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Utilization of depth-wise and spatially separable convolutional network fusion for classification of white blood cells

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ABSTRACT

White blood cells (WBCs) are an essential part of the human immune system, playing a significant role in fighting diseases and infections. Their detection and classification from microscopic blood images is a crucial step in diagnosing various diseases. Looking at cells by hand is still key, but it takes a lot of work and mistakes can happen. So, this study tries to improve how to find and sort WBCs using some cool computer tricks. The study tackling issues like cells being on top of each other, looking different, and not having a ton of data. To achieve this, image enhancement techniques were applied using contrast enhancement algorithm, contrast-limited adaptive histogram equalization (CLAHE), and image segmentation techniques using color isolation are employed, which contributes to more accurate separation of overlapping cells, and enables faster and more efficient diagnosis. To efficiently complete the classification process after the segmentation process, a neural network structure consisting of combining three types of convolutional layers (depthwise, spatially, and convolution) was used. To evaluate the proposed technique, experiments were conducted using an open-source blood cell count and detection (BCCD) dataset from the Kaggle platform, and resulted in achieving a classification accuracy of 99.06% and an F1-score of 99.05%. This highlight of the model's ability to efficiently deal with the challenges associated with WBC classification.

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1. INTRODUCTION

Blood is an essential element for assessing human health, as each drop of it contains multiple components that reveal the health status. Another pertaining assessment is the peripheral blood smear, where a blood sample spread is placed on a glass slide, stained in a particular manner, and subsequently observed in a microscope. This test figures out the different kinds of white blood cells (WBCs) and tells them apart from red blood cells and other stuff, giving info about how healthy someone is [1]. For they are able to fight bacteria, viruses, and other germs, WBCs are a crucial component of the immune system [2], [3].

Blood disorder cases, like leukemia and lymphoma, are increasing. These cells are super important because they keep your immune system working right [4]–[6]. These cells as a group cooperate to enhance

the immunity of the body by helping in removal of foreign and pathogenic elements [7]. It is also known that the blood has a set composition that is constant in each individual, which consists of five main types of cells. These are neutrophils (40-60%), lymphocytes (20-40%), monocytes (2-8%), eosinophils (1-4%), and basophils (0.5-1%). Starting from those with the lowest percentages, basophils are most rarely seen whereas each type performs various functions to protect the body [8], [9]. Changes in WBCs number, or in their morphology such as size and shape or color in blood smear, are signs of diverse body disorders. In cytopathology, the WBC morphology and their count in the slides is also helpful in the diagnosis of many disorders. Hence, the identification and characterization of the blood cells in this context, corresponds to the mechanisms that promote early diagnosis and treatment of many disease processes [6], [10], [11]. Conventional methods use blood smear as such remains costly and time consuming as it relies on a visual inspection by the clinicians trained on the hematology. Such methods are tedious and are subject to human fallibility. Whereas with computer assist vision systems, it provides more effective and dependable approach with diagnostic precision and less human interference as well as variability [12]–[14]. But, to discriminate WBCs photomicrographic pointers are used along with the image preprocessing methods and statistical measures obtained through manual feature engineering. All these procedures are laborious and can consume a lot of time, and the accuracy of the classification greatly depends on the manually selected features, which leads to low accuracy and a long time of classification [15].

With the development of computing capabilities, the use of artificial intelligence and deep learning algorithms is increasing in medical and biological applications. These techniques are used in various fields, from medical image analysis to processing big data of the human genome. Therefore, the development of low-cost and reliable systems for classifying and evaluating WBCs has become imperative [16]. Despite advances in image-based classification of WBCs, the field still faces significant challenges. Variation in cell morphology is affected by patient condition and staining techniques, making it difficult to develop accurate classification systems. Other cellular components, such as red blood cells and platelets, complicate image analysis and increase likelihood of classification errors. In addition, lack of large and diverse datasets, coupled with variations in illumination and staining intensity, limit the accuracy and optimization of systems [17], [18].

A number of methodologies based on deep learning have been proposed in this regard for the detection and classification of WBCs. One of the methods, named WBCsNet utilized the dataset-master and reported 98.92% of accuracy. However, this method did not take into consideration the segmentation of WBC images from the main image and used pre-trained deep learning models and therefore detailed analysis was not possible [15]. Similarly, another study used AlexNet, GoogLeNet, and ResNet-50 with open-access dataset from Kaggle and showed a 97.95% accuracy but again did not extract WBC images from the main image hence not affecting the granularity of their analysis [2]. The combination of ResNet-50, VGG-19, and MobileNet-V3-small with Raabin-WBC dataset resulted in 98.86% accuracy. While efficient, this method was also without segmentation of WBCs from the primary pictures and primarily depended on pre-trained models [3]. Another work using convolutional neural network (CNN) on the publicly available dataset from Kaggle achieved high accuracy 99.5%, but it did not perform the extraction of WBC images from the main image, which impacted the robustness of the classification [16].

DenseNet-121, when applied to the open-access dataset from Kaggle, attained an accuracy of 98.84%. This study had similar limitations by not extracting WBC images and using pre-trained models, potentially affecting feature extraction specificity [19]. MobileNet, applied to the same dataset, achieved 98.4% accuracy and included segmentation. However, it was based on pre-trained deep learning models and may have missed important/unique features from this dataset [20]. DenseNe-t201 and DarkNet-53, which worked on an open-access dataset synthesized from a real-world dataset, reported accuracy of 99.9%. However, the use of synthetic data and pre-trained models without the extraction of WBC images makes the findings of this study possibly inapplicable [13]. Still, another CNN-based study used open-access data from Kaggle, didn't extract WBC images from the background picture, and reported 98% accuracy [17].

Further research using CNN with the same dataset achieved 98.33% accuracy but also did not separate WBC images and thus is consistent with the limitations of previous works [21]. Convolutional attention BLSTM network (CAB-Net), when tested using the peripheral blood cell (PBC) and blood cell count and detection (BCCD) datasets, achieved 98.29% accuracy but was limited by not being able to extract WBC images from the primary image, hence limiting the detailed morphological analysis [18]. Lastly, a combined CNN and recurrent neural network (RNN) approach using the publicly available Kaggle dataset achieved 95.89% [22]. The current research didn't segment the WBC images from the parent image and also used pre-trained networks, that might not capture all the subtleties in the dataset.

Abozeid *et al.* [23] have used pretrained model (Op-YOLOv8) over BCCD dataset and obtained performance (99.2% accuracy) with little customizations. Chen *et al.* [24] introduced a dual attention model (DAFFNet) evaluated on six different datasets, with accuracies between 91.30% to 99.71%, but the winner

model presented a relatively high computational complexity, which may mitigate the real deployment. Fayyaz *et al.* [25] proposed a 3-stage CNN model to the BCCD dataset, with a reported overall accuracy of 97.59%, but it does not have a segmentation step and has a fairly complicated pipeline. The existing literature has generally shared some limitations, such as using already pre trained models of deep learning and failing to extract WBC images from original images. Even if it achieved high accuracy, these two factors actually limit the models' ability in extracting unique features necessary for the accurate classification of WBCs.

In order to resolve these issues, this paper presents an approach that employs the contrast-limited adaptive histogram equalization (CLAHE) method for image accuracy improvement and chromatic spinning-based segmentation of blood smear images. This is an image contrast enhancement technique that helps visual interpretation and performance for subsequence tasks such as image segmentation. Standard methods have several limitations, and in order to overcome these limitations CLAHE was introduced which enhances local contrast [26], [27]. A deep learning model with three sophisticated types of convolutional layers for feature extraction and WBC classification was developed in this study. The key contributions of this research are as follows:

i) Using the CLAHE method to enhance image accuracy.
ii) Implementing a new segmentation approach using chromatic spinning.
iii) Developing a robust deep learning model with three advanced convolutional layers for WBC classification.
iv) Providing an efficient and reliable solution for early diagnosis by examining blood smears.

2. METHOD

In this section, the methodology used in the proposed approach for classifying WBCs will be reviewed in detail. It comprises of two primary stages: preprocessing image and feature extraction and classification using the proposed model. Figure 1 illustrates the basic steps of this approach.

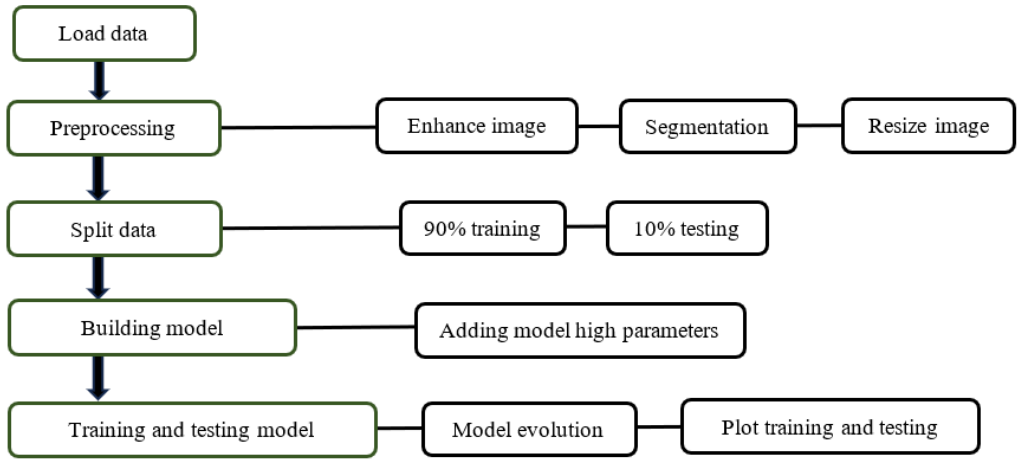

Figure 1. The general structure of the proposed method

2.1. Preprocessing image stage

To improve the efficiency and speed of diagnosis in cases of cell overlap in blood smear images, advanced image processing techniques such as the CLAHE algorithm are used to enhance the contrast of the images. The image is transformed into the Lab color model, and then the CLAHE algorithm is used on the light channel (the L channel) to boost contrast while keeping the color components intact. This procedure enhances the details in areas of low contrast, while reducing noise. After contrast enhancement, preparation for the color isolation process is carried out by converting the image to the HSV color model. In this model, the color violet—which usually represents WBCs—is determined by setting lower and upper limits for the color values. To ensure that an image containing only WBCs is extracted, the largest area is selected and cropped after color isolation process. Figure 2 illustrates the different stages of image processing, starting from contrast enhancement using CLAHE and ending with the extraction of WBCs.

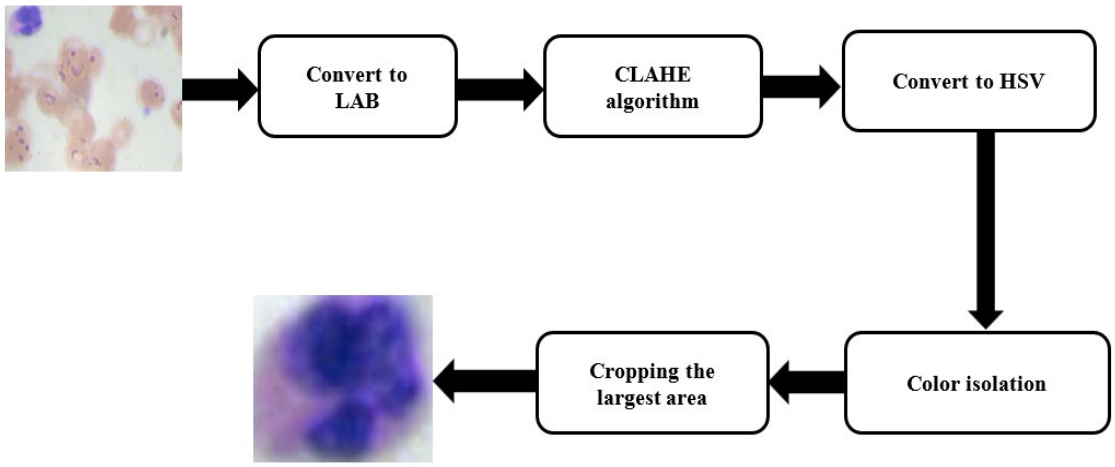

Figure 2. Stages of the proposed WBC segmentation process

2.2. Feature extraction and classification stage

In this stage, a deep learning model specifically designed for processing WBC images was developed. The model consists of three types of convolutional layers. The processing process begins with adjusting the input layer to accommodate the color WBC images with a resolution of (64×64) pixels. First, two convolutional layers are used, each containing 128 kernels, followed by a normalization layer and then a pooling layer, where pooling operations are applied using max pooling windows. This is followed by two convolutional layers across spatial dimensions, where the first contains 64 kernels to operate on the vertical dimension, while the second operates on the horizontal dimension with the same number of kernels, followed by a pooling layer. After that, the third type of convolutional layers, the depthwise convolution layer, is used. In this layer, a separate filter is applied to each input channel, and then the input channels are combined using a convolutional layer with a kernel size of (1×1), followed by a pooling layer. To align the outputs of the convolutional layers with the inputs of the fully connected layers, a global average pooling layer is applied. Then, two fully connected layers are used, which adapt to the number of nodes in the previous layer and the number of desired classes. To improve generalization and reduce the risk of overfitting to the training data, a dropout layer is added after each fully connected layer. Finally, a final layer consisting of the softmax function, which is widely used in multi-class classification problems, is included. This layer is adjusted to match the number of target classes.

The optimal design of the proposed model was determined experimentally by gradually adjusting the number of convolutional layers, the maximum pooling size, and the number of filters. This process was continued until the architecture with the best performance was selected. Table 1 shows the detailed design of the proposed model, while Figure 3 provides a visual description of the model architecture.

Table 1. The proposed model architecture

Layer	Kernel size	Kernel No.	Input shape	Output shape	Parameter no.
Convolutional 1	3×3	128	64, 64, 3	62, 62, 128	3,568
Convolutional 2	3×3	128	62, 62, 128	60, 60, 128	147,584
Batch normalization	-	-	60, 60, 128	60, 60, 128	512
Max pool. 1	2×2	-	60, 60, 128	30, 30, 128	0
Horizontal convolution	1×3	64	30, 30, 128	30, 28, 64	24,640
Vertical convolution	3×1	64	30, 28, 64	28, 28, 64	12,352
Max pool. 2	2×2	-	28, 28, 64	14, 14, 64	0
Depthwise convolution	3×3	1	14, 14, 64	12, 12, 64	640
Pointwise convolution	1×1	32	12, 12, 64	12, 12, 32	2,080
Max pool. 3	2×2	-	12, 12, 32	6, 6, 32	0
Global average pooling	-	-	6, 6, 32	32	0
Fully connected	-	-	32	512	16,896
Dropout (0.5)	-	-	512	512	0
Fully connected	-	-	512	256	131,328
Dropout (0.5)	-	-	256	256	0
Softmax	-	-	256	4	1,028

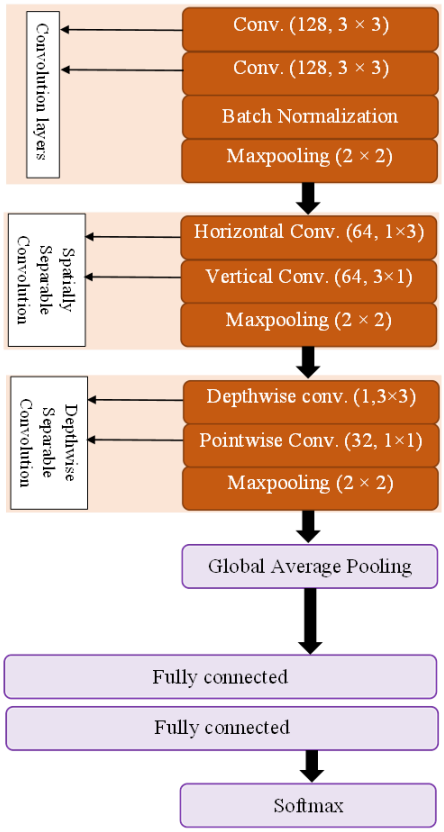

Figure 3. Architecture of the suggested deep learning model for WBC classification

3. RESULTS AND DISCUSSION

A new method for the classification of leucocytes in the WBCs was developed utilizing the free environment for programming Google Colab based on Python3. Each of the experiments was performed on a 12 GB Nvidia Tesla K80 GPU with 13 GB of RAM. For the evaluation, the open-access dataset presented on Kaggle was used. The effectiveness of the system under consideration was measured with the use of evaluation indicators such as accuracy and F1-score.

3.1. Dataset

The BCCD dataset consists of 12,500 magnified images of blood cells in JPEG format [28]. It includes about 3,000 images for each of the four types of WBCs: eosinophils, lymphocytes, monocytes, and neutrophils. Each image has a resolution of 320×240 pixels, uses 3 color channels (RGB), and has a pixel density of 96 dots per inch (DPI). Figure 4 displays sample images of WBCs from the dataset.

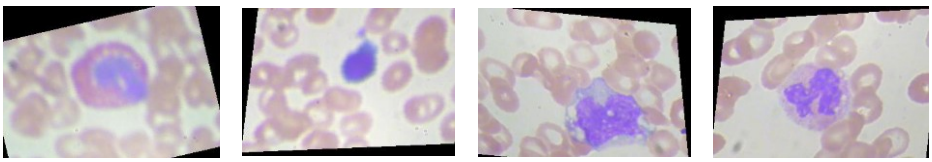

Figure 4. Samples of WBCs images

3.2. Segmentation results

The proposed method described in section 2.1 was used to extract WBC images from blood smear images and enhance their resolution. Each cropped WBC image was 64×64 pixels in size. Figure 5 shows the resulting images from the enhancement and segmentation stages.

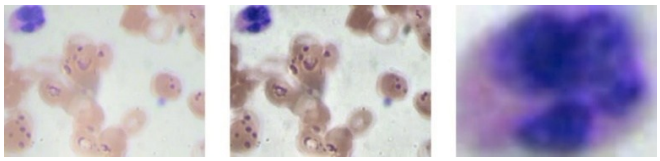

Figure 5. Segmentation stages

3.3. Evaluating the proposed technique's performance

The proposed technique in this study was evaluated using two main indicators: accuracy and F1-score. The accuracy measure is defined according to (1).

$$Accuracy = \frac{True\ positive+True\ negative}{True\ positive+Tru\ negative+False\ positive+True\ negative} \quad (1)$$

True positive represents the number of cases where WBCs were correctly classified and successfully identified. While true negative refers to the number of cases where WBCs were correctly excluded. On the other hand, false positive refers to the number of cases where WBCs were incorrectly classified as correct, while false negative refers to the number of cases where WBCs were incorrectly excluded as incorrect.

The F1-score represents the harmonic mean between precision and recall. It is calculated using (2). Both precision and recall can be calculated mathematically according to (3) and (4).

$$F1-score = \frac{2\times Precision\times Recall}{Precision+Recall} \quad (2)$$

$$Precision = \frac{True\ positive}{True\ positive+False\ positive} \quad (3)$$

$$Recall = \frac{True\ positive}{True\ positive+False\ negative} \quad (4)$$

The training process utilized Keras, which is a popular deep learning framework. In the final layer, the softmax function was applied to transform the outputs into class probabilities. The convolutional layers started with weights set by the leaky rectified linear unit (ReLU) function, which is a variation of the standard ReLU function. The Adam method was used to adjust the weights during training, with a constant learning rate of 0.001. The training lasted for 100 rounds, giving the model time to learn from the data and improve its performance by updating the weights. Several tests were done to find the best settings for the model. These tests were designed to enhance the model's accuracy and boost its overall performance. After a series of training iterations, a classification accuracy of 99.06% and an F1-score of 99.05% were achieved, which reflects the high efficiency of the proposed model. Table 2 shows the evaluation results of different parameters used in the model. The table shows the effect of changing each parameter individually while keeping the rest of the parameter's constant.

Table 2. The performance results of assessing the proposed technique

No. of filters in Conv	No. of filters Spatially Conv	No. of filters Depthwise Conv	No. of filters Pointwise Conv	Activation function	Accuracy (%)	F1-score (%)	Note
16	16	16	1x1	Leaky ReLU	90.14	90.19	-
32	32	32	1x1	LeakyReLU	92.51	92.62	-
64	64	64	1x1	Leaky ReLU	94.36	94.56	-
128	128	128	1x1	Leaky ReLU	91.75	91.77	-
128	64	32	1x1	Leaky ReLU	95.44	95.51	-
128	64	32	1x1	Leaky ReLU	96.21	96.31	-
128	64	32	1x1	ReLU	90.14	90.44	-
128	64	32	1x1	swish	93.59	93.65	-
128	64	32	1x1	Leaky ReLU	97.90	98.03	With batch normalization
128	64	32	1x1	Leaky ReLU	99.06	99.05	Batch normalization + GlobalAveragePooling2D

Figure 6 shows the relationship between the number of iterations and the accuracy of the proposed model during the training process. In the early stages of training, a sharp increase in accuracy can be observed, reflecting the model's ability to quickly learn from the basic patterns in the data. After epoch 30,

the increase in accuracy becomes more gradual. At this stage, the model has learned most of the basic patterns, and it begins to improve its ability to recognize fine details in the data. As epoch 85 approaches, the accuracy reaches a relatively stable level, indicating that the model has reached a stage of saturation. This stability indicates a balance between learning from the data and avoiding overfitting.

Figure 7 shows how the loss function, called categorical cross entropy, changes as the model trains over time. At the beginning, the loss function jumps around a lot, showing that the model is still adjusting its settings to understand the data better. As the training continues, especially after 20 epochs, the loss function starts to settle down, meaning the model is getting better at handling the data and making fewer mistakes. By the time 60 epochs is reached, the loss function keeps dropping steadily. After 90 epochs, the loss function stays between 0.03 and 0.05, which means the model has learned well and is making very few errors.

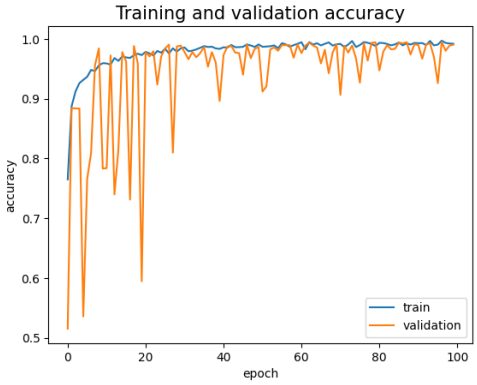

Figure 6. Accuracy of the proposed model

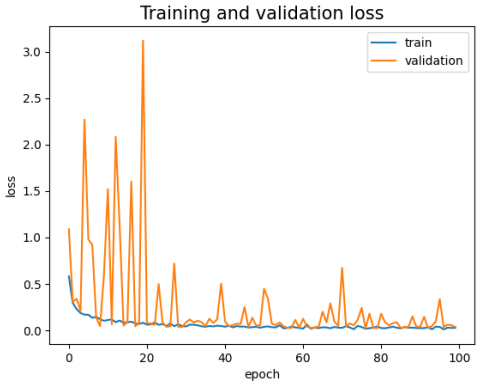

Figure 7. Loss function of the proposed model

Figure 8 shows the receiver operating characteristic (ROC) curves, which are used to evaluate the performance of the model in classifying the four types of WBCs. The horizontal axis represents the false positive rate, while the vertical axis represents the true positive rate. The ROC curves show a convergence towards the upper left corner of the graph, reflecting the high efficiency of the model in distinguishing between the different types of WBCs.

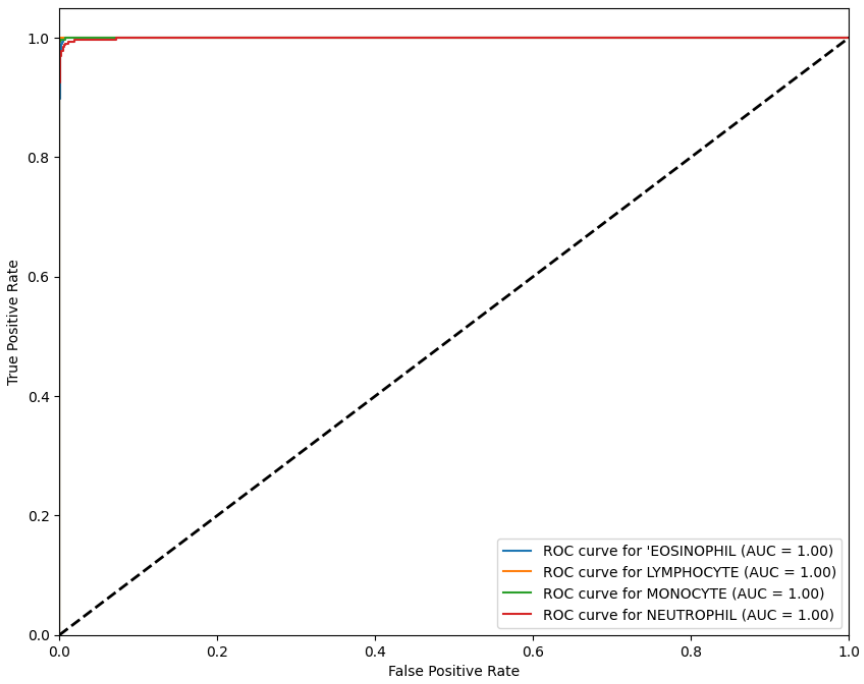

Figure 8. ROC of the proposed model

Figure 9 shows the confusion matrix of the proposed technique. The results show that the model achieved 100% accuracy in classifying lymphocyte, while the classification accuracy reached 99.06% for neutrophils, 99.34% for eosinophils and 97.77% for monocyte. These results reflect the outstanding performance of the model and its high efficiency in distinguishing between different types of WBCs.

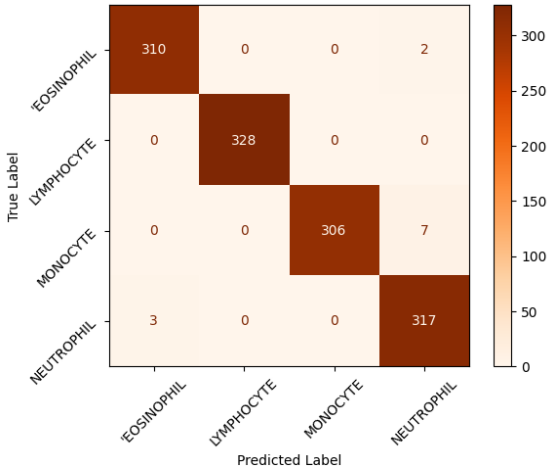

Figure 9. Confusion matrix of the proposed model

3.4. Comparison and results analysis

Despite the complex challenges posed by image resolution, overlapping cells, heterogeneity of cell types and sizes, as well as data scarcity and differences in lighting conditions, the results obtained using the proposed technique have proven to be very promising. The results show that the proposed method adopted a systematic and organized approach to build a model based on different convolutional layers. The model building process was preceded by image quality improvement and segmentation steps, which contributed to achieving highly reliable performance. In contrast to previous studies [16], [17], [21], [25], that did not rely on segmentation of blood smear images, which offered the advantage of reducing computational complexity and accelerating the training process while improving reliability. The proposed model is distinguished from traditional CNN models used in most previous studies [2], [19], [20], [22]–[24], as it was specifically designed to address the unique challenges associated with WBC classification. Table 3 provides a comparative analysis of the different methodologies and their results, with the proposed model. When comparing the results of the proposed model with recent research based on the same dataset, it is clear that the achieved results are very encouraging and highlight the efficiency of the approach in improving the accuracy and reliability of WBC classification.

Table 3. Comparison of the proposed model performance and the related works

Reference	Technique	Segmentation	Accuracy (%)
[1]	AlexNet, GoogLeNet, and ResNet-50	No	97.95
[16]	CNN	No	99.5
[19]	DenseNet-121	No	98.84
[20]	MobileNet	Yes	98.4
[17]	CNN	No	98
[21]	CNN	No	98.33
[22]	CNN and RNN	No	95.89
[23]	Op-YOLOv8	Yes	99.2
[24]	DAFFNet	Yes	99.71
[25]	CNN	No	97.59
The proposed technique	Mix CNN	Yes	99.06

4. CONCLUSION

This paper developed an advanced WBC classification technique based on deep learning approaches, focusing on the use of different types of convolutional layers. As a prelude, the CLAHE algorithm was applied to enhance image contrast, along with color isolation technology to segment images.

This approach aims to address the challenges resulting from cell overlap and different lighting conditions. Using the proposed technique, deep features were extracted from images, resulting in high classification performance with high reliability, even when dealing with a limited dataset size, which is a major challenge in deep learning applications. An open-source dataset from Kaggle was used for experiments. Several experiments were designed and implemented to understand how the parameters of the proposed model layers evolve over time. The results showed that the model is able to adapt to a variety of WBCs, resulting in high classification accuracy. When compared with other approaches, the proposed technique demonstrated superior performance. The best results achieved were a classification accuracy of 99.06% and an F1-score of 99.05%, indicating the efficiency and effectiveness of the model. In the future, adopting deep learning methodologies in all stages of the WBCs classification process is proposed, from contrast enhancement and image segmentation to the final classification. The most important contributions of this work are an integrated segmentation-classification pipeline, development of a specialized deep learning model, and applying CLAHE for training-enhanced contrast. Nonetheless, limitations such as evaluating only a single dataset and absence of clinical validation are present. In future work, the model is planned to be refined for deployment, integrate clinical tests, and validate the model clinically, as well as optimize testing on other datasets and incorporate attention mechanisms focused on feature extraction.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

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Ahmed Nooruldeen Alsafi	✓		✓			✓			✓	✓	✓			
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C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

DATA AVAILABILITY

The data that support the findings of this study are openly available in Kaggle at https://www.kaggle.com/datasets/paultimothymooney/blood-cells, reference [28].

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