Blood Cell Identification Employing Images Combining CNN and ResNet

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Abstract—Clinical pathology tests, such as the Complete Blood Count (CBC), are essential for accurately counting blood cells and are used to diagnose a variety of diseases [19]. These tests have shown to be useful in diagnosing major illnesses including cancer, leukemia, and bone marrow failure as well as ailments like infections, inflammations, and malaria [1], [1], [19]. The classification of different blood cells such as basophil, eosinophil, erythroblast, ig, lymphocyte, monocyte, neutrophil, and platelets are the main topic of this study. The study uses a variety of deep learning models, such as Basic CNN, AlexNet architecture, CNN with data augmentation, complicated CNN with data augmentation, ResNet 50, and Transfer learning using ResNet 50, to obtain appropriate categorization. In addition for classification of blood cells SoftMax is used . The study explores the analysis of white blood cells (WBCs), with a particular emphasis on the differentiation of basophil, neutrophils, eosinophils, lymphocytes, and monocytes [8]. It also covers the measurement of platelet characteristics [10], [11] and the morphological categorization of red blood cells (RBCs) [3]. The potential of automated analysis of blood cell pictures is demonstrated by the application of these various methodologies. The objective is to enable quicker clinical diagnosis procedures by offering pathologists and hematologists invaluable support in classfication of blood cells [14]. The efficiency and accuracy of clinical pathology could be improved with this automated method, which would eventually improve patient outcomes and treatment.

Index Terms—Blood Cells, CNN, ResNet 50, AlexNet, data augmentation, Transfer Learning, basophil, eosinophil, erythroblast, ig, lymphocyte, monocyte, neutrophil, platelets, SoftMax.

I. Introduction

The development of algorithms for the automated analysis of medical pictures through advanced techniques in computer graphics, image processing, and artificial intelligence has seen a spectacular surge in attention in recent years [6]. This explosion has led to the development of a number of automated medical diagnosis systems that help doctors diagnose diseases by giving them useful data that greatly improves the accuracy and efficacy of medical evaluations [6].CBC determines hemoglobin(HB) measurements, mean red blood cell volumes [?] as well as three important parts of Blood Cells that are White Blood Cells(WBCs), Red Blood Cells(RBCs) and Platelets are also determined [4]. The characteristic shape of red blood cells (RBCs) is that of a flat disc or ball [7]. This form is spherical and has a central depression, but it is not hollow. Unlike white blood cells (WBCs), red blood cells (RBCs) are characterised by the absence of a nucleus, which allows them to change shape more easily and circulate more easily throughout the human body [7]. An RBC has a lifetime of about 120 days [7].In the context of normal blood, red blood cells (RBCs), also known as erythrocytes, play a crucial role, with their count ranging from 4.2 to 5.9 million cells per square centimeter [11]. Their vital functions include the transportation of oxygen throughout the body and the removal of waste products and carbon dioxide from tissues [4]. However, due to these essential roles, RBCs become susceptible to infection by parasites such as Babesia and Malaria, which actively penetrate and infect these cells [11]. This weakness draws attention to the possible health hazards connected to infections that target red blood cells.On other hand, white blood cells (WBCs) are categorised using light microscopy and standard staining procedures, which help distinguish distinct cell types according to whether or not they have granules in their cytoplasm. However, because of their similarities, differentiating between different types of leukocytes in blood smears can be difficult. WBCs are essential for fighting infectious agents such as bacteria, viruses, foreign invaders, and malignant or diseased cells. They make up around 1(perct) of the blood volume in a healthy body [17]. Leukocytes are a subset of white blood cells (WBCs) that have one nucleus or several segmented nuclei [7]. Notwithstanding the challenges associated with classification, the central function of WBCs in the immune response emphasises the significance of examining their morphological characteristics for diagnostic and therapeutic objectives. In a similar vein, platelets, small blood cell fragments crucial for blood clotting, typically present in counts ranging from 150,000 to 450,000 per microliter, play a vital role in maintaining hemostasis [11]. Close monitoring of platelet counts is necessary in certain diseases, such as dengue infection, and platelet transfusion may be required if levels drop dangerously low. Blood smear

abnormalities typically indicate the existence of an infection or illness [11].Blood cells that show differences that correspond to particular health situations include neutrophils, erythroblasts, platelets, basophils, eosinophils, lymphocytes, monocytes, and immunoglobulins (ig). An important part of mounting a non-specific immune response is played by basophils [[?]]. Their unique appearance is typified by a two-lobed nucleus that is difficult to view

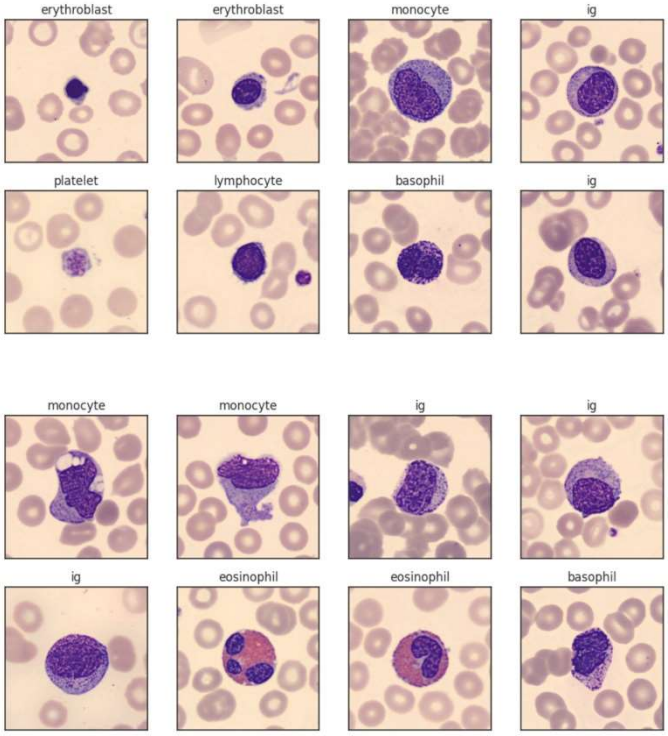


Fig. 1. Blood Cell Images

and a pale pink-tan cytoplasm that is packed with purple/blueblack granules. These granules help to distinguish basophils as distinct entities within the immune system, with certain physical characteristics that facilitate recognition and categorization [16]. Making up 3(percent) of white blood cells (WBCs), eosinophils are essential for responding to parasite infections as well as battling bacterial infections. Eosinophils are distinguished morphologically by a pale pink-tan cytoplasm that contains big orange and red granules and a two-segmented blue nucleus. These distinguishing characteristics help identify eosinophils and highlight their unique roles in the immune system, especially in the fight against parasitic and bacterial infections [16]. Thirty percent of white blood cells (WBCs) are lymphocytes, which are categorised into two types: B and T lymphocytes. T cells actively participate in the destruction of foreign invaders, whilst B cells are in charge of producing antibodies. Lymphocytes can be distinguished morphologically by their big, spherical or oval shape [1]. They have a pale blue cytoplasm with occasionally purple-reddish granules, and a dark-staining nucleus. The distinct cellular architecture of lymphocytes in the immune system is a reflection of their specialised responsibilities, which include both direct defence against foreign threats and the creation of antibodies [16]. Six percent of white blood cells (WBCs) are monocytes, and they are essential to the immune system because they remove dead cells [1]. Monocytes are distinguished morphologically by a single, kidney-shaped nucleus that stain blue-gray and is accompanied by little granules. Their unique cellular makeup is in harmony with their essential role of preserving tissue integrity by eliminating old or damaged cells [16]. White blood cells (WBCs) that include 60(percent) neutrophils are known to be the first to react to invasive pathogens like bacteria or viruses [1]. Neutrophils have a characteristic multilobed nucleus that stains dark purple, and their cytoplasm has granules and looks pale pink-tan. Neutrophils' ability to quickly identify and eliminate foreign invaders is facilitated by their cellular arrangement, which aids in the innate immune response against microbial threats [16]. Also, Immunoglobulins (ig) are responsible for protecting the body against viruses, fungi, bacteria which is made from blood having antibodies. Also, the paper follows following pattern where Section- II contains Related Works, Section-III has Dataset and Methods which the paper follows, which follows by References.

II. Related Works

Hematology's peripheral blood smear microscopic analysis is acknowledged for its time-consuming and expensive nature. However, researchers have shown a keen interest in developing algorithms for the automatic examination of medical images, particularly microscopic blood smears, utilizing image processing, computer vision, artificial neural networks, and machine learning algorithms [1]. The study further delves into the use of digital image processing [15] for automated blood cell counting, positioning it as a cost-effective alternative to the labor-intensive and costly manual techniques employed in peripheral blood smear microscopy analysis [1]. Unlike conventional counting methods, the methodology prioritizes pre-processing and enhancing blood cell images to enhance accuracy and efficiency [15]. The positive results validate the potential practical application of this approach in medical settings [15]. The study also emphasises how important it is to standardise blood smear preparation in order to produce high-quality pictures [15]. Blood cell analysis approaches, such as image processing, computer vision, artificial neural networks, and machine

learning algorithms, are being actively developed by researchers in the field [1]. Convolutional neural networks (CNNs) are now widely used for automated image processing; state-of-the-art performance has been achieved by architectures including LeNet, VGG-16, and AlexNet [1]. Furthermore, quantitative phase imaging (QPI) facilitates the examination of blood constituents by ascertaining the morphology of red blood cells under varying illumination conditions or in scenarios that overlap [20]. Numerous segmentation methods, such scale-space filtering and the Snakeballoon model, are intended for cell analysis, while support vector machines provide precise and adaptable classification for cell type identification [21], [22]. Strong feature selection and rigorous independent validation for reliable automated lymphoid cell analysis are presented, highlighting the recent focus on end-to-end pipelines for identifying particular cell categories [13].

III. Dataset and Method

A. Description of Dataset

The collection includes 17,092 pictures of single normal cells that were taken in the Hospital Clinic of Barcelona's Core Laboratory using the CellaVision DM96 analyzer. Neutrophils, eosinophils, basophils, lymphocytes, monocytes, immature granulocytes (promyelocytes, myelocytes, and metamyelocytes), erythroblasts, and platelets or thrombocytes are the eight different groups into which these pictures are divided. Clinical pathologists with extensive experience annotated the 360 × 363 pixel JPG pictures. However, the dataset only includes photos of people who were free of hematologic or oncologic conditions, infections, or pharmacologic treatments at the time of blood collection, guaranteeing a healthy and representative cell sample for study.

B. Feature Extraction and Classification Of CNN Model

In the feature extraction process, six distinct models were employed, each serving a unique purpose in classifying blood cell types. These models, designated as Model-1 through Model-6, which include a variety of structures and approaches.

Model-4 and Model-6 exhibit the highest accuracies, with

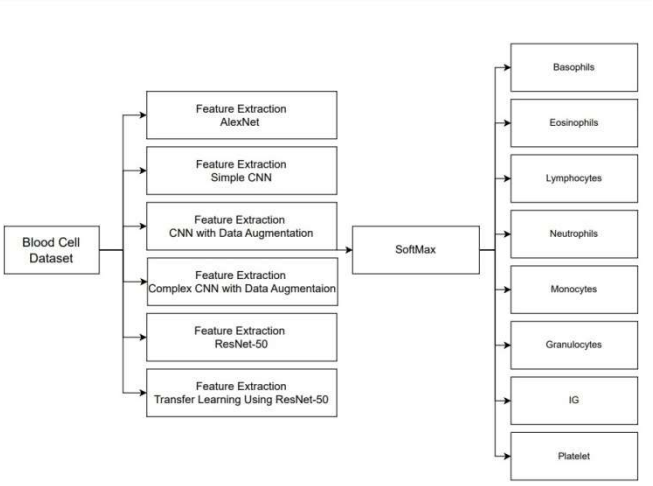
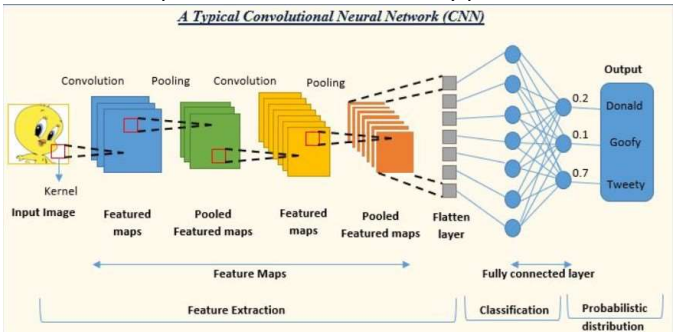


Fig. 2. Working Process

Model-4 achieving 0.96 accuracy and Model-6 reaching 0.99 accuracy. It's important to remember, though, that Model-6's very high accuracy could be a sign of overfitting—a situation in which the model has grown unduly adapted to the training set, which could cause problems when trying to apply the model to fresh data. For Model-4, a Convolutional Neural Network (CNN) is utilised, capitalising on a meticulously crafted architecture to proficiently categorise mistakes within photographs. The following is a description code and architecture: CNNs process the input data through a network of interconnected layers. Convolutional layers are often the first hidden layer in a CNN. They work by applying a series of filters to the input data in order to identify particular



patterns. By swiping over the input data and multiplying each filter entry element-by-element, a feature map is produced for each filter. The model is then given non-linearities to learn more intricate patterns in the data by combining these feature maps and passing them via non-linear activation functions like the ReLU function. Additional convolutional layers, pooling layers, and fully-connected layers are examples of subsequent layers in a CNN. Feature maps are

smaller when pooling layers are used. This improves the model's computational efficiency by lowering the total number of parameters. In most CNNs, fully-connected layers may be found following the convolutional and pooling layers. The model may learn potential non-linear combinations of the features learnt by the convolutional layers thanks to fully-connected layers, which link all of the neurons in one layer to all of the neurons in the layer above. A CNN's softmax layer, which generates a probability distribution over all potential class labels for the input data, is usually its last layer. The class with the highest probability is selected as the model's forecast. A convolutional neural network is developed for image classification using the Keras Sequential API.The TensorFlow random seed is set to 42 for reproducibility. The model architecture consists of the following key components:

- Input Layer:- The input layer of the model is first defined to hold photos with dimensions (IMGHEIGHT, IMGWIDTH, 3), where 3 is the number of RGB colour channels.
- Rescaling Layer:- To normalise pixel values and scale them to the range [0, 1], a rescaling layer is created. The training process is accelerated and stabilised with the help of this normalisation.
- Data Augmentation:- By producing a variety of training instances, data augmentation techniques are integrated to improve the generalisation of the model. This aids in the model's learning to withstand a variety of real-world situations.
- Convolutional Layer:- Conv2D adds three layers in order to extract features. He typical kernel initialization, ReLUactivation,'same' padding, and various filter sizes (8, 16, and 32) are applied to each layer's convolution process. Max pooling layers are used to down-sample spatial dimensions after every convolution.
- Flatten Layer:- To prepare the data for the following dense layers, the Flatten layer is used to transform the 2D feature maps into a 1D vector.
- Dense Layer(Classifier):- A Dense layer with eight neurons and a softmax activation function, appropriate for multi-class classification, rounds out the model. Probability distributions for each of the specified classes are generated by this layer. A brief synopsis of the model's architecture, including the number of parameters in each layer, is given in the model summary. After the model is constructed, it is assembled with sparse categorical crossentropy as the loss function and the Adam optimizer. After that, the model is trained for 20 epochs using the given training dataset, and its performance is tracked using the validation dataset. The callback that is supplied is used to implement early stopping, which guarantees that the training process ends when validation accuracy does not improve.

C. Feature Extraction and Classification of Transfer Learning Using Resnet-50

The theory behind transfer learning is that models are able to extract generic features from massive datasets and use this information to do new, related tasks with a little amount of labelled data. Transfer learning lets us use pre-trained models as a starting point, saving us the trouble of building a deep neural network from scratch.A deep convolutional neural network architecture called ResNet-50 (Residual Network with 50 layers) is well-known for its efficiency in image categorization applications. It is made up of residual blocks with skip links in them, which help the network learn and spread information more efficiently. Large datasets like ImageNet, which have millions of photos spanning hundreds of classifications, have been used to pre-train ResNet-50. Transfer Learning Process using Resnet-50 the process is as follows:-

- Loading Pre-trained Model:- First, the pre-trained ResNet-50 model needs to be loaded. During its training on ImageNet, this model has acquired hierarchical and abstract features from a variety of images.
- Removing Top Layers:- The top layers that handled the particular classification task (such as ImageNet classification) during the initial training are eliminated. The bottom layers that have picked up general traits are left behind.
- Freezing Layers:- In the early phases of transfer learning, the layers of the pre-trained model are frozen in order to preserve the knowledge it has learnt. By freezing, these layers' weights are kept from changing while they are being trained for the new task.
- Adding Custom Head:- On top of the previously trained model, a new set of layers is added. Global pooling layers, fully linked layers, and an output layer appropriate for the current task are usually included in this custom head.
- Fine-Tuning (Optional):- Some or all of the frozen layers may get unfrozen in subsequent stages of transfer learning, enabling the model to adjust its parameters for the

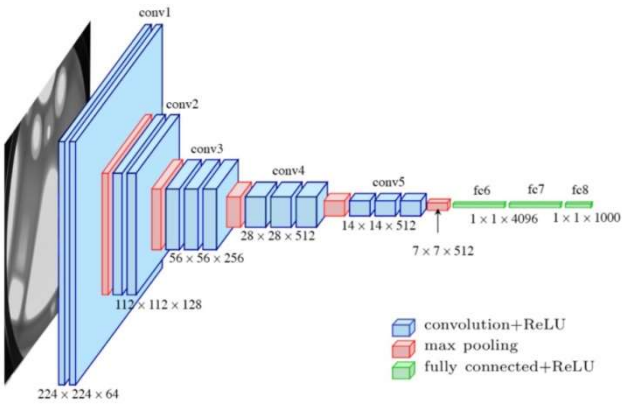


Fig. 3. Transfer Learning Using Resnet-50

new job. When the new task differs significantly from the previous task, this phase is really helpful.

The working of the code for Model-6 is as follows:-

- Unfreezing Layers:- The feature extraction layer of the pre-trained ResNet-50 model is unfrozen by the first line of code. Unfreezing in transfer learning enables the model to modify its parameters while being trained on a particular dataset.
- Architecture Model:-The architecture for Model6 is constructed in the next block of code. Using Keras, it is built as a sequential model. The model starts with data augmentation, which applies random alterations to the training set of data to improve the model's generalisation. The ResNet-50 layers that were previously frozen are then added, acting as a feature extractor. The spatial dimensions are decreased by global average pooling, and a dense layer with softmax activation is added for the final eight-class classification.
- Compilation:- Model6's training procedure is configured using the compile function. Sparse Categorical Crossentropy, an appropriate loss function for multi-class classification applications, is specified. 0.0001 learning rate is used with the Adam optimizer to regulate the weight updates during training. Accuracy is the selected evaluation metric, which gauges the model's effectiveness using the validation data.
- Model Training:- Model6 is trained using the fit method, which is started by the last block of code. The model is validated on valdatasetresnet after being trained for 20 epochs on the supplied traindatasetresnet dataset. History6 contains the training history, together with metrics and losses. For early halting, which stops training if the model's performance on the validation set stops, the earlycb callback is utilised to improve. Finally, this code illustrates how transfer learning with ResNet-50 is continued, with previously frozen layers being unfrozen to accommodate the particular classification problem. After then, the model is assembled and trained, allowing the target dataset to be used to fine-tune the ResNet-50 architecture for increased accuracy and generalisation.

D. Results

The Test results on respective test sets are as follows :-

Model-1 :0.20
Model-2 :0.20
Model-3 :0.20
Model-4 :0.96
Model-5 :0.21
Model-6 :0.99

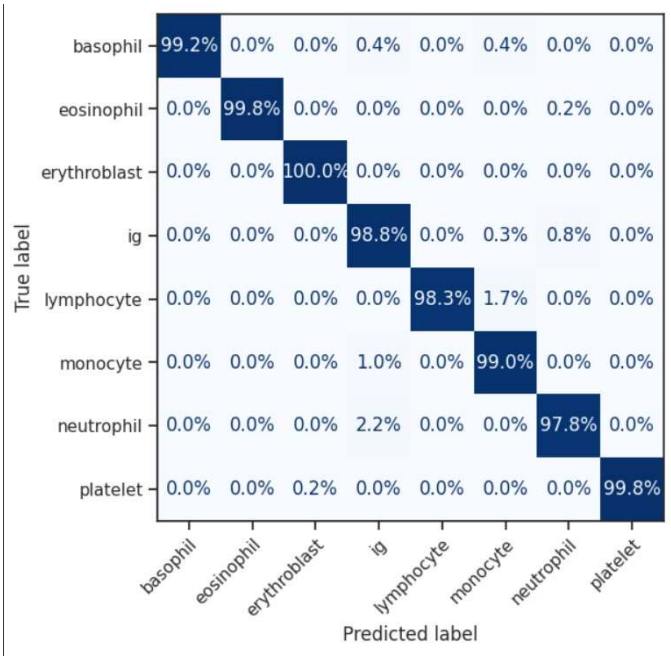


Fig. 4. Confusion-Matrix of Model-6

Among all the test sets, Model-4 and Model-6 emerged as the best-performing models. However, the 0.99 accuracy achieved by Model-6 suggests a potential risk of overfitting. In order to investigate the reasons behind this overfitting, a set of 40 misclassified images was plotted and analyzed.

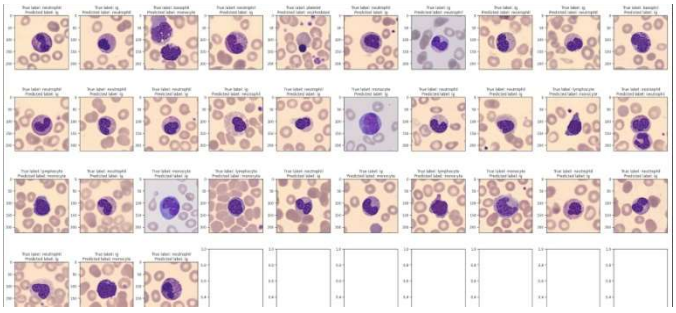


Fig. 5. Wrongly Predicted Images

The Confusion Matrix drawn for Model-6 there are two visualisations produced: one with normalised data and another with a colour variation to highlight inaccurate predictions.Theoffdiagonal elements draw attention to incorrect classifications, whereas diagonal elements show the proportion of accurate predictions for each class. The first visualisation gives each class a relative accuracy measure based on normalised values. In the following figure the confusion matrix drawn which gives darker hues in the visualisation denote higher error rates and highlight sections of the matrix where the model has trouble.

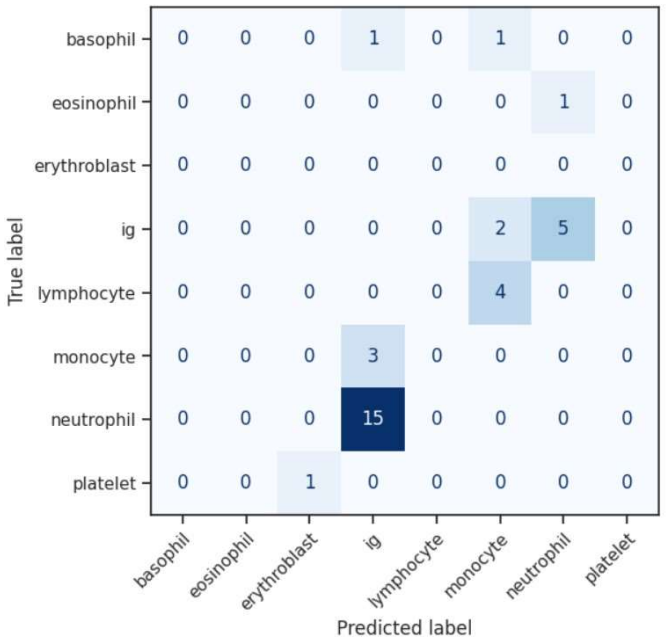


Fig. 6. Confusion matrix with zero weight in the correct predictions

Three criteria have been employed by most researchers to assess performance: specificity, sensitivity, and accuracy. The percentage of right predictions is called accuracy, the percentage of true negatives (TN) that the system correctly identified is called specificity, and the rate of true positives (TP) that the model classified is called sensitivity. Equations are used to compute these parameters [8].

$$\text{Precision} = \frac{TP}{TP + FP} \quad (1)$$

In Equation 1, TP represents True Positive and FP represents False Positive [16]

$$\text{Sensitivity} = \frac{TP}{TP + FN} \quad (2)$$

The sensitivity is given by above Equation 2, TP represents True Positive and FN represents False Negative. [16] The F1 Score is given by Equation 3 [16]:

$$\text{F1 Score} = \frac{2 \times \text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \quad (3)$$

The Accuracy is given by Equation 4 [16]:

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \quad (4)$$

The conclusion drawn from Classification Report for Model-6 is as follows:-

TABLE I
CLASSIFICATION REPORT OF MODEL-6

Class	Precision	Recall	F1-score	Support
Basophil	1.00	0.99	1.00	237
Eosinophil	1.00	1.00	1.00	596
Erythroblast	1.00	1.00	1.00	294
IG	0.97	0.99	0.98	602
Lymphocyte	1.00	0.98	0.99	241
Monocyte	0.98	0.99	0.98	307
Neutrophil	0.99	0.98	0.98	679
Platelet	1.00	1.00	1.00	462
Accuracy	0.99	0.99	0.99	3418
Macro avg	0.99	0.99	0.99	3418
Weighted avg	0.99	0.99	0.99	3418

Conclusion

Blood cell Identification has been done with the use of Convolutional Neural Network and Residual Network. These methods are so popular and effective in Healthcare industry for various disease identification and prediction. The data set is collected and applied feature extraction methods by using various methods. The SoftMax activation function is used for prediction of blood cells. The execution results are compared with all effective existing methods and highlighted the efficiency of Model-6 for blood cell identification. The accuracy of this model-6 is 99% and the execution time for this model is comparatively low. In future, the research focus will be on platelets identification with this effective model to provide novel solution.

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