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Research Article

A Novel Framework for Accurate Multiclass Blood Cell Classification Using Deep Learning

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Abstract – This work introduces a new approach for classification of blood cells that handles issues imbalance dataset between different categories and the presence of several classes. The main part of the proposed approach is ResNet-18, a deep neural network designed for both strong and efficient feature extraction and classification. We implemented class balancing techniques to eliminate the problem of imbalanced classes in the training data. The model was able to classify Plasma Cell, Basophil, Eosinophils, Erythroblast, Lymphocyte, Monocyte, nRBC and Platelet among the blood cell types. The study showed that the model achieved an accuracy of 99.12%, precision of 99.12%, recall of 99.13% and F1-score of 99.12%. A deep learning framework makes blood cell analysis dependable and easily scalable, helping solve major issues with classifying medical images.

Keywords – CNN, Blood Cells, Plasma, RBC, Deep Learning, Imbalanced Dataset.

I. INTRODUCTION

This Human blood contains various cellular formations which have distinct functions including immune protection, coagulation, repair and transport of oxygen [1]. In peripheral blood, the main constituents include platelets, leukocytes (white blood cells, WBCs), erythrocytes (red blood cells, RBCs), and plasma [2]. These cells are used in the diagnosis of diseases such as malaria, anemia and leukemia as pointed out by [3]. In contrast to the clear geometric shapes of RBCs and platelets, WBCs have various forms and types and subtypes, which makes them the main object of analysis in medical image segmentation and classification [4, 5].

RBCs, which make up 40-50% of the total blood volume, carry out gas exchange throughout the body beginning with the lungs. WBCs are cells that are involved in the protection of the body from pathogens such as bacteria, viruses and parasites [6]. Depending on their shape and size, WBCs are subdivided into erythroblasts, platelets, immature granulocytes: promyelocytes, myelocytes, metamyelocytes, monocytes, lymphocytes, basophils, eosinophils, and neutrophils, all of which have different functions in pathogen elimination [7]. The identification of WBCs and RBCs is therefore an important clinical decision. WBC classification is much more efficient and accurate when done automatically; it also cuts out manual work and human errors [8, 9]. These systems enhance accuracy, free

from bias and time efficient diagnostic outcomes that are useful in early detection of pathology and assist clinicians in making timely decisions [10].

Several papers examined the different approaches to diagnose and predict blood cells, and these works show the promise of AI in this area. This section gives a brief idea about the research done on the prediction of blood cell classification using AI method. Heni et al. [11] presented deep learning for WBC classification with data augmentation and the EK-means segmentation algorithm. Their method of categorizing images of WBCs includes breaking them into subtypes which include neutrophils, eosinophils, lymphocytes, and monocytes. The approach involves a new method of data augmentation known as checkerboard image, which complements pixelization or hole images to improve the performance of the model. The k-means and the fuzzy c-means are combined in the EK-means algorithm, for image segmentation. In the case of the validation of the system, the VGG19 model returned a validation accuracy of 96.24%. Tahiri et al. [12] put forward a WBC classification method based on quaternion Meixner-Charlier hybrid moments and deep learning. For moment parameter tuning, the approach employs Grey Wolf Optimization, and classification is performed with the help of a convolutional neural network. It gave detection rates of neutrophils to the tune of 98.53%, lymphocytes 98.16% and monocytes and eosinophils at 97.43%. Currently, Dong et al. [13] introduced an ensemble Convolutional Neural Network (CNN) for WBC classification; it can arise difficulties in cell segmentation and feature extraction as compared to traditional methods. To diversify the model, the approach uses three CNN frameworks; VGG16, ResNet50, and Inception V3 as base models. The Gompertz function is implemented to accurately model the ensemble learning strategy as it relates to confidence in predictions and fuzzy levels. The proposed model in this paper had an overall accuracy of 96.5 percent. Another study presenting a framework for WBC classification was conducted by Ferdousi et al., [14] who used a deep learning model that incorporated both SRGAN and VGG19. SRGAN improves low-quality microscopic images into high-quality ones then classify it with a pre-trained VGG19 classifier. The study used a dataset of 12,447 WBC images (Eosinophil, Lymphocyte, Monocyte, Neutrophil) and the model obtained a test accuracy of 94.87 percent. Song and Wang [15] presented a semi-supervised CNN for WBC classification with only a few labeled samples available. The experiments used a VGG network pre-trained on 10% labeled data for predicting the unlabeled samples with entropy and confidence filtering to produce high-quality pseudo-labels. They obtained an average accuracy of 94.4 with 500 labeled samples, while the fully supervised model yielded 97.9% with 9069 labeled samples.

Challenges remain in BC classification, despite advancements. We aim to design a robust framework that performs accurate multi-class BC classification in the imbalanced dataset, and computational efficiency. Techniques of deep learning (DL) promise solutions to these challenges. By automating the identification, counting, and classification of WBCs, DL based approaches reduce human error and increase efficiency and accuracy [8]. Medical image analysis tasks, such as WBC detection, segmentation and classification, have shown significant success using CNN based methods [16]. R-CNN [17], SSD and YOLO [18] improve detection performance but at high computational cost because they are based on sliding windows and selective search. This research addresses these challenges with the following key contributions:

1- We built an efficient ResNet based framework that can classify 8 distinct WBC classes: Plasma Cell, Basophil, Eosinophils, Erythroblast, Lymphocyte, Monocyte, nRBCs and Platelet.

2- We tackled the dataset imbalance through data augmentation enhancement, representative training samples and classification performance.

3- We developed blood cell classification framework, a complete solution for blood cell classification, which successfully enhanced classification accuracy.

II. MATERIALS AND METHOD

This section discusses the data, preparation methods and the deep learning algorithm applied for blood cell (BC) classification. To classify microscopic blood cells, we use a lightweight and efficient architecture called ResNet-18.

A. Dataset Description

The model was trained and evaluated on Kaggle datasets [19, 20], consisting of ten blood cell classes. To address class imbalance, images were curated and split into 80% for training and 20% for testing. Figure 1 shows sample images.

B. Data Preprocessing

The blood cell images are improved using pre-processing before being used for training. All images are resized to be 227×227 pixels to help with classification. After that, the images are changed into a format that models can process and normalized to help training stay reliable. A blurring effect based on the Gaussian method. Preprocessing helps to make sure that images can be correctly categorized.

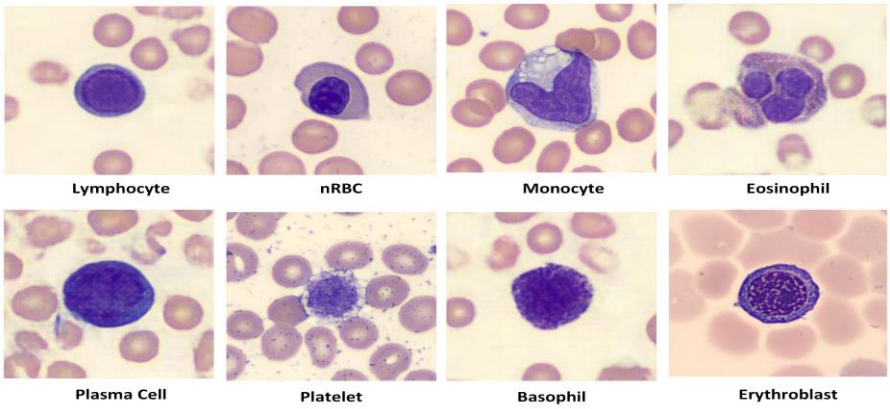

Fig. 1 Sample Images of Dataset

C. Data Augmentation

The augmentations of the dataset included automatic types (shifts, shears, zooms, flips) and manual types (rotations and contrast modifications). These changes, performed on each image. Augmented dataset size in terms of classes by 8%, improving blood cell classification with ResNet-18. Augmented images shown in Figure 2.

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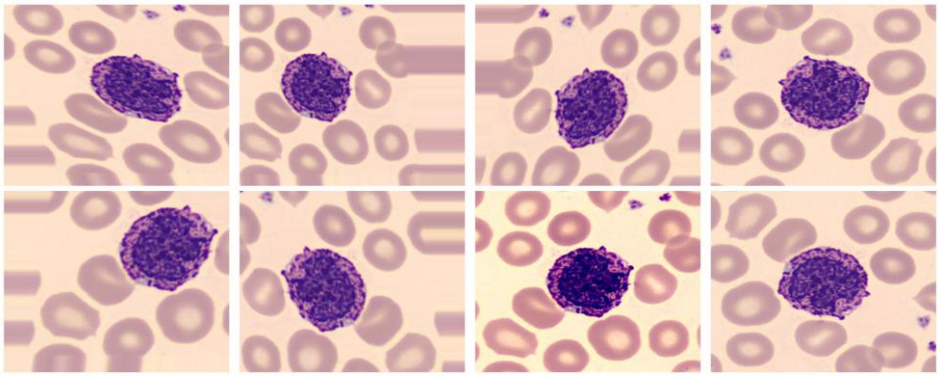

Fig. 2 Augmented Images from Dataset

Table 1. Dataset Details

Class Name	Before Augmentation	After Augmentation
Plasma Cell	250	2000
Basophil	250	2000
Eosinophils	250	2000
Erythroblast	250	2000
Lymphocyte	250	2000
Monocyte	250	2000
nRBC	250	2000
Platelet	250	2000
Total	**2500**	**20,000**

D. Proposed Model

Proposed models take 227x227x3 input image which then moves through various convolutional and pooling layers. At the start, 64 filters of 7x7 size are applied with a stride of 2 which provides an output of 113x113x64 and is then downsized by max-pooling to 57x57x64. After that, more convolutional layers use 128 filters at 29x29, 256 filters at 15x15 and 512 filters at 8x8, to find increasingly complex features. The network uses residual blocks, made up of two convolutional layers, ReLU and batch normalization which help it learn residual functions and make the learning process easier by solving the vanishing gradient problem. Its architecture aids in the classification of blood cell by reliably extracting important features from images of blood cells.

Adding these residual blocks allows the network to be built deeper without losing performance. There is an 8x8x512 final feature map which is reduced to 1x1x512 with average pooling, flattened and then sent to a fully connected layer. The model produces an 8-dimensional output which can classify 8 blood cell types, i.e. Plasma Cell, Basophil, Eosinophils, Erythroblast, Lymphocyte, Monocyte, nRBCs and Platelet. Details of ResNet-18 described in Table 2. Each layer's transformation can be mathematically simplified with Eq. (1).

$$y = F(x, w) + x \qquad (1)$$

where $F(x, w)$ functions as the residual function and the input is x. If we need to change the dimensionality, a linear w_s is used on the vector x. So, the SoftMax layer assigns probabilities to each of the 8 blood cell class, making it possible to accurately identify blood cells. The strong performance of ResNet-18 when recognizing complex patterns is why it is useful in automatic detection of blood cell. The structure of ResNet-18 is shown in Figure 3.

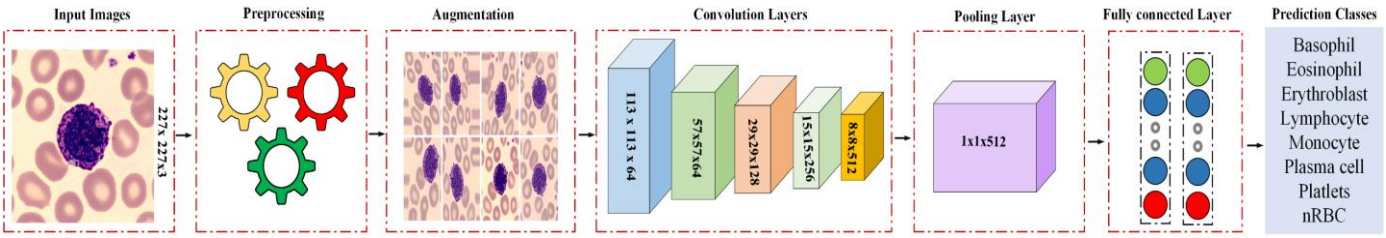

Fig. 3 Architecture diagram of proposed model

Table 2. Layer Details of Proposed Model

Layer	Conv 1	Conv2.x	Conv3.x	Conv4.x	Conv5.x	Pooling
Output Size	113 × 113 × 64	57 x 57 × 64	29 × 29 × 128	15 × 15 × 256	8 × 8 × 512	1 × 1 × 512
Filter	7 × 7, 64, stride 2	3 × 3, 64 (×2)	3 × 3, 128 (×2)	3 × 3, 256 (×2)	3 × 3, 512 (×2)	Average Pooling

III. RESULTS

In this section we explain model's performance by using evaluation measures on the test dataset. The model's performance checking various blood cell types is shown using accuracy, precision, recall, F1-score and the confusion matrix.

A. *Evaluation Metric*

We assessed our proposed model utilizing various measurements, including accuracy, precision, recall, and F1 score. The equations are presented below.

$$Accuracy = \frac{\text{True Positive} + \text{True Negative}}{\text{Total Positive} + \text{Total Negative}} \quad (2)$$

$$Percision = \frac{\text{True Positive}}{\text{True Positive} + \text{FalsePositive}} \quad (3)$$

$$Recall = \frac{\text{True Positive}}{\text{True Positive} + False\text{Negative}} \quad (4)$$

$$F1\ Score = 2\ \text{x}\ \frac{\text{PercisionRate x Recall Rate}}{\text{PercisionRate} + \text{Recall Rate}} \quad (5)$$

B. *Proposed Model Results*

Overall performance of the blood cell classification model demonstrates its high accuracy and reliability as given in Table 3. The model achieved an impressive accuracy of 99.12%, reflecting its ability to correctly classify most samples. With a precision of 99.12%, the model effectively minimizes false positives, while a recall of 99.13% indicates its strong capability to identify true positives. The F1-score of 99.12% further emphasizes the model's balanced performance in terms of precision and recall. These metrics collectively underscore the model's robustness and effectiveness in handling the classification task with high precision and minimal errors.

Table 3. Results of Proposed Model

Accuracy	Precision	Recall	F1-score
99.12 %	99.12%	99.13%	99.12%

In Figure 4, we presented the matrix of confusion for the blood cell classification model which shows the exact match between the predicted class and the true class for every classification model. This visualization just concerns the distribution of the correct and wrong classified samples and allows a very comprehensive check of the performance of the model for all the class at a very quick glance

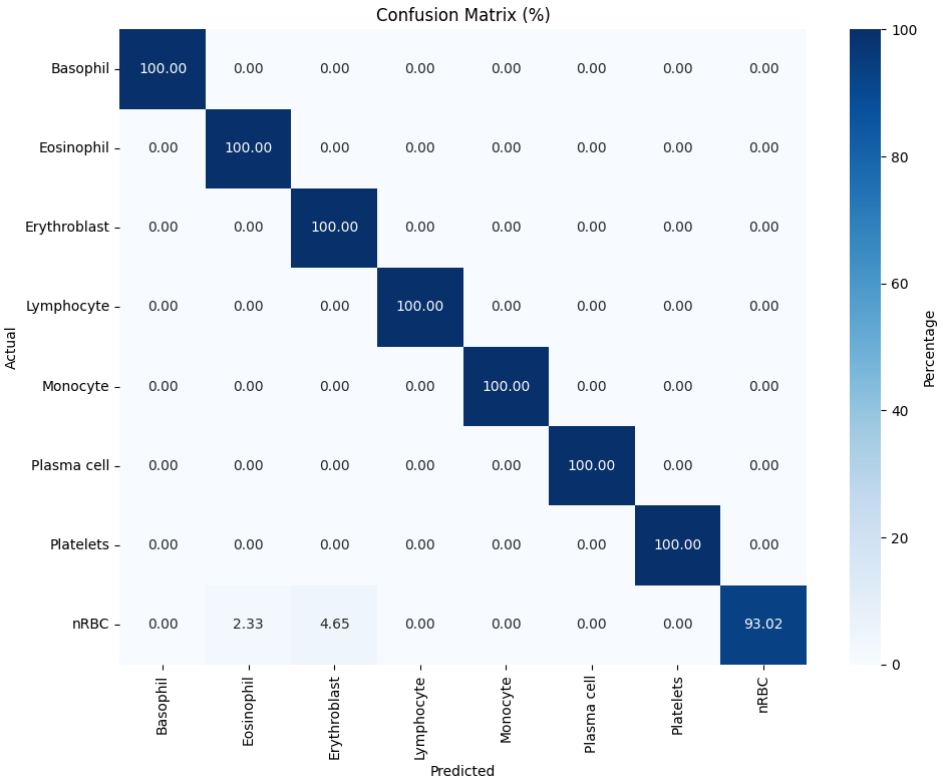

Fig. 4 Confusion Matrix of proposed model

The training of the model was also regulated through indicators such as accuracy and loss. Figures 5 shows how the precision and loss changes with respect to the epochs in training session. An accuracy curve applied to the training data shows thereby proving that the model improves with each training epoch. Likewise, the loss curve decreases gradually implying the correct identification of the signature for learning error rates during the training phase of the model.

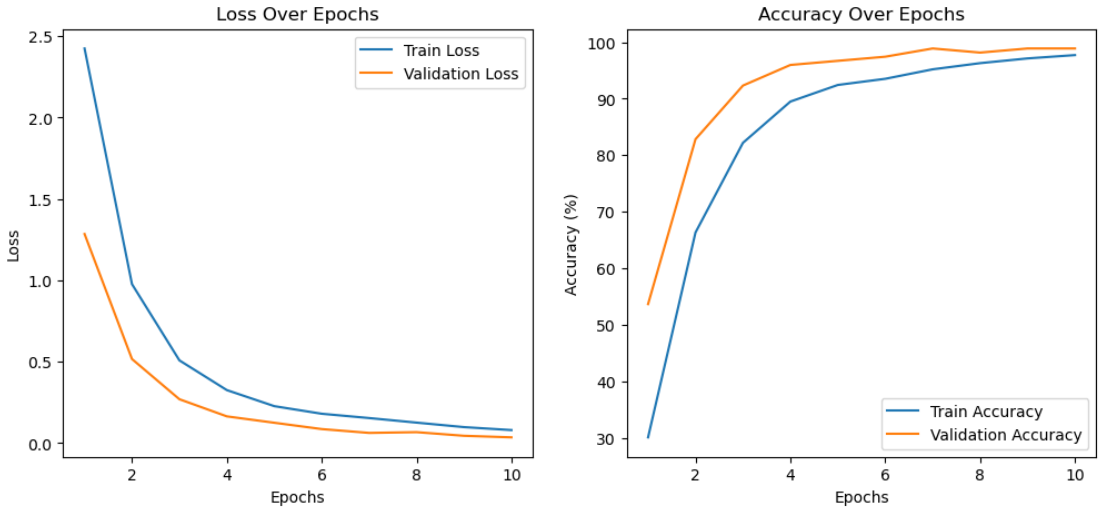

Fig. 5 Loss and accuracy graph of proposed model

C. *Evaluation with existing state of art*

The proposed model is also very effective in classifying 8 types of blood cells with an accuracy of 98.5%. It performs better than several existing approaches that deal with fewer classes. For instance, Heni et al. [11] obtained 96.24% with VGG19 on 4 classes and Dong et al. [13] got 96.5% on 5 classes using

ensemble CNN. Tahiri et al.[12] obtained 98.43%-97.53% for 4 classes. Ferdousi et al.[14] with SRGAN + VGG19 obtained 94.87% for 4 classes, while Song et al. [15] got 94.4% - 97.9% for 5 classes. Compared with the proposed BC-Net, it successfully completes the 8 class classification task with higher precision (99.12%), recall (99.13%), and F1-score (99.12%), indicating its applicability to complicated classification issues. Comparison is represented by Table 4 and graphically shown in Figure 6.

Table 4. Comparison of proposed model with previous models

Reference	Model used	Classes	Accuracy (%)
Heni et al. [11]	VGG19	4	96.24%
Tahiri et al. [12]	CNN + Quaternion Moments	4	98.43-97.53 %
Dong et al. [13]	Ensemble CNN (VGG16, ResNet50, Inception V3)	5	96.5%
Ferdousi et al. [14]	SRGAN + VGG19	4	94.87%
Song et al. [15]	Semi-Supervised CNN (Mean Teacher, VGG)	5	94.4-97.9%
Proposed Model	**ResNet-18**	**8**	**99.12%**

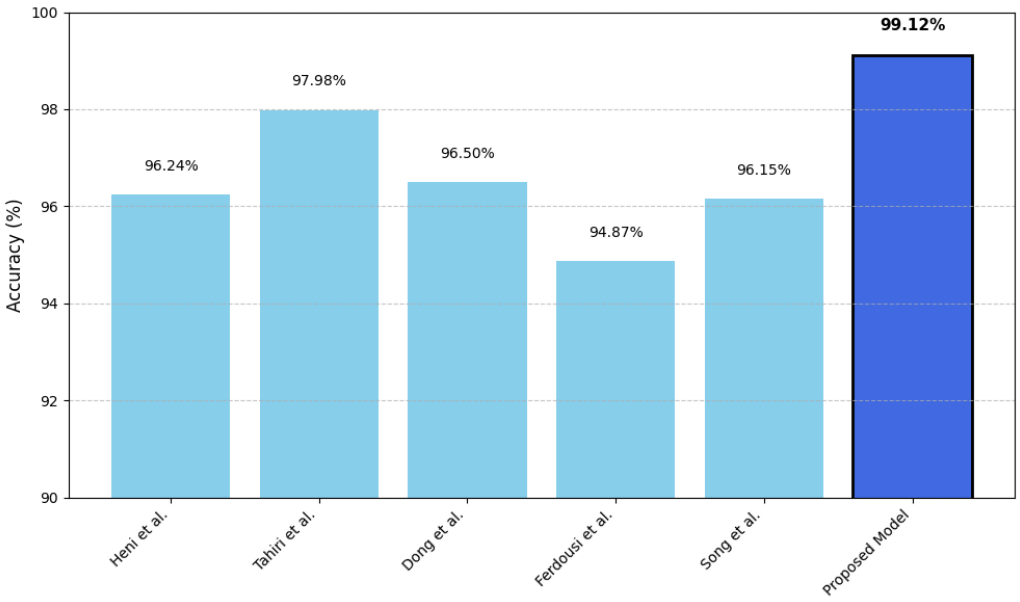

Fig. 6 Loss and accuracy graph of proposed model

IV. DISCUSSION

The strong performance and high accuracy of the proposed model reflect its ability to learn about different kinds of blood cells. While earlier models had restrictions on class numbers or required complicated ensembles, this approach manages to classify well with a light residual network, proving the effectiveness of residual learning in biomedical imaging. Being able to use the model for eight different classes is a step toward creating more widely useful diagnostic tools. Since our approach surpasses leading methods, it suggests that combining deep abstract features with a simple structure is better for automated analysis of

blood. By doing this, the work establishes a new approach for using deep learning in similar, complicated classification tasks.

V. CONCLUSION

The proposed model based on ResNet-18 is to deliver state-of-the-art performance in blood cell classification, targeting 10 distinct classes: Basophil, Eosinophils, Erythroblast, Lymphocyte, Monocyte, nRBC, Plasma Cell, Platelet. ResNet-18 for efficient and accurate feature extraction and classification the proposed model yields high accuracy of 99.12%. The combination of these methods guarantees better classification of the micro blood cell images, even if the program is used in the areas with limited access to resources. The main advantage of the model is evident when it comes to the performance; however, the dependency on the high-quality training data and the computational power points out the directions for the further development. Additional improvements of the preprocessing pipeline as well as tuning the hyperparameters might improve its stability on different datasets. Future work will focus on the application of the model to different, larger datasets and the integration of other methods to address the problem of imbalanced classes and noise for further classes. These developments will help to progress the application of the model to clinical practice and provide accurate, efficient diagnostic support for blood cells.

REFERENCES

[1] A. Girdhar, H. Kapur, and V. Kumar, "Classification of white blood cell using convolution neural network," Biomedical Signal Processing and Control, vol. 71, p. 103156, 2022.

[2] K. Balasubramanian, N. Ananthamoorthy, and K. Ramya, "An approach to classify white blood cells using convolutional neural network optimized by particle swarm optimization algorithm," Neural Computing and Applications, vol. 34, no. 18, pp. 16089-16101, 2022.

[3] R. B. Hegde, K. Prasad, H. Hebbar, and B. M. K. Singh, "Comparison of traditional image processing and deep learning approaches for classification of white blood cells in peripheral blood smear images," Biocybernetics and Biomedical Engineering, vol. 39, no. 2, pp. 382-392, 2019.

[4] K. G. Dhal, R. Rai, A. Das, S. Ray, D. Ghosal, and R. Kanjilal, "Chaotic fitness-dependent quasi-reflected Aquila optimizer for superpixel based white blood cell segmentation," Neural Computing and Applications, vol. 35, no. 21, pp. 15315-15332, 2023.

[5] R. I. Agustin, A. Arif, and U. Sukorini, "Classification of immature white blood cells in acute lymphoblastic leukemia L1 using neural networks particle swarm optimization," Neural Computing and Applications, vol. 33, no. 17, pp. 10869-10880, 2021.

[6] W. Stock and R. Hoffman, "White blood cells 1: non-malignant disorders," The Lancet, vol. 355, no. 9212, pp. 1351-1357, 2000.

[7] X. Yao, K. Sun, X. Bu, C. Zhao, and Y. Jin, "Classification of white blood cells using weighted optimized deformable convolutional neural networks," Artificial Cells, Nanomedicine, and Biotechnology, vol. 49, no. 1, pp. 147-155, 2021.

[8] S. Khan, M. Sajjad, T. Hussain, A. Ullah, and A. S. Imran, "A review on traditional machine learning and deep learning models for WBCs classification in blood smear images," Ieee Access, vol. 9, pp. 10657-10673, 2020.

[9] A. Patil, M. Patil, and G. Birajdar, "White blood cells image classification using deep learning with canonical correlation analysis," Irbm, vol. 42, no. 5, pp. 378-389, 2021.

[10] S. Sharma et al., "[Retracted] Deep Learning Model for the Automatic Classification of White Blood Cells," Computational Intelligence and Neuroscience, vol. 2022, no. 1, p. 7384131, 2022.

[11] A. Heni, I. Jdey, and H. Ltifi, "Blood Cells Classification Using Deep Learning with customized data augmentation and EK-means segmentation," J. Theor. Appl. Inf. Technol, vol. 101, no. 3, 2023.

[12] M. A. Tahiri, A. Bencherqui, H. Karmouni, H. Amakdouf, M. Sayyouri, and H. Qjidaa, "White blood cell automatic classification using deep learning and optimized quaternion hybrid moments," Biomedical Signal Processing and Control, vol. 86, p. 105128, 2023.

[13] N. Dong, Q. Feng, J. Chang, and X. Mai, "White blood cell classification based on a novel ensemble convolutional neural network framework," The Journal of Supercomputing, vol. 80, no. 1, pp. 249-270, 2024.

[14] J. Ferdousi, S. I. Lincoln, M. K. Alom, and M. Foysal, "A deep learning approach for white blood cells image generation and classification using SRGAN and VGG19," Telematics and Informatics Reports, vol. 16, p. 100163, 2024.

[15] H. Song and Z. Wang, "Automatic Classification of White Blood Cells Using a Semi-Supervised Convolutional Neural Network," IEEE Access, 2024

[16] S. K. Pandey and A. K. Bhandari, "A systematic review of modern approaches in healthcare systems for lung cancer detection and classification," *Archives of Computational Methods in Engineering,* vol. 30, no. 7, pp. 4359-4378, 2023.

[17] B. Leng, C. Wang, M. Leng, M. Ge, and W. Dong, "Deep learning detection network for peripheral blood leukocytes based on improved detection transformer," Biomedical Signal Processing and Control, vol. 82, p. 104518, 2023/04/01/ 2023, doi: https://doi.org/10.1016/j.bspc.2022.104518.
[18] Z. Han *et al.*, "One-stage and lightweight CNN detection approach with attention: Application to WBC detection of microscopic images," *Computers in Biology and Medicine,* vol. 154, p. 106606, 2023/03/01/ 2023, doi: https://doi.org/10.1016/j.compbiomed.2023.106606.
[19] UncleSamulu. *Blood Cells Image Dataset*. [Online]. Available: https://www.kaggle.com/datasets/unclesamulus/blood-cells-image-dataset
[20] M. Nickparvar. *White blood cells dataset.* [Online]. Available: https://www.kaggle.com/datasets/masoudnickparvar/white-blood-cells-dataset