classifier (ETC) are implemented as baseline approaches using extracted features like cell shape, size, and texture. Although ETC improves performance compared to DTC due to ensemble learning, both methods remain constrained by limited feature representation. To overcome these challenges, a Convolutional Neural Network (CNN) is introduced to automatically learn discriminative features directly from microscopic blood smear images. The proposed CNN effectively captures cellular morphology and structural abnormalities, achieving accuracy above 95% with improved precision, recall, and F1-score. The system enables rapid, reliable classification, reduces dependency on manual analysis, and supports real-time screening. Overall, this intelligent framework highlights the effectiveness of deep learning in enhancing diagnostic accuracy, accessibility, and early disease detection.

Keywords: Red Blood Cell Infections, Decision Tree Classifier, Extra Trees Classifier, Convolutional Neural Networks, Automated Diagnosis

1. INTRODUCTION

Red Blood Cell (RBC) infections, including malaria and sickle cell disease, pose a significant health crisis in India. Malaria alone accounted for over 4 million cases in 2020, with a majority of cases reported in Odisha, Chhattisgarh, Jharkhand, and West Bengal. Sickle cell disease, an inherited blood disorder, is also highly prevalent in tribal regions of central and eastern India. Traditional diagnostic methods such as microscopic examination of stained blood smears, ELISA, and PCR-based techniques have been the gold standard for detection. These methods are labour intensive, time-consuming, and require skilled pathologists. The increasing burden of RBC infections highlights the need for automated solutions that ensure fast, accurate, and cost-effective diagnosis, reducing mortality rates and improving healthcare outcomes. AI-powered deep learning models offer a transformative solution by automating RBC infection classification, ensuring rapid and error-free detection of diseases from microscopic images. Deep learning has revolutionized medical diagnostics by automating microscopic image analysis, as shown in Fig. 1. AI-driven models can rapidly classify RBC infections such as malaria and sickle cell disease, reducing human errors. These models help healthcare professionals detect diseases in real time, improving patient outcomes. AI-based RBC infection detection is used in hospitals, research labs, and remote healthcare centers for enhanced medical decision-making.

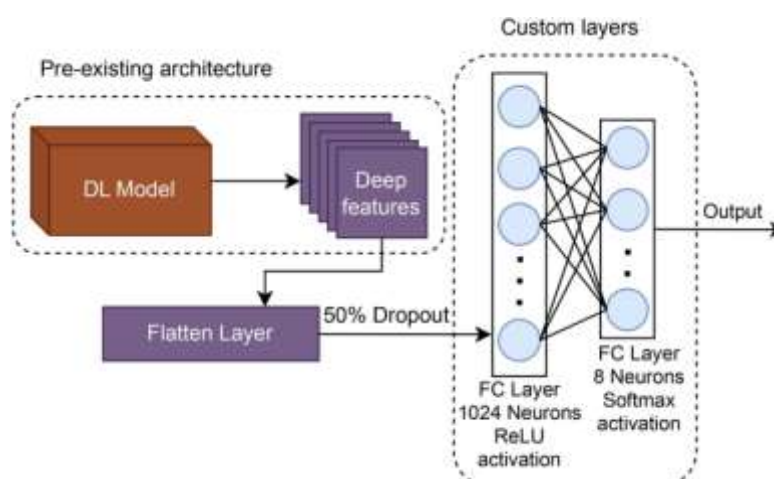


Fig. 1: Red blood cell infection defects.

2. LITERATURE SURVEY

Patil et al. [1] introduced a technique for identifying and counting the RBCs. They used a threshold of global Otsu with a threshold value of 140 for converting the image to binary. Then, the labeling algorithm is employed for counting the cells. Alomari et al. [2] utilized the Circular Hough Transform (CHT) algorithm with multi-iteration. Bhagvathi and Thomas et al. [3] performed the red component extraction from the RGB image, while the FIS editor with rules is used for circulatory detecting. Note that the RBCs count is the same as the number of circles. Furthermore, Hough transform is employed for separating the white blood cells (WBCs) away from the RBCs. Maitra and Gupta et al. [4] set up a counter for counting the cells. To highlight the RBCs, the green component was extracted from the RGB image. Mazalan et al. [5] performed image cropping for obtaining small image partitions to determine the maximum and minimum radius. The RBCs count process was accomplished by using CHT. CHT used the computed radius values, which acted as input values to it.

Tulsani, et al. [6] applied the extraction of the second component of YCbCr format for highlighting the presence of RBCs in the blood smear. In addition, they set up a counter for counting the RBCs, while the watershed transformation technique is employed for separating the overlapped cells. They applied some morphological operations as well. Sreekumar and Bhattacharya et al. [7] have utilized CHT for calculating the number of cells. In their approach, the WBCs have a more circular shape than that of the RBCs, as they assumed. A distance tool is utilized for determining the radius range required by the CHT algorithm. In contrast, the mean radius value is calculated by Chintawar et al. [8] for detecting the sickle cells. Their system diagnosed 12 types of anemia disease. The proportion of each type is counted using a counter. Khot et al. [9] computed the form factor for detecting the existence of various types of RBCs such as dacrocytes and elliptocytes. The classification method is based on a set of specific range values of the form factor. On the other hand, the fractal dimension approach is employed for identifying the sickle cells. Rexcy et al. [10] used the component Labelling algorithm for counting the cells, whereas Rakshita and Bhowmik et al. [11] introduced an approach utilizing edge detection, as well as morphological operations for identifying the sickle cells. The edge detection is performed using a Sobel operator. The form factor was calculated as well. The abnormal cells have a form factor of less than 0.5, and those from 0.5 to 1 were considered normal cells.

Revathi and Jeevitha et al. [12] presented another approach for diagnosing the sickle cells. First, the gradient watershed transform is used for determining regional minima in real images. Second, the

resulting gradient map is exposed for detecting the nuclei. Third, the shape descriptors were employed for retaining the valid nuclei. Besides, other features were computed such as the mean square error, peak signal-to-noise ratio, and root mean square error. This approach achieved the well-behaved performance of ellipse adjustment utilizing natural images. Bala and Doegar et al. [13] proposed watershed segmentation for detecting the sickle cells. The form factor was calculated for identifying the abnormal cells, while the contour plot was employed for highlighting the target and sickle cells. Hidalgo et al. [14] presented a technique for analyzing the shape of red blood cells smear of sickle cell diseases by utilizing ellipse adjustments and a new technique for identifying significant points. They also employed a set of constraints that aided in avoiding the use of image preprocessing steps.

Parvathy et al. [15] presented watershed segmentation and Otsu's segmentation as an approach for detecting the sickle cells. Compactness and form factor were calculated for differentiating the abnormal cells from the normal ones. Veluchamy et al. [16] applied artificial neural networks for identifying normal/abnormal cells. Thresholding techniques and some morphological operations were used for segmenting the image. Next, the features were extracted using algebraic moment invariants and statistics of the first and second gray level. Lastly, the extracted features were analysed for differentiating the normal/abnormal cells. Poomcokrak and Neatpisarnvani et al. [17] employed neural networks as a technique for identifying the sickle cells. The individual RBCs were extracted using an edge detection algorithm. Then, the neural network was utilized for analysing and classifying the individual cells. Fadhel et al. [18] introduced a watershed transform and the CHT for detecting the sickle cells. CHT was used for identifying the normal RBCs, which had a circular shape. While the effectiveness factor was calculated during the watershed segmentation for differentiating normal/sickle cells, the RBCs count was achieved using a counter.

Sharma et al. [19] presented an approach for diagnosing thalassemia and SCA. The marker-controlled watershed transform was used for separating the touching erythrocytes. The extracted features were classified using the K Nearest Neighbor. Rodrigues et al. [20] introduced another approach for differentiating various types of erythrocytes. First, the image was converted to binary using the global Otsu's threshold. Next, feature extraction was performed after applying morphological operations. Lastly, the features were categorized utilizing some classifiers, hence, selecting the best one. Chen et al. [21] presented a technique for diagnosing hemolytic anemia. The concavity information was employed for isolating the overlapped cells, whereas different classifiers were used for classifying different types of hemolytic anemia. Tanwar V et al. [22] ensured the reliability of the results, that conducted rigorous statistical validation through fivefold cross-validation on our primary dataset. Paired t-tests ($\alpha=0.05$) comparing each model against the ResViT baseline [44] (accuracy: 0.82) yielded statistically significant improvements ($p < 0.01$) with large effect sizes. Ren et al [23] Specifically, implemented task of medical cell counting, researchers have proposed a series of deep learning network architectures. Faster R-CNN introduces a region proposal network (RPN) and ROI pooling layer, combining object localization and classification.

4. PROPOSED SYSTEM

Proposed methodology involves a structured pipeline for automated RBC infection classification using artificial intelligence. Initially, a diverse and well-annotated microscopic blood smear dataset containing parasitized and uninfected cells is collected and enhanced through augmentation techniques such as rotation, flipping, and contrast adjustment to improve generalization. The images then undergo preprocessing, including resizing to a uniform dimension, normalization, noise reduction, and contrast enhancement, ensuring consistent input quality for model training. A DTC and an ETC are first applied as baseline models, utilizing manually extracted features such as cell shape, size, and texture; while

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ETC offers improved stability and generalization over DTC due to its ensemble learning strategy, both approaches remain limited by weak deep feature representation. To overcome these limitations, a CNN is proposed as the primary model, leveraging convolutional, pooling, and fully connected layers to automatically learn hierarchical cellular features and detect infection patterns. Comparative evaluation using metrics such as accuracy, precision, recall, and F1-score demonstrates that the CNN significantly outperforms both DTC and ETC, achieving over 95% accuracy and providing robust, reliable, and scalable classification suitable for AI-assisted medical diagnosis.

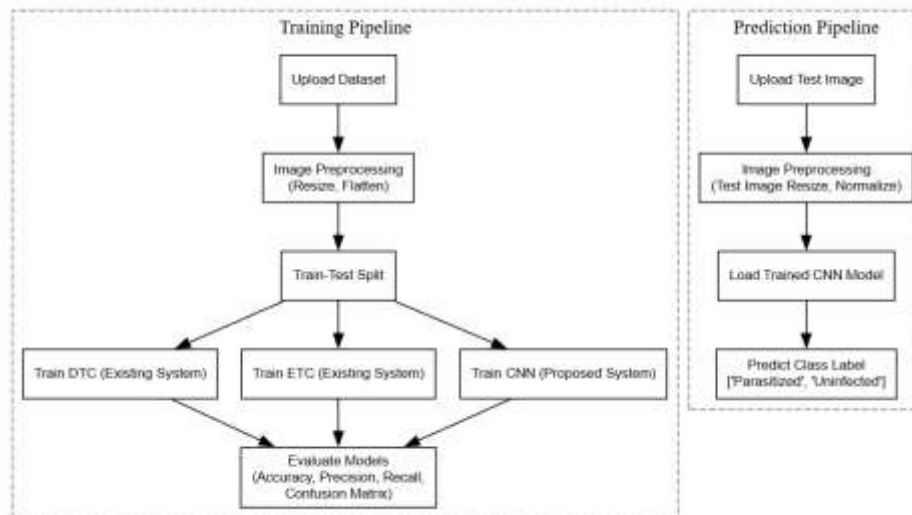


Fig. 2: Proposed system workflow

4. RESULTS DESCRIPTION

Fig. 3 shows that dataset consists of labelled images categorized into two main classes: "parasitized" and "uninfected". These labels indicate whether a given Red Blood Cell (RBC) sample is infected with malaria parasites or remains healthy. The presence of these classes enables supervised learning, where the model learns from labelled data to make accurate classifications. Fig. 4 shows that After loading the dataset, it is split into training (19,966 samples) and testing (4,992 samples) sets to ensure proper learning and evaluation. Each image is resized to a fixed dimension (e.g., 64×64 pixels) and flattened into a 12,288-feature vector ($64 \times 64 \times 3$ for RGB images). To enhance model efficiency, pixel values are normalized between 0 and 1. This preprocessing step ensures consistency in image size and scale, helping the model learn relevant patterns effectively. The training dataset is used for model learning, while the testing dataset evaluates performance, ensuring the classifier generalizes well for accurate RBC infection detection.



Fig. 3: Uploaded the Dataset



Fig. 4: After Image processing



Fig. 5: After ETC Classifier trained

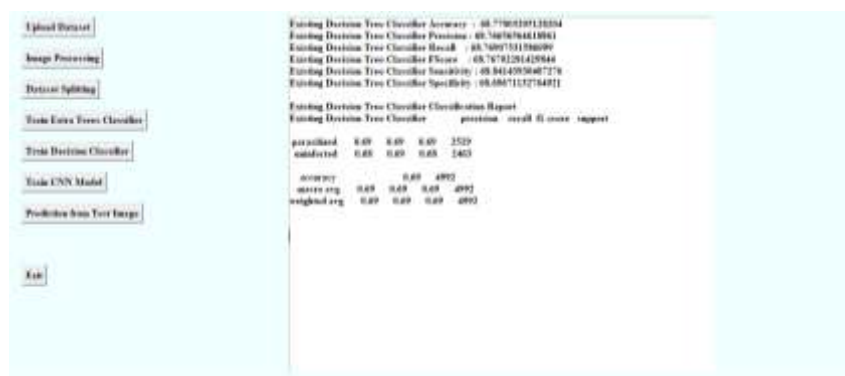


Fig. 6: After trained DTC.

Fig. 5 shows that after training the ETC on the dataset, the model achieved an accuracy of 67.53%, indicating its overall correctness in classifying RBC infections. The precision (67.69%) reflects the proportion of correctly predicted positive cases among all predicted positives, while the recall (67.58%) measures the model's ability to identify actual positive cases. The F1-score (67.49%), which balances precision and recall, suggests moderate classification performance. Fig. 6 presents the after training the Decision Tree Classifier (DTC) on the dataset, the model achieved an accuracy of 68.77%, indicating a moderate classification capability. The precision of 68.77% suggests that when the model predicts a

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sample as a particular class, it is correct approximately 68.77% of the time. The recall score of 68.77% implies that the model correctly identifies 68.77% of actual positive cases, showing its ability to capture relevant instances. Additionally, the F1-score of 68.77% balances precision and recall, confirming the model's overall consistency.

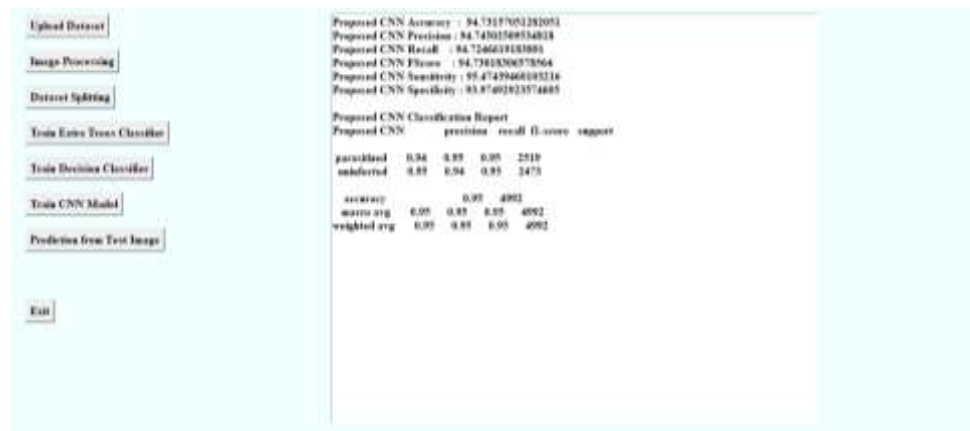


Fig. 7: CNN Calculation metrics.

Fig. 7 shows that CNN model demonstrates superior performance in classifying parasitized and uninfected samples compared to traditional machine learning models like Decision Trees and Extra Trees Classifiers. The CNN achieves an impressive accuracy of 94.73%, indicating that it correctly classifies the vast majority of images in the dataset. The precision of 94.74% suggests that when the model predicts a sample as positive (parasitized), it is correct most of the time, minimizing false positives. The recall of 94.72% signifies that the model effectively identifies parasitized cases, reducing false negatives. The F-score of 94.73% further confirms the balance between precision and recall, indicating the model's robustness. Additionally, the sensitivity of 95.47% highlights the model's ability to correctly detect infected cases, making it highly reliable for disease detection. The specificity of 93.97% ensures that uninfected samples are also accurately classified, reducing the risk of misdiagnosis. Fig. 8 illustrates the output of an AI-based microscopic image classification system for RBC infection detection. The model predicts the cell as parasitized, indicating the presence of infection-related features. Performance metrics show high accuracy, precision, recall, and F1-score, demonstrating reliable classification capability. The system uses a convolutional neural network to analyse cellular morphology and detect abnormalities. The classification report confirms balanced performance across infected and uninfected classes. This result highlights the effectiveness of deep learning for automated microscopic diagnosis.

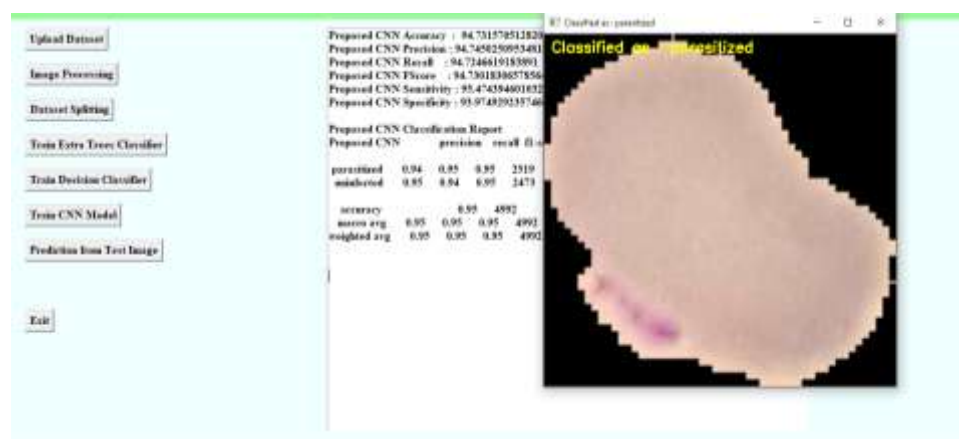


Fig. 8: Predicted as parasitized

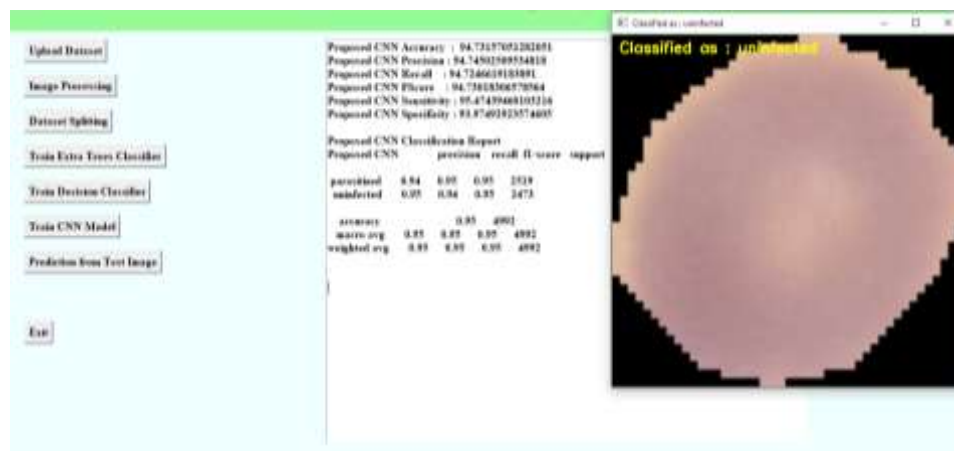


Fig. 9: Predicted as Uninfected

Fig. 9 presents the classification result of the AI-based microscopic image analysis system identifying a red blood cell as uninfected. The prediction indicates that no infection-related morphological patterns were detected in the analysed cell. The model demonstrates strong performance metrics, reflecting high reliability in distinguishing healthy cells from infected ones. The convolutional neural network effectively evaluates cellular structure and texture features for diagnosis. The classification report confirms consistent precision, recall, and F1-score values. This outcome validates the system's capability for accurate automated screening of blood smear samples.

5. Conclusion

The study demonstrates that the proposed Convolutional Neural Network (CNN) significantly improves malaria detection performance compared to a traditional Decision Tree classifier. The CNN achieved an accuracy of 94.73% along with high precision, recall, and F1-score, indicating reliable classification of parasitized and uninfected cases. Sensitivity and specificity values above 93% further confirm its effectiveness in identifying both classes with strong confidence. The confusion matrix shows that the model detects parasitized samples accurately, though it produces a few false positives for uninfected cases. In contrast, the Decision Tree model performed poorly due to its limited ability to handle complex image patterns. The superior results of CNNs stem from their capability to learn deep spatial features directly from images. However, challenges such as computational cost, training time, and dataset imbalance remain. Overall, the findings validate CNNs as a powerful approach for automated malaria diagnosis and suggest that enhancements like data augmentation and transfer learning could further improve performance.

REFERENCES

- [1] Patil, P.R.; Sable, G.S.; Anandgaonkar, G. Counting of WBCs and RBCs from blood images using gray thresholding. *Int. J. Res. Eng. Technol.* 2014, 3, 391–395.
- [2] Alomari, Y.M.; Abdullah, S.; Huda, S.N.; Zaharatul Azma, R.; Omar, K. Automatic detection and quantification of WBCs and RBCs using iterative structured circle detection algorithm. *Comput. Math. Methods Med.* 2014, 2014, 979302.

10.48047/jocaaa.2025.34.06.22

- [3] Bhagavathi, S.L.; Niba, S.T. An automatic system for detecting and counting RBC and WBC using fuzzy logic. *Arpn J. Eng. Appl. Sci.* 2016, 11, 6891–6894.
- [4] Maitra, M.; Gupta, R.K.; Mukherjee, M. Detection and counting of red blood cells in blood cell images using Hough transform. *Int. J. Comput. Appl.* 2012, 53, 16.
- [5] Mazalan, S.M.; Mahmood, N.H.; Razak, M.A.A. Automated red blood cells counting in peripheral blood smear image using circular Hough transform. In *Proceedings of the 2013 1st IEEE International Conference on Artificial Intelligence, Modelling and Simulation*, Kota Kinabalu, Malaysia, 3–5 December 2013; pp. 320–324.
- [6] Tulsani, H.; Saxena, S.; Yadav, N. Segmentation using morphological watershed transformation for counting blood cells. *IJCAIT* 2013, 2, 28–36.
- [7] Sreekumar, A.; Bhattacharya, A. Identification of sickle cells from microscopic blood smear image using image processing. *Int. J. Emerg. Trends Sci. Technol.* 2014, 1, 783–787.
- [8] Chintawar, I.A.; Aishvarya, M.; Kuhikar, C. Detection of sickle cells using image processing. *Int. J. Sci. Technol. Eng.* 2016, 2, 335–339.
- [9] Patil, D.N.; Khot, U.P. Image processing based abnormal blood cells detection. *Int. J. Tech. Res. Appl.* 2015, 31, 37–43.
- [10] Rexcy, S.M.A.; Akshaya, V.S.; Swetha, K.S. Effective use of image processing techniques for the detection of sickle cell anemia and presence of plasmodium parasites. *Int. J. Adv. Res. Innov. Ideas Educ.* 2016, 2, 701–706.
- [11] Rakshit, P.; Bhowmik, K. Detection of abnormal findings in human RBC in diagnosing sickle cell anaemia using image processing. *Procedia Technol.* 2013, 10, 28–36.
- [12] Revathi, T.; Jeevitha, S. Efficient watershed based red blood cell segmentation from digital images in sickle cell disease. *Int. J. Sci. Eng. Appl. Sci.* 2016, 2, 300–317.
- [13] Bala, S.; Doegar, A. Automatic detection of sickle cell in red blood cell using watershed segmentation. *Int. J. Adv. Res. Comput. Commun. Eng.* 2015, 4, 488–491.
- [14] Gonzalez-Hidalgo, M.; Guerrero-Pena, F.A.; Herold-Garcia, S.; Jaume-i-Capó, A.; Marrero-Fernández, P.D. Red blood cell cluster separation from digital images for use in sickle cell disease. *IEEE J. Biomed. Health Inform.* 2014, 19, 1514–1525.
- [15] Parvathy, H.B.; Hariharan, S.; Aruna, S.N. A Real Time System for the Analysis of Sickle Cell Anemia Blood Smear Images Using Image Processing. *Int. J. Innov. Res. Sci. Eng. Technol.* 2016, 5, 6200–6207.
- [16] Veluchamy, M.; Perumal, K.; Ponuchamy, T. Feature extraction and classification of blood cells using artificial neural network. *Am. J. Appl. Sci.* 2012, 9, 615.
- [17] Poomcokrak, J.; Neatpisarnvanit, C. Red blood cells extraction and counting. In *Proceedings of the 3rd International Symposium on Biomedical Engineering*, Changsha, China, 8–10 June 2008; pp. 199–203.
- [18] AbdulraheemFadhel, M.; Humaidi, A.J.; RazzaqOleiwi, S. Image processing-based diagnosis of sickle cell anemia in erythrocytes. In *Proceedings of the 2017 Annual Conference on New*

10.48047/jocaaa.2025.34.06.22

Trends in Information & Communications Technology Applications (NTICT) IEEE, Baghdad, Iraq, 7–9 March 2017; pp. 203–207.

- [19] Sharma, V.; Rathore, A.; Vyas, G. Detection of sickle cell anaemia and thalassaemia causing abnormalities in thin smear of human blood sample using image processing. In Proceedings of the 2016 International Conference on Inventive Computation Technologies (ICICT), Coimbatore, India, 26–27 August 2016; pp. 1–5.
- [20] Rodrigues, L.F.; Naldi, M.C.; Mari, J.F. Morphological analysis and classification of erythrocytes in microscopy images. In Proceedings of the 2016 Workshop de Visão Computacional, Campo Grande, Brazil, 9–11 November 2016; pp. 1–6.
- [21] Chen, H.M.; Tsao, Y.T.; Tsai, S.N. Automatic image segmentation and classification based on direction texton technique for hemolytic anemia in thin blood smears. *Mach. Vis. Appl.* 2014, 25, 501–510.
- [22] Tanwar, V.; Sharma, B.; Yadav, D.P.; Dwivedi, A.D. Enhancing Blood Cell Diagnosis Using Hybrid Residual and Dual Block Transformer Network. *Bioengineering* 2025, 12, 98.
- [23] Ren, S.; He, K.; Girshick, R.; Sun, J. Faster R-CNN: Towards Real-Time Object Detection with Region Proposal Networks. *IEEE Trans. Pattern Anal. Mach. Intell.* 2025, 39, 1137–1149.