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RESEARCH ARTICLE

Classification of Blood Cells from Blood Cell Images Using Dense Convolutional Network

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HIGHLIGHTS

- *A Dense CNN model is proposed for white blood cell classification*
- *Comparison in terms of accuracy, precision, recall, and F1 measure with other classifiers*
- *The overall accuracy rate of 94% was obtained with DenseNet121 model*
- *Use of publicly available dataset for state-of-the-art comparison with other studies*

Keywords:

- White blood cells
- Classification
- Deep learning
- DenseNet
- Pre-trained model

GRAPHICAL ABSTRACT

This study aims to classify white blood cells from blood cell images. Input image goes along multiple convolutions and acquire high-level features with standard CNN. In Dense Convolutional Network (DenseNet), each layer acquires additional inputs from all previous layers and transfers on its own feature-maps to all next layers as shown in graphic. DenseNet is a dense-connected convolutional network that forward connects each layer to the other layers. DenseNet gives superior performance for various computer vision problems. DenseNet reduces the gradient descent problem, increases feature reuse, and reduces parameter usage. The advantage of DenseNet architectures is to allow feature propagation and feature reuse. Thus it minimizes the number of parameters. The main structure block of DenseNet121 is the Dense Block. These Dense Blocks consist of convolution layers. DenseNet121 contains 121 connected convolutional layers with a fully-connected layer of 1000 units as the final output layer.

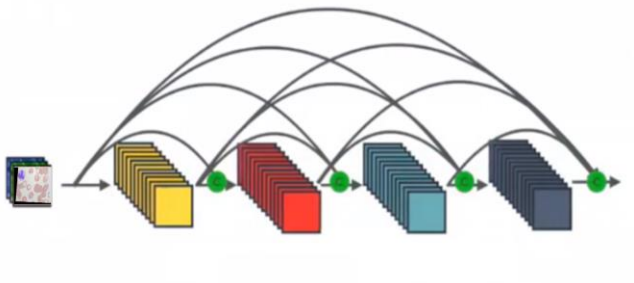

Figure A. Fundamental architecture of one dense block in DenseNet

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Aim of Article : *This study aims to classify white blood cells from blood cell images.*

Theory and Methodology: *In this study, blood cells are classified from blood cell images using dense convolutional neural network. This paper intends to utilize a dense convolutional neural network model (DenseNet121) to overcome the blood cell classification problem that is one of the most compelling problems in blood diagnosis.*

Findings and Results: *The data in the experimental study: 70% is reserved for training, 10% for validation, and 20% for testing. DenseNet121 model is built with batch size 128 and with 100 epochs at training. The total number of parameters is 7,628,484 for this model. DenseNet-121 has achieved the best feature extractor pre-trained model with accuracy rate of 94%.*

Conclusion: *Considering the high accuracy value obtained with this model, automatic detection of which class the cells belong to will speed up the diagnosis and allow more data to be examined.*

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ABSTRACT

Classification of white blood cells plays a significant role in the detection of diseases which are infections caused by abnormalities in the immune system, allergies, anemia, leukemia, cancer, AIDS, etc. In traditional methods, experts manually examine the white blood cells under the microscope, and since this process is tedious, takes more time and can be more error-prone, automated systems have become necessary. Making this classification automatically will help experts in the detection of diseases. In this study, blood cells are classified from blood cell images using dense convolutional neural network. This paper intends to utilize a dense convolutional neural network model to overcome the blood cell classification problem that is one of the most compelling problems in blood diagnosis. In this study, a DenseNet121 model is built to classify blood cell images. Experiments are conducted on an open-access BCCD dataset (12507 white blood cell images that contain four types of white blood cells). Performance evaluations are performed on the accuracy of the techniques, and the results are compared with state-of-the-art deep learning-based approaches as Xception, VGG19, EfficientNetB1. In experimental studies, the highest accuracy (94%) is obtained with the proposed DenseNet121 model. Considering the high accuracy value obtained with this model, automatic detection of which class the cells belong to will speed up the diagnosis and allow more data to be examined by doctors.

Keywords: *White blood cells, Classification, Deep learning, DenseNet, Pre-trained model*

I. INTRODUCTION

White blood cells (WBC) are one of the most essential cells for the human immune system. They are the cells that protect the human body against various infectious diseases and foreign invaders. While most white blood cells are produced in the bone marrow, some are produced by important glands in the body [1], [2]. Information that will be useful for diagnosing diseases can be learned in the blood, which is examined under the microscope. Recognition and examination of WBC in peripheral blood can help hematologists in diagnosing diseases like allergies, anemia, leukemia, cancer, AIDS, and blood cancer [3]. Studies in this context have become one of the most critical steps in hematological procedures. Classification of white blood cells plays a significant role in the detection of diseases which are infections caused by abnormalities in the immune system. Making this classification will help experts in the detection of diseases. One of the challenges in medical science is the detection and recognition of white blood cells, since red blood cells

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are much more numerous than white blood cells in body [4]. In a healthy adult individual, white blood cells make up about 1% of the total blood volume [5]. Due to this low ratio of white blood cells in the blood, the classification and recognition of white blood cells and especially their subtypes becomes a more difficult problem. A change in the number of any white blood cell subtype could mean that something is wrong with body and body is reacting to some type of pathogen. If we can recognize the white blood cells and their subtypes, we can get an idea about the future course of any disease and take various precautions in advance based on this information. Existing manual methods are error-prone and heavily time-consuming. There is a need for faster and more real solutions with less chance of error and to eliminate these disadvantages [6].

In this study, a DenseNet model is built to classify blood cell images. The rest of the work is organized as follows. In Section 2, the related works in literature are presented. Material and method are explained in Section 3. In this section, the data set used in the experimental study and the DenseNet model applied are explained in detail. In Section 4, experimental results are given, and the discussion and conclusion part of the study is given in Section 5.

II. RELATED WORKS

Researchers have recently proposed many methods for classifying blood cells because of the importance of blood cell classification in diagnosis. Related studies using similar open-access dataset [7] with this study are summarized as follows. In 2018, Liang et al. [8] proposed a model that assembles features of CNN (used Xception) and RNN (used LSTM). They classified cells using CNN & RNN with an accuracy rate of 90.79%. D. Bani-Hani et al. [9] proposed using CNN for the image classification of four blood cells with optimized CNN's hyperparameters with Genetic Algorithm. They classified cells using CNN & Genetic Algortm with accuracy rate of 91.00%. In 2019, Şengür et al. [10] used LSTM model which is based on shape and deep feature to classify white blood cells. They achived 92.89% accuracy with LSTM model. Banik et al. [11] proposed fused CNN model to classify blood cell images. They achieved 90.79 classification accuracy on WBC dataset. In 2020, Patil et al. [12] used to merge CNN and RNN to reinforce the perceiving of image content. Moreover, they used Canonical Correlation Analysis to overcome problem of multiple cells overlap. They classified cells using this technique with a accuracy rate of 95.48%. In 2020, Mohamed et al. [13] studied the performance ten different pretrained models with six types of machine learning techniques. They reported that DenseNet-169 has achieved the best feature extractor pre-trained model with accuracy rate of 92.00%. In 2020, Dekhil [14], proposed a customized CNN architecture with extracted ROI. This technique achieved rate of accuracy with 92.50%. In 2021, Ghosh and Kundu [15] built a multi-layer network model by combining RNN+CNN to classify different blood cells. They obtained 87.29% accuracy with RNN+CNN model. Ekiz et al. [16] classified cells using the convolutional features in the SVM classifier with an accuracy rate of 85.96%. Other hybrid deep learning methods are summarized as follows. In 2017, X. Li et al. [17] used feature extraction with PCA and then compared the results obtained using an 8-layer CNN architecture with a trained SVM. They presented that CNN was 30% more successful than SVM. Yu et al. [18] classify WBC sub-types by using transfer learning and fine-tuning methods. At the end of their studies, they achieved better results than conventional methods and a standard CNN. Jiang et al. [19] first pre-processed the datasets (data augmentation, PCA, etc.) and then trained the datasets with a 33-layer CNN architecture.

As can be observed in the literature, despite it is possible to achieve high success measures with deep learning, the need for a large amount of data during training process a major problem for researchers working with medical images [20]. For this reason, it is observed that researchers benefit from data augmentation techniques in data sets, thus trying to increase the number of data to an adequate level. Essentially, accuracy can be increased even more with original data. In addition, as observed in the studies, some researchers used transfer learning/fine-tuning methods to overcome with the insufficient data problem, while others used hybrid models in their studies. Also, despite deep learning methods can make extraction directly from the image itself, it has been observed that researchers benefit from pre-processing processes in order to increase the accuracy rate. On the other hand, in cases where the examples in the classes of the data set are insufficient, it has been observed in some studies that some classes are not included in the training.

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III. MATERIAL AND METHOD

A. *Material*

The blood consists of three different components, these are white, red blood cells, and thrombocytes. White blood cells consist of five different types of cells. The cells are exist in the rate of Basophil 0-1%, Monocyte 2-10%, Eosinophil 1-5%, Lymphocyte 20-45%, and Neutrophil 50-70% [21]. Neutrophils are the most abundant type of white blood cell in the body. This cell type protects against infections from toxic substances, deals with viruses, bacteria, fungi, and even cancer cells. Lymphocyte deals with infection and prevent infections. Eosinophil deals with and prevents parasitic and bacterial infections. Eosinophils are white blood cells that control inflammation that causes asthma and allergies. Monocyte removes microorganisms, unknown agents and dead cells. Basophil is a kind of WBC that assists prevent and treat wound infections. It contains suitable substances that help relieve allergies and control blood clotting [22].

Blood cell images in this study are obtained from the BCCD dataset of the popular Kaggle database [7]. This data set consists of images referring to four different classes as Eosinophil, Lymphocyte, Monocyte, and Neutrophil. Fig. 1 shows samples of four cells types in the dataset. Size of all images in the dataset is same and in the dimension of 240x320x3. A total of 12.507 augmented images of blood cells in JPG format are available as 3133 Eosinophil, 3108 Lymphocyte, 3095 Monocyte, and 3171 Neutrophil images. Fig. 2 shows categorical distribution of the blood cells data used in this study as 70% training, 10% validation, and 20% testing.

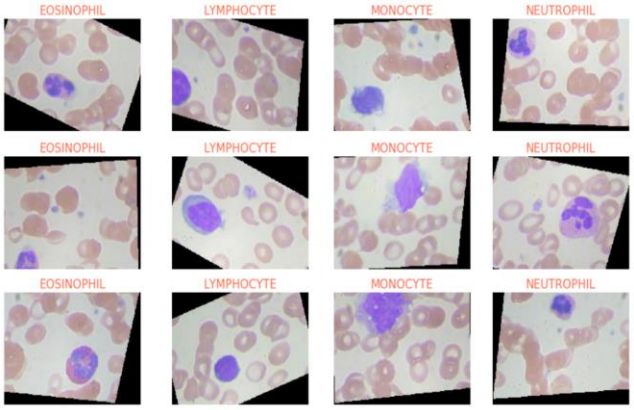

Figure. 1. The sample cell types in dataset (4 different cell types are Eosinophil, Lymphocyte, Monocyte, and Neutrophil).

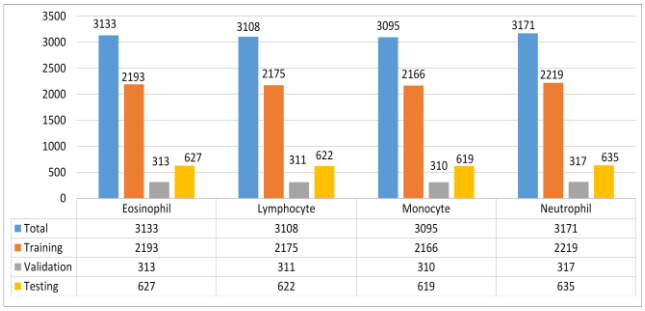

Figure. 2. Categorical distribution of the blood cells in the dataset.

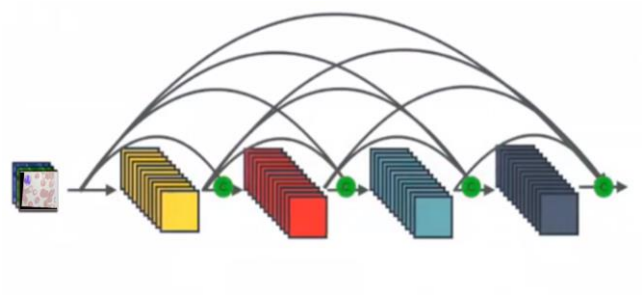

Figure. 3. Fundamental architecture of one dense block in DenseNet [23].

B. *Method*

Deep learning has emerged as an exciting trend in machine learning in recent years. Deep learning is an extension of classical machine learning. This extension is defined as the use of functions that add more depth to the model and allow data to be represented in several hierarchical ways. The high hierarchical structure and wide learning capacity of deep learning models allow classification and predictions to be made with consistency. Deep neural networks are the multi-layered and multi-neuron version of Neural Network. The most important feature is automatic feature extraction in accordance with the problem and these features are obtained by the learning of the network. CNN architecture stands out with its popularity among various algorithms of deep learning. Inspired by the visual cortex of the brain, CNN is mainly used to classify images, signals, cluster similarities and perform object recognition [24], [25]. This architecture consists of convolution layers, pooling layers, nonlinear layers, and fully connected layers by processing the image with various layers. The convolution layer is the layer that the most intensive mathematical processing takes place, and some filters are applied to the image to detect low and high level features in the image. In the nonlinear layer, which is also called the activation layer, nonlinearity is introduced to the system and the ReLu function is used because it usually gives the best results.

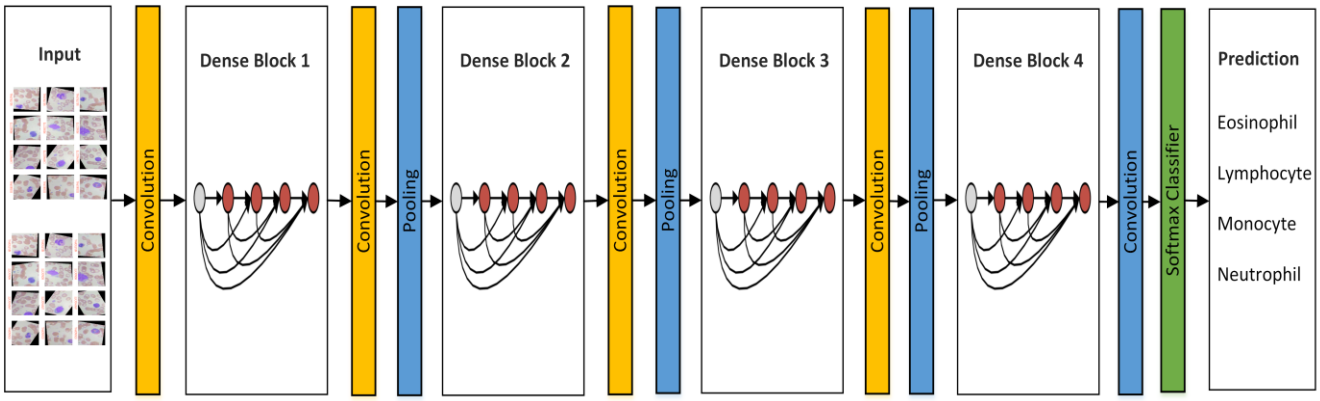

Figure. 4. The workflow of DenseNet121 architecture used in this study to classify blood cells from blood cell images.

The pooling layer reduces the number of weights on the system by reducing the size of the feature maps in order to reduce the parameters in the network. Fully connected layers act as a classifier in the model by establishing a connection between the input and output layers [26].

Input image goes along multiple convolutions and acquire high-level features with standard CNN (ConvNet). In Dense Convolutional Network (DenseNet), each layer acquires additional inputs from all previous layers and transfers on its own feature-maps to all next layers as shown in Fig. 3 [23]. DenseNet is a dense-connected convolutional network that forward connects each layer to the other layers. DenseNet gives superior performance for various computer vision problems. DenseNet reduces the gradient descent problem, increases feature reuse, and reduces parameter usage. The advantage of DenseNet architectures is to allow feature propagation and feature reuse. Thus it minimizes the number of parameters. The main structure block of DenseNet121 is the Dense Block. These Dense Blocks consist of convolution layers. DenseNet121 consists of 121 connected convolutional layers with a fully-connected layer of 1000 units as the final output layer [27]. CNN architectures are generally hierarchical, so feature maps of l-1 layer is given as an input to the l.layer. Feed-forward networks just like convolutional networks connect the output of the l.layer as input to the (l+1).layer, that gives source to the sequent layer transition: $X_l = H_l(X_l - 1)$ which l indexes the layer. H_l is a composite function and that contains some of operations as batch normalization, ReLU, pooling, or Convolution. On the other hand in DenseNet, the feature maps of all previous layers are combined and used as input for any specific layer. In other words, DenseNet is a connectivity model that further improves the flow of information between layers. Direct connections from any layer to all following layers are performed. In addition, its own feature maps are used as input for all subsequent layers. Therefore, the feature maps of all previous $X_0, X_1, ..., X_{l-1}$ layers are combined and used as input for layer X_l. As a result, the l.layer receives the feature-maps of all preceding layers, $X_0, X_1, ..., X_{l-1}$, as input eq. (1) where $[X_0, X_1, ..., X_{l-1}]$ indicates the integration of the feature-maps produced in layers 0 ,....., $l-1$. For ease of fulfillment, the multiple inputs of $H_l(\cdot)$ in eq. (1) are concatenated into a single tensor [27], [28].

$$X_l = H_l([X_0, X_1, ..., X_{l-1}]) \quad (1)$$

As shown in Fig. 4, DenseNet121 has four Dense blocks and a transition layer between each Dense blocks. Any Dense block contains some convolution layers, and any transition layer contains a batch normalization, a pooling and convolution layer. Activation function (ReLU) is used in DenseNet to increase nonlinearity. In this model, global average pooling layer which is the last layer of DenseNet121, generates features from the input image. Then, obtained features are operated by the classifier to perform the final prediction. Thus, a fully-connected layer is followed by a softmax classifier that uses softmax activation function. A fully connected three-unit layer is used for classification (four classes for blood cells). The output of the fully connected layer is normalized and probability distribution over the predicted output classes is created by softmax activation. This particular model improves the pass of information over the network and decreases the vanishing gradient problem. In addition, DenseNet improves feature reuse and parameter efficiency and provides combined information of the network to each layer [29]. The most significant reason for choosing is

that dense connectivity has a regularized effect and reducing overfitting at training.

IV. EXPERIMENTAL RESULTS

The experimental studies in this study are conducted on a desktop computer with Intel Core (i7) 8700U CPU @ 3.20 GHz, NVIDIA 4 GB GeForce-GTX 1050 Ti graphics and 16GB primary memory. The software was implemented using Python 3.7 and its related libraries. The data in the experimental study: 70% is reserved for training, 10% for validation, and 20% for testing. The input image resolution of the model is (240x320x3). DenseNet121 model is built with batch size (mini-batch) 128 and with 100 epochs at training. The total number of parameters is 7,628,484 for this model. At this stage, the performance evaluation of the method is performed over four performance criteria as Precision, Recall, F1-Score, and Accuracy. These values are calculated over confusion matrix (as shown in Fig. 5) for each class (Eosinophil, Lymphocyte, Monocyte, and Neutrophil). Performance parameters of the experiment are given in Table I. The calculated scores about Precision, Recall, F1-Score for each class and average results are given in this table. According to this experimental study, the accuracy value obtained with the proposed DenseNet121 technique is 94%.

Table I.
Performance parameters of the DenseNet121 model

Accuracy: **94.00%**	Precision	Recall	F1-Score
Eosinophil	0.9535	0.8501	0.8988
Lymphocyte	0.9851	0.9598	0.9723
Monocyte	0.9919	0.9855	0.9887
Neutrophil	0.8382	0.9543	0.8925
Average:	0.9422	0.9374	0.9381

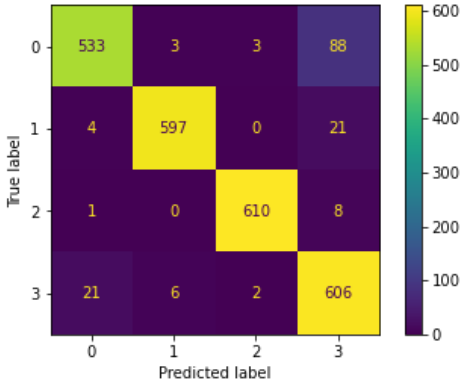

Figure. 5. Confusion matrix of DenseNet121 model.

As shown in Table II, transfer learning and CNN-based different popular techniques as Xception, VGG19, and EfficientNetB1 have been compared with the proposed DenseNet121 technique. It was observed that the DenseNet121 model in this study gives superior results than other models.

Table II.
Comparison of other deep learning techniques with DenseNet121 model

Model	Precision	Recall	F1-Score	Accuracy (%)
Xception	0.7897	0.7869	0.7844	78.59
VGG19	0.8490	0.8478	0.8466	84.70
EfficientNetB1	0.8892	0.8680	0.8668	86.72
DenseNet121	0.9422	0.9374	0.9381	94.00

In Fig. 6, training/test accuracy and training/test loss graphs for 100 iterations of the DenseNet121 model are presented. Both training and test accuracy curves show a rising curve as the number of iterations increases. Moreover, decrease in error rate is shown from loss curve. It shows that training and learning process of the network are at a good learning rate. As shown in Fig. 6, while the loss value decreases in each iteration, the accuracy rate increases with the given training set and learning occurs.

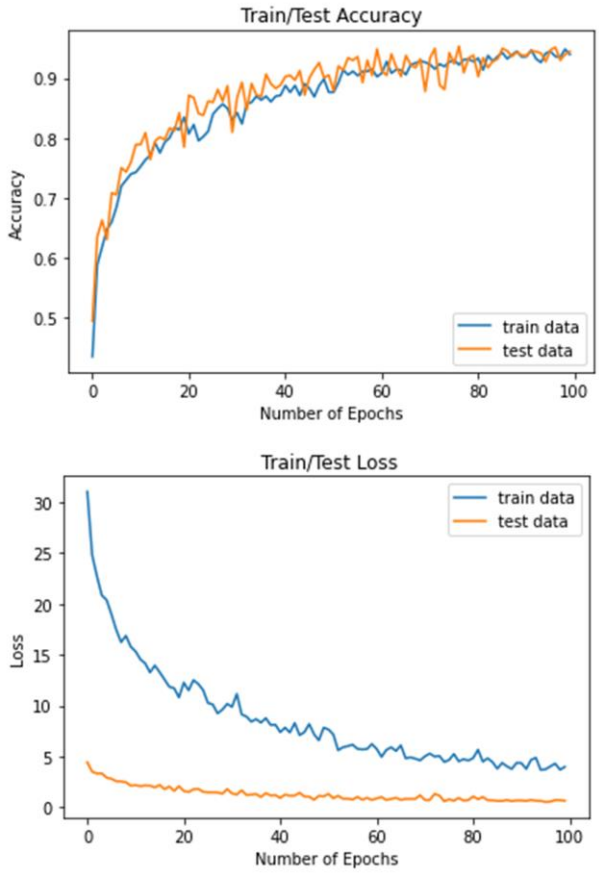

Figure. 6. Training/test accuracy and training/test loss graphs of the DenseNet121 model.

Table III.
Performance comparison of this study with other studies using same BCCD dataset

Study	Year	Method	Accuracy (%)
Liang et al. [8]	2018	CNN + RNN	90.79
Bani-Hani et al. [9]	2018	CNN + Genetic Algorithm	91.00
Şengür et al. [10]	2019	LSTM	92.89
Banik et al. [11]	2019	Fused CNN	90.79
Patil et al. [12]	2020	CNN + RNN	95.48
Mohamed et al. [13]	2020	DenseNet-169	92.00
Dekhil [14]	2020	CNN with extracted ROI	92.50
Ghosh & Kundu [15]	2021	CNN + RNN	87.29
Ekiz et al. [16]	2021	Con-SVM	85.96
This study	2021	DenseNet121	**94.00**

Performance comparison of the current study with other studies using same BCCD dataset is given as shown in Table 3. In this table, the state-of art studies using same BCCD dataset are discussed. At this stage, we studied the experimental results which divide randomly whole data as training and testing in literature (like this study 70% training, 10% validation, and 20% testing). DenseNet121 model in this study gives the reasonable accuracy score of 94% for BCCD dataset when compared to other techniques. For instance, a similar study by Mohamed et al. [13] about DenseNet-169 was conducted on the BCCD dataset (for approximately 80% training and 20% testing). They achieved the best feature extractor pre-trained model by DenseNet-169 with accuracy rate of 92.00%.

V. CONCLUSION

White blood cells are one of the immune systems that play a role in protecting the body from infectious diseases and foreign invaders. There are different categories of white blood cells, and each category may indicate a disorder of the body. Currently, WBC diagnosis is usually studied manually by a doctor. This process is prone to a lot of time, costs and errors compared to automatic computerization. Therefore, an automated classification technique for WBC images is proposed in this study. In this paper, a dense convolutional neural network model is studied. Parameters and layers of this architecture are specially adjusted to get high performance from this model.

Experimental studies are conducted on an open-access BCCD dataset. In this dataset, there are a total of 12507 images belonging to four classes: Eosinophil, Lymphocyte, Monocyte, and Neutrophil. For this purpose, a DenseNet121 model is applied, which is able to classify blood cell images. The data in the experimental study: 70% is reserved for training, 10% for validation, and 20% for testing. Performance evaluations are performed on the accuracy of the techniques, and the results are also compared with state-of-the-art (popular) deep learning-based approaches like Xception, VGG19, EfficientNetB1. In experimental studies, the highest accuracy (94%) is obtained with the proposed DenseNet121 model.

According to experimental results, both training and test accuracy curves show a rising curve as the number of iterations increases. Thus, decrease in error rate is shown from loss curve. It shows that training and learning process of the network are at a good learning rate. Considering the high accuracy value obtained with this model, automatic detection of which class the cells belong to will speed up the diagnosis and allow more data to be examined by doctors. In further studies, other deep learning-based techniques and new dataset include abnormal white blood cells (recognizing other kinds of cell types) will be studied and comparisons will be made to complete the diagnostic system. We can also work on making the system more stable, reducing noise and improving overall performance with pre-processing and post-processing stages.

CONFLICTS OF INTEREST

There is no conflict of interest.

RESEARCH AND PUBLICATION ETHICS

The author declare that this article does not require ethics committee approval or any special permission.

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