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Advances in Medical Imaging: Using Convolutional Neural Networks for White Blood Cell Identification

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Abstract: White blood cells (WBC) perform a vital function within the immune system by actively protecting the body from a wide range of diseases and foreign substances. Diverse types of WBCs exist, including neutrophils, lymphocytes, eosinophils, and monocytes, each possessing distinct roles within the immune response. Neutrophils are typically the initial immune cells to mobilize in response to infections and inflammation, exhibiting a rapid and robust reaction. Conversely, lymphocytes play a pivotal role in the recognition and targeted elimination of pathogens. Nevertheless, identifying and classifying WBCs poses significant challenges and demands considerable time, even for seasoned medical practitioners. The process of manual classification is frequently characterized by subjectivity and is susceptible to errors, thereby potentially compromising the precision of both diagnosis and treatment. In response to this challenge, scholars have devised deep learning methodologies that can automate the process of WBC classification, thereby enhancing its precision. This study employs a convolutional neural network (CNN) to classify WBCs based on imaging data. The CNN underwent training using a substantial dataset comprising body cell images. This training facilitated the acquisition of discerning characteristics specific to various WBC types, thereby enabling accurate classification. The methodology was evaluated within a simulated environment, yielding encouraging outcomes. The approach that was proposed successfully achieved an average accuracy rate of 98.33% in the classification of WBCs. This outcome serves as evidence of deep learning techniques enhancing the speed and accuracy of WBC classification.

Index Terms: Deep Learning, CNN, Classification, White Blood Cells classification, Feature extraction.

1. Introduction

White blood cells (WBCs) are a category of blood cells that assume a crucial role in the immune system of the human body, serving to protect it from infections and diseases [1]. White blood cells, also referred to as leukocytes, are generated within the bone marrow. These entities are distinguished by the lack of hemoglobin, a protein responsible for

transporting oxygen in erythrocytes. They encompass various subtypes, including neutrophils, lymphocytes, monocytes, and eosinophils, each possessing distinct physiological roles. The average white blood cell count in adult humans ranges from 4000 to 10,000 [2]. The insufficiency of these cells within the human body can result in symptoms such as persistent infections, abrupt loss of weight, debility, and exhaustion, which may also precipitate a range of illnesses [3].

The primary diagnostic approach utilized in clinical examinations for these cases involves acquiring microscopic images of the patient and subsequently subjecting them to examination by specialized physicians [4]. Nevertheless, the process of manually classifying WBCs is a laborious undertaking that necessitates the expertise of a well-trained specialist who must meticulously analyze microscopic images. Furthermore, it should be noted that manual classification is susceptible to human error, thereby potentially leading to inaccuracies in the obtained outcomes [5]. Automated techniques utilizing computer vision and machine learning methodologies have been devised by researchers to tackle the difficulties entailed in manually classifying white blood cells.

The healthcare industry has been influenced by recent advancements in Artificial Intelligence (AI) and Machine Learning (ML) [6, 7]. The utilization of these technologies has facilitated the advancement of healthcare solutions in real-time, thereby enhancing the efficiency and precision of diagnoses and aiding in the exploration of novel treatment alternatives. Nevertheless, traditional machine learning models may encounter difficulties in attaining optimal efficacy and accuracy because of the complex and time-intensive requirements of tasks like pre-processing, segmentation, and feature extraction [8]. These processes have the potential to influence the efficacy and accuracy of the models, thereby posing challenges in attaining precise and dependable outcomes [9].

Deep learning (DL) has emerged as a highly effective methodology for extracting features in various domains, such as image and speech recognition, natural language processing, and medical imaging. This approach has been widely acknowledged for its ability to achieve remarkable results in these applications [10-14]. DL can extract prominent features from input images and use them proficiently for diagnosis and classification. This approach effectively addresses the limitations observed in previous machine-learning methodologies. CNNs are highly suitable for processing image data due to their ability to learn at various scales and their robustness in extracting significant features from images through multiple layers of filters [15]. This study's objective is to harness DL's capabilities to accurately identify and classify the several types of white blood cells present in a blood sample. Consequently, the present study has devised a classification methodology employing CNN to discern various categories of WBCs.

The key objectives of our study are listed as follows:

- To present an overview of the current state-of-the-art WBC classification field using deep learning techniques.
- Identify the challenges and limitations of using deep learning for WBC classification.
- To analyze the performance of the proposed methods using publicly available datasets.
- To compare and evaluate different deep learning architectures and methods for WBC classification.

This article has the following organizational structure. The research on determining the kind of WBC from blood microscopic images is covered in Section 2. The background techniques used in this article are further explained in Section 3. The proposed methodology is depicted in section 4. Section 5 mentions experimental findings and discussions. The final conclusions are presented in Section 6.

2. Literature Review

Types of WBC in blood smear images have been classified using various methods. The most widely used of these typically employ some combination of machine learning, deep learning, fuzzy logic, or all three.

B. Karthik et al. [16] implemented an approach to segment and classify blood cells. At first, they acquired microscopic blood cell images using a digital microscope, followed by an image pre-processing approach to eliminate noise. They used the k means approach for segmenting the microscopic images; finally, they used the Enhanced CNN approach to classify normal and abnormal cells. Burhan Ergen et al. [17] proposed a model which consists of three stages. In the first stage, they used GoogleNet, ResNet-50, and AlexNet for extracting the features. In the second stage, Maximal Information Coefficient and Ridge Regression were employed for selecting the features. At last, they used those selected features which were common in MIC and RR for classification purposes using the Maximal Information Coefficient classifier. Pradeep Kumar Das et al. [18] suggested a novel hybrid transfer learning-based approach for detection and classification purposes which consists of ResNet18 and MobilenetV2. For containing the advantages of both approaches, they proposed a probability-based weight factor during hybridization. M.D. Patil et al. [19] proposed a classification approach of WBC images. They first applied canonical correlation analysis which extracts multiple nuclei patches and represents the effects of overlapping features. After that the output is fed into CNN and RNN models; finally, the output is merged, and the prediction is made by a dense softmax layer.

To improve segmentation accuracy, Yan Lu et al. [20] implemented a WBC-Net model which was based on ResNet and UNet++. It contained three stages: feature extraction, feature reconstruction, and feature fusion. WBC-Net showed better robustness among various states of models. Engin Avci et al. [21] implemented a novel automatic approach for the detection and classification of white blood cells. Here they used the R-CNN approach for identifying the regions and the transfer learning approach for classification purposes. They used several CNN architectures like

VGG16, GoogleNet, ResNet, and AlexNet, however, ResNet50 outperformed all models. Himani Kapur et al. [22] suggested a classification approach that utilized the concept of a Convolutional Neural Network for classifying types of white blood cells in blood smear images. The implemented approach showed maximum performance in 20 epochs. An automatic nucleus-based segmentation and classification approach was proposed by Rappy Saha et al. [23]. They used the k-means algorithm for nucleus segmentation. For classification, they fused the features of the first and last layers of convolution of CNN which provided better accuracy than other CNN models. Table 1 shows the comparative summary of relevant studies.

- As a result of this study's extensive literature evaluation, the authors have drawn the following findings.
- Classifying WBC classes has been accomplished using both conventional image processing and Neural Networks (NN).
- Second, a well-performing Convolution Neural Network (CNN) can be built from scratch to solve the WBC classification problem.
- Third, there is still a significant lag between the time spent training CNNs and their ability to classify WBCs.

Our motivation for developing a CNN-based categorization strategy comes from the information provided above.

Table 1. Comparative summary of relevant studies

Study	Methodology	Image Pre-processing	Segmentation	Classification	Models Used
Karthik et al. (2022) [16]	Digital microscope, image pre-processing, k-means, Enhanced CNN	Yes	K-means	Enhanced CNN	Not specified
Ergen et al. (2020) [17]	GoogleNet, ResNet-50, AlexNet, Maximal Information Coefficient, Ridge Regression, Maximal Information Coefficient classifier	No	Not specified	Maximal Information Coefficient classifier	GoogleNet, ResNet-50, AlexNet
Das et al. (2021) [18]	ResNet18, MobilenetV2, transfer learning, probability-based weight factor	No	Not specified	ResNet18, MobilenetV2	ResNet18, MobilenetV2
Patil et al. (2021) [19]	Canonical correlation analysis, CNN, RNN, softmax	No	Canonical correlation analysis	CNN, RNN, softmax	Not specified
Lu et al. (2021) [20]	WBC-Net, ResNet, UNet++, feature extraction, feature reconstruction, feature fusion	No	Not specified	WBC-Net	ResNet, UNet++
Avci et al. (2020) [21]	R-CNN, transfer learning, VGG16, GoogleNet, ResNet, AlexNet	No	R-CNN	Transfer learning	VGG16, GoogleNet, ResNet, AlexNet
Kapur et al. (2022) [22]	Convolutional Neural Network	No	Not specified	Convolutional Neural Network	Not specified
Saha et al. (2020) [23]	K-means, CNN	No	K-means	CNN	Not specified

3. Preliminaries

3.1 Convolution neural networks

Convolutional Neural Networks (CNNs) are a specialized form of deep learning algorithm that exhibits exceptional efficacy in the domain of image classification tasks [24]. CNNs are founded upon the concept of convolutional operations. These operations entail the application of a diminutive matrix, referred to as a kernel or filter, to localized regions of an image. Subsequently, the kernel is traversed across the entirety of the image, thereby enabling the extraction of distinctive features at various spatial locations. CNNs consist of multiple layers, as stated in previous research [25]. Each layer within the network is responsible for executing a distinct computational operation on the input image. In general, the initial layers of a CNN are responsible for conducting convolution and subsampling operations. These operations are aimed at extracting fundamental features at a lower level, such as edges and textures, as mentioned in reference [26]. The subsequent layers amalgamate these characteristics to construct elevated-level depictions of the image. In conclusion, the image is classified based on the extracted features using a fully connected layer, as mentioned in reference [27]. CNNs have demonstrated their efficacy in various image classification tasks, such as object recognition and detection. Notably, CNNs have exhibited remarkable performance in the classification of WBCs. In a conventional image classification task utilizing CNNs, the network layers fulfil specific functions as illustrated in Fig. 1.

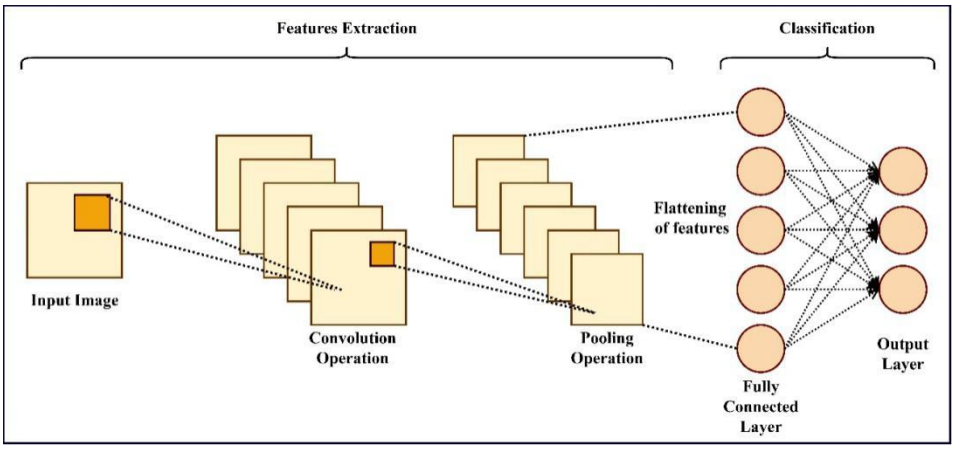


Fig.1. Basic Convolution Neural Network

- *Convolutional layer:* Convolutional layers constitute a fundamental element within CNNs. The primary function executed by this layer is the convolution operation, wherein a collection of filters is applied to localized regions of the input image. These filters are subsequently shifted across the entire image to extract features from various locations [28]. Every filter is represented by a small matrix that undergoes convolution with a specific local region of the input image. The outcome of this convolution operation is then saved in a feature map. The procedure is iteratively performed for every filter, leading to the generation of feature maps. These feature maps are then consolidated by concatenation to produce the final output of the convolutional layer.
- *Pooling layer:* Pooling layers are commonly employed after convolution layers to decrease the spatial dimensions of the feature maps [29], thereby enhancing the network's resilience to minor translations in the input. Activation functions, such as Rectified Linear Unit (ReLU), sigmoid, and others, are utilized in neural networks to introduce non-linearity.
- *Fully connected layer:* Fully connected layers are used in classification to analyze the features extracted by the convolution layers and make a final decision on the class of the cell. It is performed by computing the dot product of the input and weight matrix and then adding a bias term. A SoftMax activation function [30] is typically applied at the output of the fully connected layer to produce a probability distribution over the classes.

4. Proposed Methodology

In this section, the proposed methodology adopted for WBC classification is discussed. It comprises mainly three tasks, namely data pre-processing, feature selection, and model training. The in-depth description of each task is given in subsequent subsections. Fig. 2 depicts the proposed architecture for blood cell image classification.

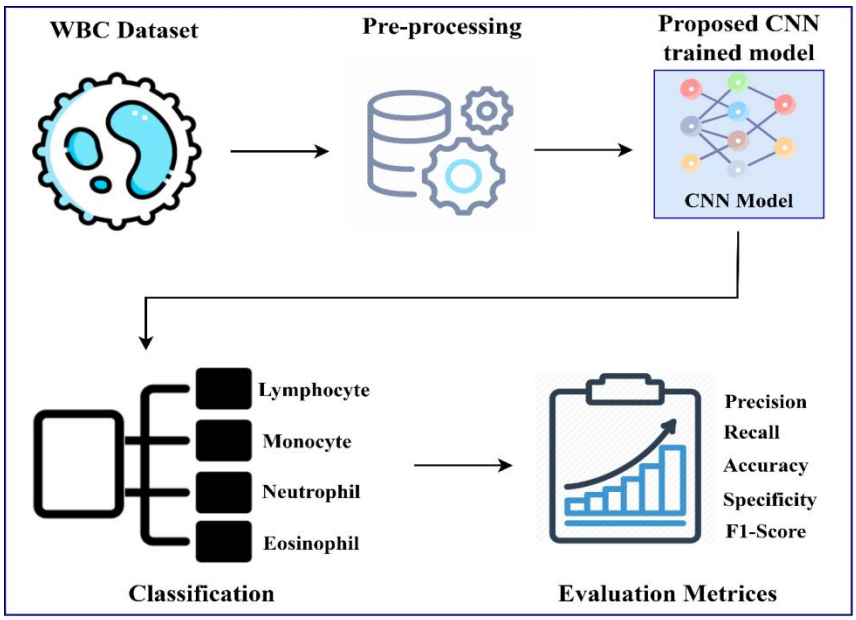


Fig. 2. Workflow of the proposed model for Classification of WBC images

4.1 Data preprocessing

Data preprocessing plays a crucial role in the image classification pipeline [31] as it helps to ensure that the data is clean, consistent, and suitable for use by a machine learning model. Proper data preprocessing can improve the model's performance, reduce overfitting, and make the model more robust to variations in the input data. Further, data preprocessing can also help to reduce computational costs and improve the efficiency of the machine learning model.

In our presented approach, the following data preprocessing steps are adopted to clean, transform, and prepare the data before being used by the machine learning model.

- Data Cleaning: Data cleaning is significant for image classification tasks as the quality and relevance of the images can impact the performance of the machine learning model. Similarly, irrelevant images can lead to bias in the model or poor generalization of new data. The dataset considered for analysis contains only three Basophil-type WBC images, which are small. Therefore, these three images are discarded from the original dataset to improve the performance, robustness, and generalization ability of the model.
- Image Resizing: This involves changing the size of the images to a specific size or aspect ratio. This step ensures that the machine learning model can process the images consistently and efficiently. In our research, all the original dataset images are resized to 128 * 128.
- Noise Reduction: Noise can obscure essential features in the images, making it harder for the model to classify the images correctly. The model can extract more relevant features by removing or reducing the noise, leading to improved performance. The median filter [32] is an effective technique commonly used to reduce the noise of a salt-and-pepper variety in images. The median filter works by analyzing the pixel values in a given neighborhood and replacing the current pixel value with the median value of the neighborhood.
- Image Augmentation: Image augmentation artificially increases the size of the dataset by applying various transformations (rotation, scaling, flipping, and cropping) to the existing images [33] to create more diverse and varied images. By applying various transformations, the original dataset size is increased to 12,444 images.
- Dataset Splitting: It refers to dividing the data into training, validation, and test sets. This is important for evaluating the performance of the model and ensuring it generalizes well to new data. Dataset images are split into a 70:30 ratio for training and testing the proposed model.

4.2 Feature extraction

Feature selection is the next stage in the process of performing image classification [34] . When CNN is being trained, the initial layers called convolution, and pooling layers, along with the non-linear activation function, are used to extract the features of the input blood cell images. CNN's feature extractor comprises specialized neural networks whose weights are determined during training. A deeper neural network (more number layers) improves the image classification process using CNN. The initial layers of the proposed model are used to learn the non-linear features from the input blood cell images, which are used for classifying images into Lymphocyte, Monocyte, Neutrophil, and Eosinophil classes.

4.3 Classification

In the field of artificial intelligence, CNN represents a subset of the feed-forward neural networks [35] . It has found extensive applications in automatic picture identification. In its most basic form, CNN is an image categorization structure. To identify images, CNN first extracts feature from them. Therefore, the classes or labels of the classes that a typical CNN has learned to classify are represented in the CNN's outputs. There are as many neurons in the CNN's output layer as there are classes in the data set. The proposed model contains four neurons in the output layer with SoftMax as an activation function to classify the input image into four classes: Lymphocyte, Monocyte, Neutrophil, and Eosinophil.

Table 2. Components of proposed CNN architecture

Model: "Sequential"		
Layer (type)	Output Shape	Param #
batch_normalimtion (BatchNormalimtion)	(None, 128, 128, 3)	12
conv2d (Conv2D)	(None, 128, 128, 32)	896
activation (Activation) (ReLu)	(None, 128. 128, 32)	0
max_pooling2d (MaxPooling2D)	(None, 64,61, 32)	0
dropout (Dropout)(0.25)	(None, 64, 64, 32)	0
conv2d_l (Conv2D)	(None,64,64,32)	9248
activation_ (Activation) (ReLu)	(None, 64, 64, 32)	0
max_p001ing2d_1 (MaxP001ing2D)	(None, 32, 32, 32)	0

conv2d_2 (Conv2D)	(None, 32, 32, 64)	18496
activation_2 (Activation) (ReLu)	(None, 32, 32, 61)	0
max_pooling2d_2 (MaxPooling2D)	(None, 16, 16, 64)	0
conv2d_3 (Conv2D)	(None. 16, 16. 64)	36928
activation_3 (Activation) (ReLu)	(None, 16, 16, 61)	0
max_pooling2d_3 (MaxPooling2D)	(None, 8,8,64)	0
conv2d_4 (Conv2D)	(None, 8,8, 128)	73856
activation_4 (Activation) (ReLu)	(None, 8, 8, 128)	0
max_pooling2d_4 (MaxPooling2D)	(None, 4,4, 128)	0
conv2d_5 (Conv2D)	(None, 4,4, 128)	147584
activation_5 (Activation) (ReLu)	(None, 4,4, 128)	0
max_p001ing2d_5 (MaxP001ing2D)	(None, 2,2, 128)	0
flatten (Hatten)	(None, 512)	0
dense (Dense) (128)	(None, 128)	65664
activation_6 (Activation) (ReLu)	(None, 128)	0
dense_1 (Dense) (64)	(None, 64)	8256
activation_7 (Activation) (ReLu)	(None, 64)	0
dropout_1 (Dropout)	(None, 64)	0
dense_2 (Dense) (32)	(None, 32)	2080
activation_8 (Activation) (ReLu)	(None, 32)	0
dense_3 (Dense) (4)	(None, 4)	132
activation_9 (Activation) (Softmax)	(None, 4)	0
Total params: 363,152 Trainable params: 363,146 Non-trainable params: 6		

5. Experimental Results and Discussion

This section presented the experimental discussion of proposed work to evaluate the performance of proposed framework. An i7 2.50 GHz processor and 16 GB of main memory have been used for all experiments. The most recent release of Python, 3.11, includes the sci-kit library necessary to train models. Data collection, detailing the specifics of the analyzed data, performance evaluation metrics, and results with discussion make up the three following sub-sections.

5.1 Dataset description

The dataset was obtained from Kaggle's public repository. Dye-labeled white blood cell micrographs (WBC) were the subject of this dataset's 364 colored images. In some cases, researchers use data collected in-house, while in others, they use a publicly available database. The dataset from this group has been selected for use in training and validation.

The provided dataset contains 12,500 images depicting blood cells. The four primary classifications are Eosinophils, Lymphocytes, Monocytes, and Neutrophils. Fig. 3 illustrates a few sample images extracted from the dataset. The total number of images exceeds 3,000, and they are uniformly distributed across all categories. Table 3 presents the comprehensive count of images pertaining to several types of white blood cells (WBCs). To assess the efficacy of the proposed framework, the dataset is partitioned into train-test splits of 70%-30%, 80%-20%, and 90%-10%. Additionally, in order to address the challenges associated with over-fitting, a preliminary stopping criterion is proposed, wherein the training process is halted when the system demonstrates minimal or no improvement over a few iterations.

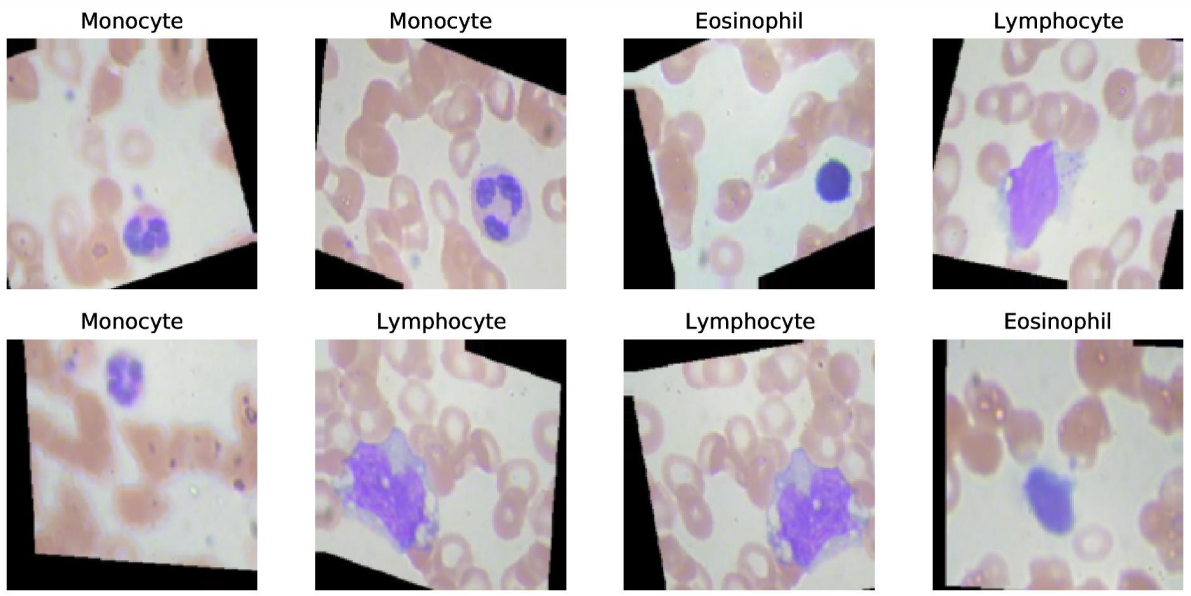


Fig. 3. Sample Blood Cell Images

5.2 Evaluation measures

Multiple evaluation measures are employed to assess the efficacy of the classifier. Among the various established metrics, classifier accuracy stands out as the predominant quality index utilized to assess the performance of classifiers. It quantifies the proportion of correctly classified samples in relation to the total number of data samples. Table 4 presents a depiction of the characteristics of the confusion matrix [36], consisting of four partitions that represent distinct features: True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN). The performance measures are computed in order to assess the efficacy of the proposed framework.

Table 4. Confusion Matrix

Actual	Predicted	
	Yes	No
Yes	True positive	False positive
No	False positive	True negative

1) Accuracy

The metric assesses the classifier's capacity to accurately forecast sample data. The measure of accuracy is determined by dividing the number of correctly predicted outcomes by the total number of predictions made for classification.

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

2) Precision

Precision is calculated by dividing the total number of correctly predicted positive cases (True Positives or TP) by the overall count of predicted positive cases, specifically within the population of infected patients.

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

3) Recall or Sensitivity

The recall metric is employed to assess the effectiveness of a classifier in accurately predicting positive instances. The calculation involves determining the proportion of accurate positive predictions in relation to the overall number of individuals who are positively infected.

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

4) Specificity

In contrast to sensitivity, specificity quantifies the capacity to make accurate negative predictions.

$$Specificity = \frac{TN}{TN + FP} \tag{4}$$

5) F1-score

The F1-score is a metric that measures the classifier's accuracy by considering both recall and precision.

$$F1 - score = 2 \times \frac{Recall \times Precision}{Recall + Precision} \tag{5}$$

5.3 Results and discussions

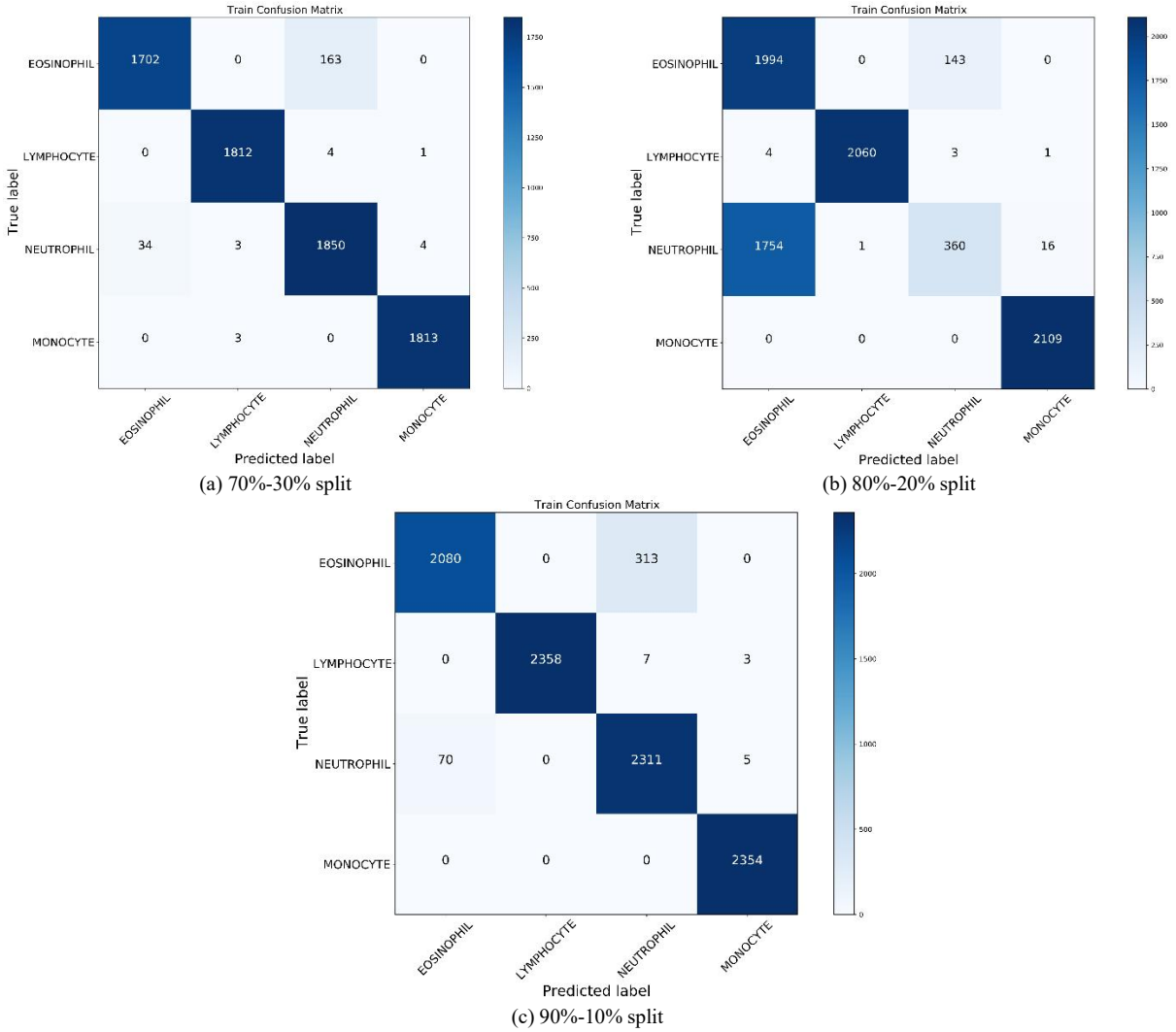
The framework that has been proposed is specifically developed with the objective of categorising images of blood cells into four distinct categories. The dataset utilised for training this framework comprises numerous images, with each image being assigned a corresponding category label. Throughout the training procedure, the hyperparameters of the convolutional neural network (CNN) model under consideration are systematically adjusted in an iterative manner with the objective of minimising the loss function and ultimately achieving convergence. In order to accomplish this objective, we have implemented the Adam optimizer, which is widely recognised for its adaptability and robustness as an optimisation algorithm. The optimizer was utilised to establish the learning rate, which governs the rate at which the model adjusts its parameters in accordance with the loss function. In order to optimise the training process, the model is trained using batches consisting of 32 samples, where each batch contains the training data and its corresponding loss function. This implies that the model undertakes the processing of 32 images simultaneously and adjusts its parameters by considering the average loss across this batch. Table 5 presents a comprehensive list of the experimental variables, encompassing the hyperparameters of the model, the settings of the optimizer, and the batch size.

Table 5. Hyper-parameter for fine-tuning

Parameter	Value
Type of pooling layer	Max Pooling
Learning rate	Reducing
Mini-batch size	32
Optimizer algorithm	Adam
Loss function	Cross-Entropy
Maximum epoch	50

The evaluation of the proposed CNN model is conducted by utilising a confusion matrix. This matrix serves as a comprehensive table that effectively summarises the classification outcomes obtained from a designated test dataset. The confusion matrix for the model is depicted in Figures 4 to 7. In order to achieve a more comprehensive assessment of the classifier's performance, we have taken into account three distinct training and test divisions. The purpose of these splits is to partition the sample data into distinct proportions for the purposes of training and testing, in order to evaluate the performance of the model across various scenarios. The initial partition involves a division of the data into two subsets, with a ratio of 70% to 30%. Specifically, 70% of the data is allocated for training purposes, while the remaining 30% is reserved for testing. The second division of the dataset follows an 80%-20% partition, wherein 80% of the data is allocated for the purpose of training, while the remaining 20% is reserved for testing. The third partition employs a 90%-10% division, wherein 90% of the dataset is allocated for training purposes, while the remaining 10% is reserved for testing.

Through the assessment of the model's performance on these distinct partitions, we can enhance our comprehension of how the model operates when exposed to differing quantities of training data. This information possesses utility in ascertaining the ideal quantity of data necessary to attain a desired level of performance, as well as in detecting any potential challenges that may arise during the training of the model using datasets of varying sizes.



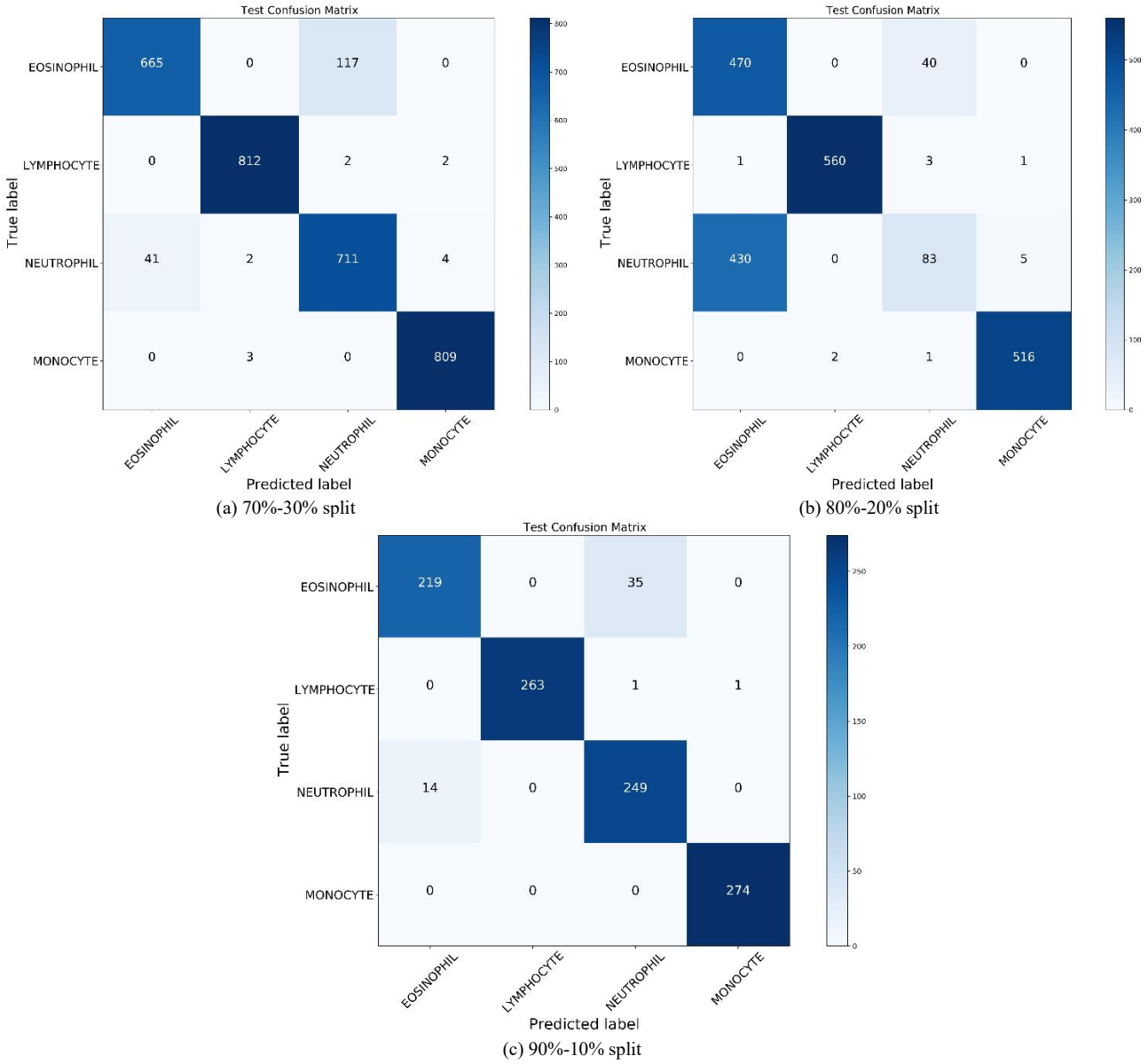
(a) 70%-30% split

(b) 80%-20% split

(c) 90%-10% split

Fig. 4. Confusion Matrix for Training data for 25 Epochs

The performance evaluation of the proposed CNN model is depicted in Figs. 4 and 5. The presented figures depict confusion matrices corresponding to various training and test splits, offering significant insights into the predictive accuracy of the model across different blood cell classes. Fig. 4 illustrates the training confusion matrix obtained after 25 epochs on various data partitions. The confusion matrices depicted in Figs. 4(a)-(c) demonstrate the accurate predictions made by the proposed CNN model. Specifically, for the 70%-30%, 80%-20%, and 90%-10% splits, the model successfully predicts 7177, 6523, and 9103 sample data, respectively. These predictions are made out of a total of 10557 training samples. Fig. 5(a) displays the confusion matrix for test data in the 70%-30% split. It reveals that the proposed model accurately predicts 2997 out of 3168 samples to their corresponding class with an accuracy of 94%. Fig. 5(b) shows the confusion matrix for test data in the 80%-20% split. The proposed model accurately predicts 1629 out of 2112 samples to their correct class with an accuracy of 77%. Finally, Fig. 5(c) presents the confusion matrix for test data in the 90%-10% split. The proposed model accurately predicts 1005 out of 1056 blood cell images to their correct classes with an accuracy of 96%.



(a) 70%-30% split

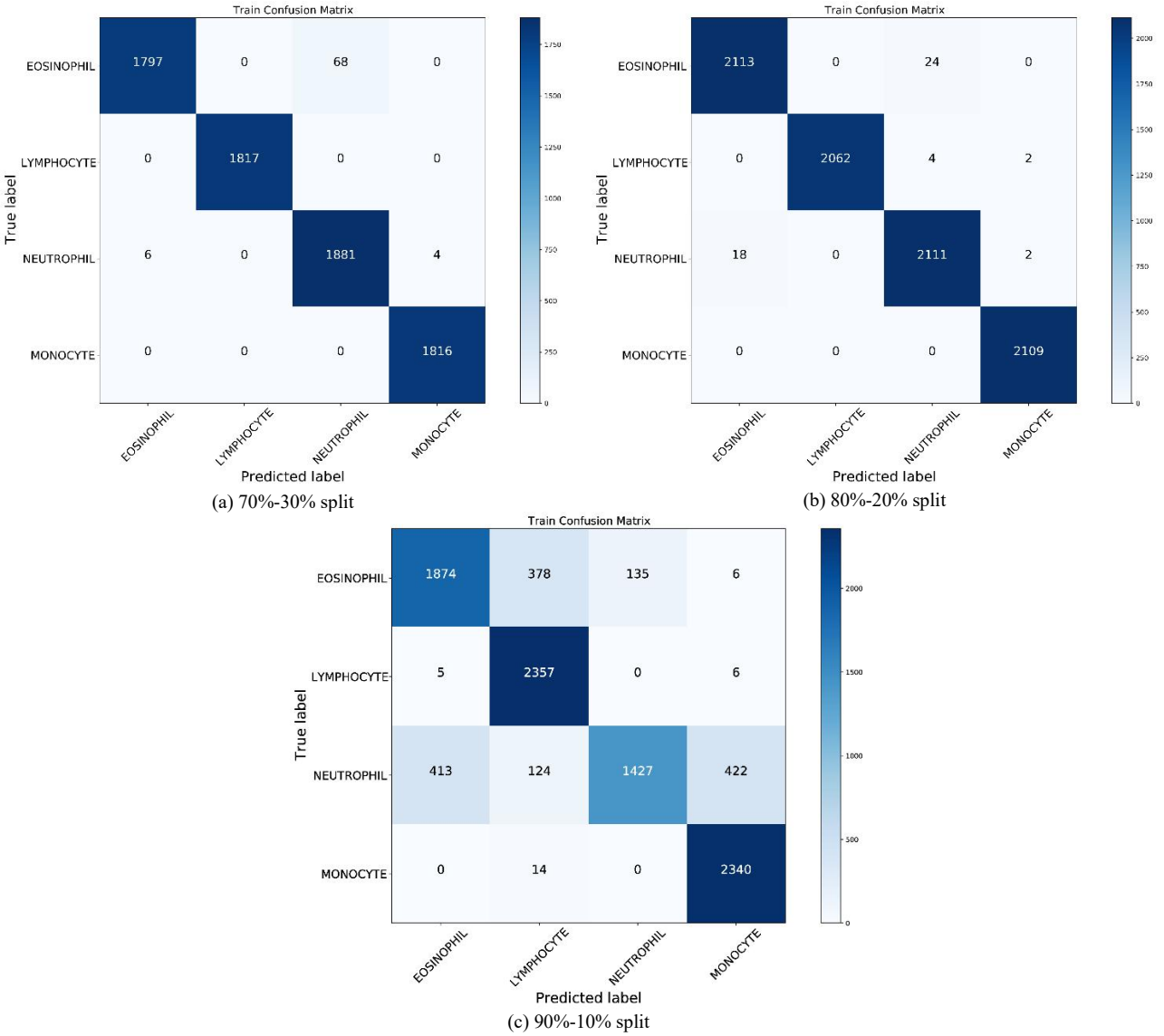
(b) 80%-20% split

(c) 90%-10% split

Fig. 5. Confusion Matrix for Test data for 25 Epochs

The average accuracy for the proposed CNN model over 25 epochs for different splits is 89%. These results indicate that the model is effective in classifying blood cells into their respective categories and has high accuracy for all three data splits.

Fig. 6 and 7 show the confusion matrix obtained from a comparable parameter over 50 epochs. Fig. 6 (a)-(c) illustrates the accurate predictions made by the proposed Convolutional Neural Network (CNN) model. Specifically, the model correctly predicts 7311, 8395, and 7998 sample data for the 70%-30%, 80%-20%, and 90%-10% splits, respectively, in relation to their respective classes. These predictions were obtained when the total number of training samples amounted to 10557. Fig. 7(a) illustrates that out of a total of 3168 images, 3078 images were accurately classified, resulting in an accuracy rate of 99.0%. The confusion matrix for the data split of 80%-20% is presented in Fig. 7 (b). The findings indicate that the model achieved a classification accuracy of 98% by accurately categorizing 2066 blood cell images into their respective classes. Finally, utilizing a data split of 90% for training and 10% for testing, the model demonstrates a remarkable accuracy rate of 98%. Based on the empirical findings, it is apparent that the model proposed in this study demonstrates superior performance, as indicated by an average accuracy of 98.33% when tested on a dataset comprising blood cell images.



(a) 70%-30% split

(b) 80%-20% split

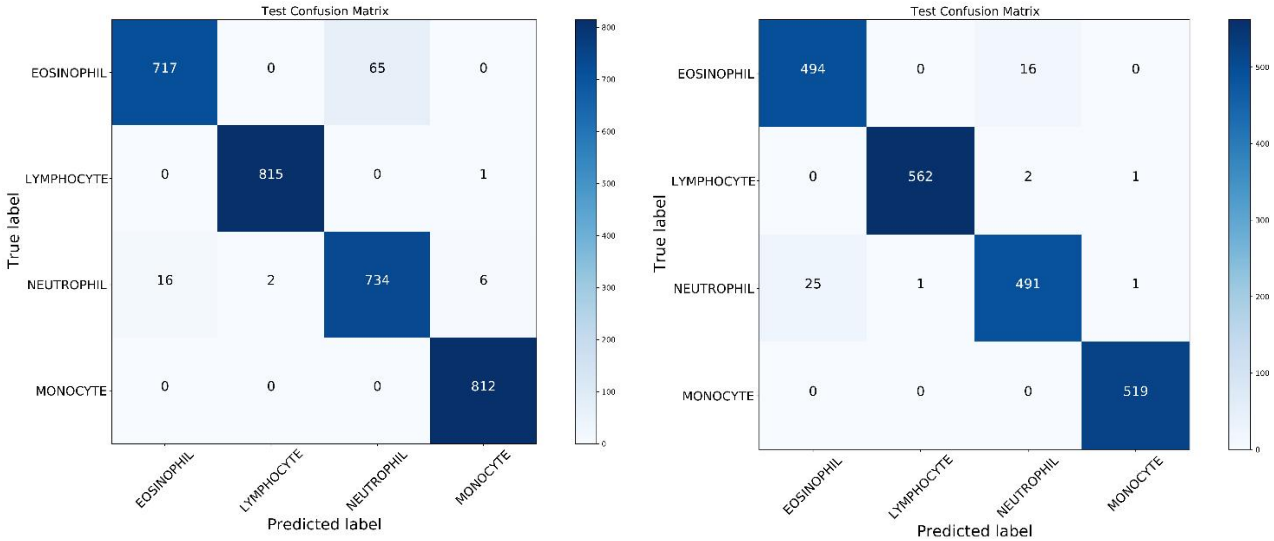
(c) 90%-10% split

Fig. 6. Confusion Matrix for Training data for 50 Epochs

Figs 8 and 9 provide a visual representation of the accuracy and loss metrics obtained during the training and validation phases of the proposed model for 25 and 50 epochs, respectively. This experiment was conducted by employing three different data splits, as previously mentioned. During each epoch, the accuracy, training error, and validation error were computed.

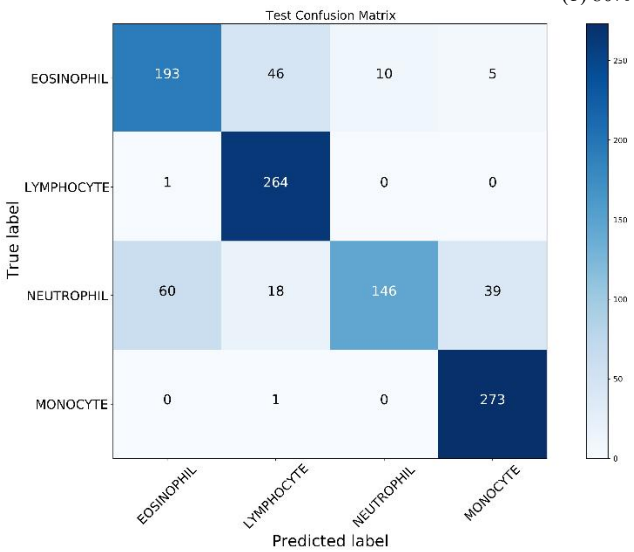
It is worth noting that the proposed model achieved the highest classification accuracy and demonstrated the lowest training and validation loss when compared to other architectures. This indicates that the proposed model outperformed other existing models in accurately classifying the data with minimal errors during the training and validation phases. These results emphasize the effectiveness and potential of the proposed model in practical applications.

Table 6 gives a summary of experimentation results with a pre-trained model and designed transfer learning classifier model. From the results, it is evident that the proposed architecture outperforms existing CNN architectures and achieves the highest classification accuracy of 99% when trained using 90-10 train-test split. On the contrary, ResNet-50, Inception-V3, and VGG 19 attain average accuracy of 97%, 98%, and 85% respectively.



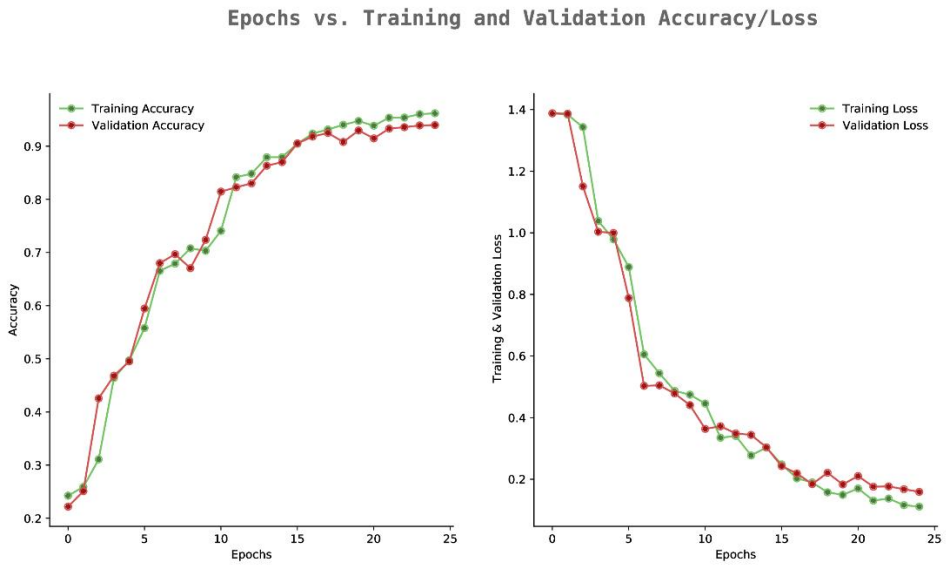
(a) 70%-30% split

(b) 80%-20% split

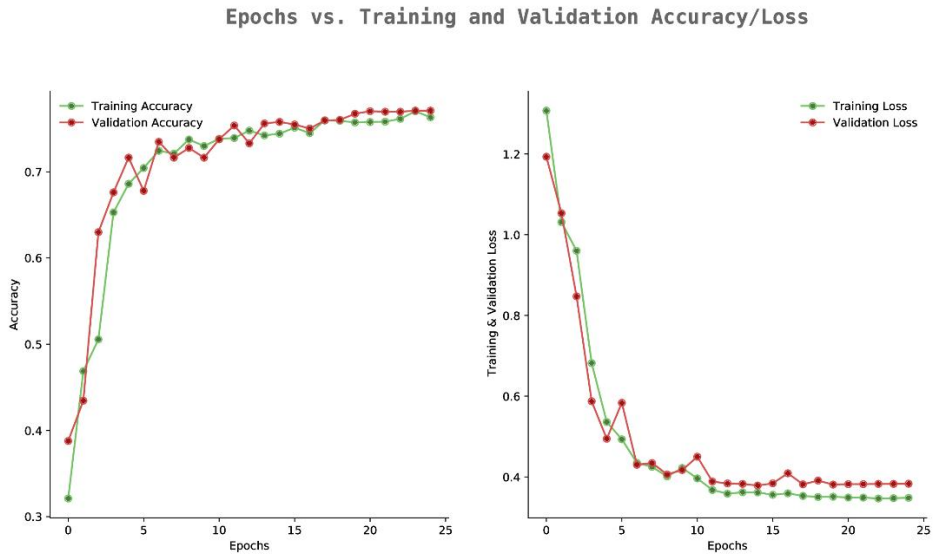


(c) 90%-10% split

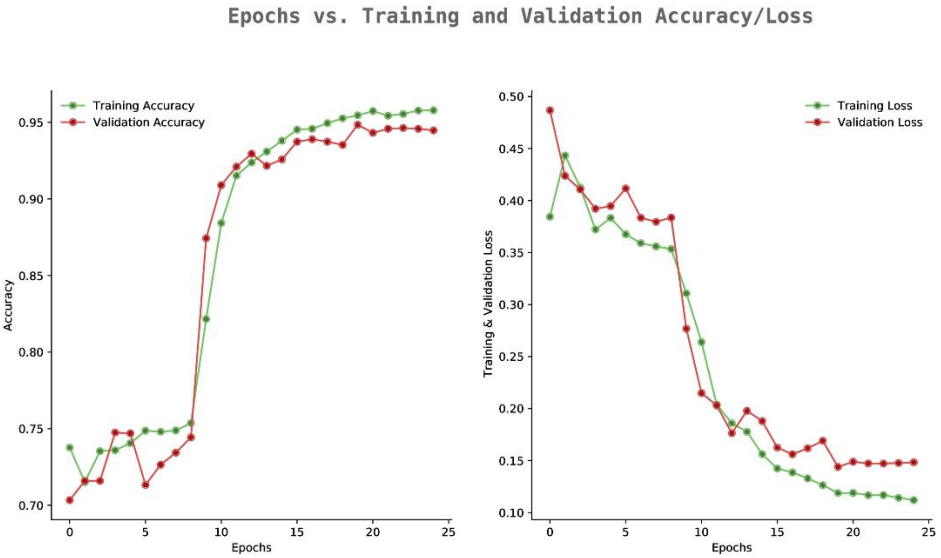
Fig. 7. Confusion Matrix for Test data for 50 Epochs



(a) 70%-30% split

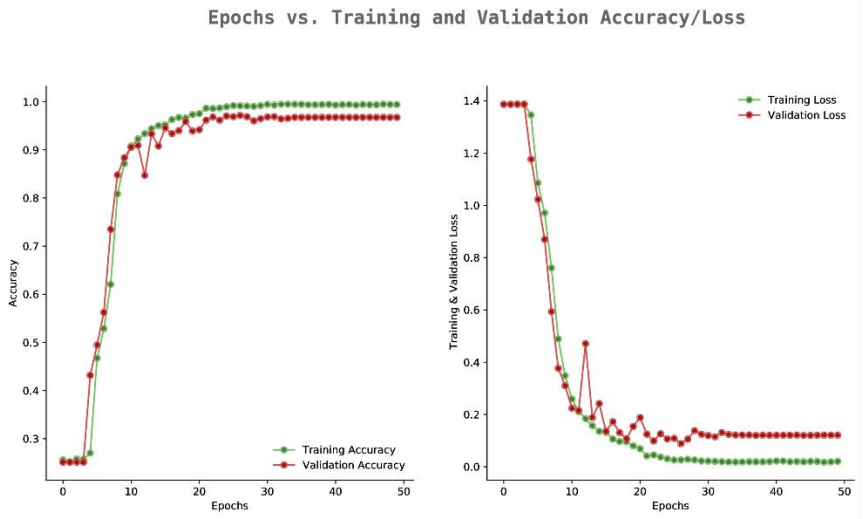


(b) 80%-20% split

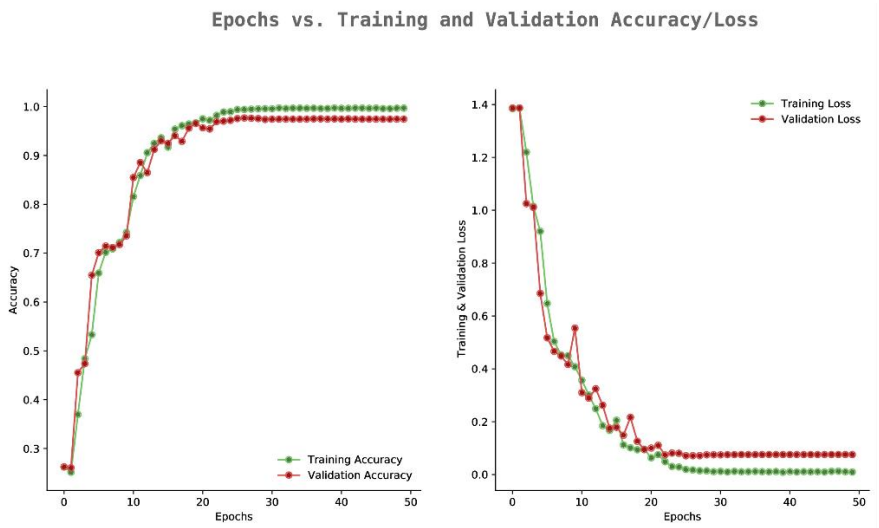


(c) 90%-10% split

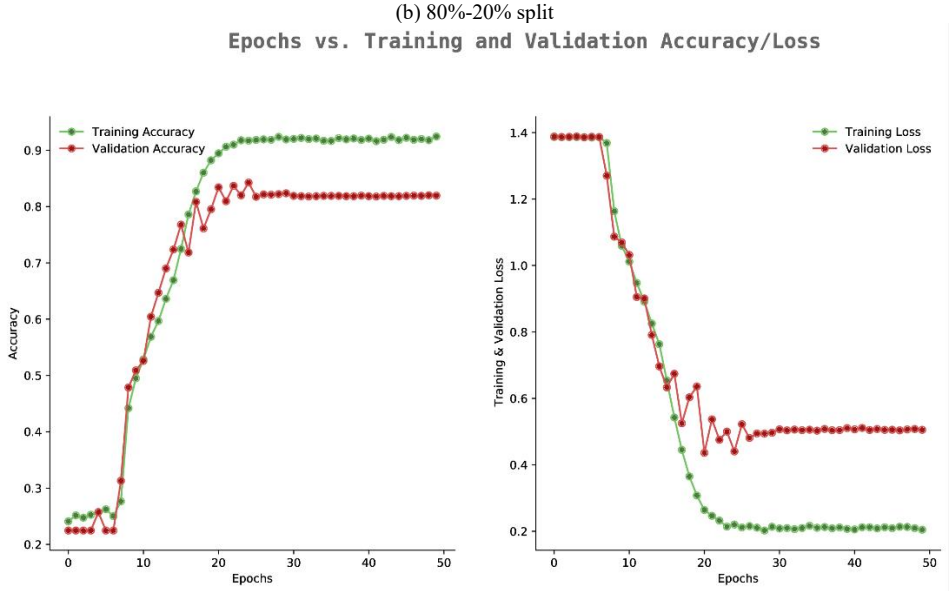
Fig. 8. Epochs vs. training and validation Accuracy/Loss for 25 Epochs



(a) 70%-30% split



(b) 80%-20% split



(c) 90%-10% split

Fig. 9. Epochs vs. training and validation Accuracy/Loss for 50 Epochs

Table 6. Performance of the Proposed Model Under Different Epochs

Epochs	Train-Test split	Class Type	Precision	Recall	F1 -Score	Accuracy	Average Accuracy
25	70:30	E	0.94	0.85	0.89	0.94	0.89
		L	0.99	1.00	0.99		
		N	0.86	0.94	0.90		
		M	0.99	1.00	0.99		
	80:20	E	0.53	0.93	0.68	0.77	
		L	1.00	1 .00	1.00		
		N	0.71	0.17	0.27		
		M	0.99	1.00	1.00		
	90:10	E	0.94	0.86	0.91	0.96	
		L	1.00	0.99	1.00		
		N	0.87	0.95	0.92		
		M	1.00	1.00	1.00		

50	70:30	E	1.00	0.96	0.98	0.99	98.33
		L	1 .00	1.00	1.00		
		N	0.97	0.99	0.98		
		M	1.00	1.00	1.00		
	80:20	E	0.95	0.97	0.96	0.98	
		L	1.00	0.99	1.00		
		N	0.96	0.95	0.96		
		M	1.00	1.00	1.00		
	90:10	E	0.96	0.94	0.96	0.98	
		L	0.89	1.00	0.93		
		N	0.94	0.91	0.88		
		M	0.89	1.00	0.92		
E: "EOSINOPHIL", L: "LYMPHOCYTE", N: "NEUTROPHIL" and M: "MONOCYTE"							

1) A comparison of recent works

Furthermore, a comparative analysis is conducted to evaluate the overall efficacy of the proposed strategy in relation to previous studies conducted within the same field. The empirical results of the proposed framework and other contemporary investigations are presented in Table 7, with a focus on metrics such as accuracy and other relevant parameters. According to the findings in Table 7, the performance approach demonstrates higher accuracy than previous studies.

Table 7. Comparative analysis with recent works

Ss8	Year	Model	Dataset	Accuracy
B. Karthik et al. [16]	2022	K-means followed by Enhanced CNN	1542 blood cell microscopic images	95%
Burhan Ergen et al. [17]	2020	CNN models followed by QDA	12435 WBC microscopic images	97.95%
Pradeep Kumar Das et al. [18]	2021	Hybrid Deep CNN based approach	ALLIDB1, ALLIDB2 contains 108 and 260 microscopic leukocytes images respectively	ALLIDB1=97.92% ALLIDB2=96%
M.D. Patil et al. [19]	2021	CCA applied to CNN and RNN	12442 microscopic blood cell images	95.89%
Yan Lu et al. [20]	2021	WBC-Net	Four datasets containing 300,100,242 and 231 WBC images respectively	Dataset1=96.3 Dataset2=97.1 Dataset3=94.18 Dataset4=97.4
Engin Avci et al. [21]	2020	R-CNN with transfer learning	BCCD=410 images LISC=242 images	97.0%
Himani Kapur et al. [22]	2022	CNN	BCCD	97.8%
Rappy Saha et al. [23]	2020	CNN	BCCD, ALL-IDB2, JTSC, CellaVision	BCCD=96.2% ALL-IDB2=97.2% JTSC=97.57% CellaVision=96.5%
Our Work	-	CNN	12444 WBC blood cell microscopic images	**Accuracy=98.33%**

6. Conclusion

This study presents a novel approach utilising convolutional neural networks (CNN) to classify the subtype of white blood cells (WBC) based on blood smear images. In contrast to the classifiers currently available, the proposed convolutional neural network (CNN) exhibited a notable overall accuracy rate of 98.33% in the identification of white blood cell (WBC) types. This outcome underscores the potential of the CNN in enhancing the precision and efficiency of WBC classification. The proposed convolutional neural network (CNN) architecture was developed from the ground up. Following a series of approximately 25 iterations, the model attained an accuracy rate of 89%. The CNN-based classification method under consideration has the potential to effectively tackle various classification challenges, including the classification of red blood cells (RBCs). The utilisation of transfer learning techniques has the potential to further enhance the accuracy rates. It is important to acknowledge that the proposed convolutional neural network (CNN) model was trained and evaluated using images of single cells, which are not commonly found in blood samples. In forthcoming investigations, our intention is to employ the model on white blood cell (WBC) images featuring the presence of multiple cells, overlapping instances, and occlusion. This particular approach has the potential to effectively

tackle the difficulties linked to manual classification, thereby resulting in enhanced outcomes in terms of diagnosis and treatment.

Data Availability Statement

The data supporting this study's findings are available from the corresponding author upon reasonable request.

Conflict of Interest

The authors declare that they have no conflict of interest.

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