Classification of White Blood Cell Using Machine Learning & Image Processing Model

Prof. Yogesh R Risodkar
dept. Electronics and Telecommunication.
Sandip Institute of Engineering and Management
Nashik, India
yogesh.risodkar@siem.org.in

Dr. Mosam K Sangolei
dept. Electronics and Telecommunication.
Sandip Institute of Engineering and Management
Nashik, India
mosam.sangole@siem.org.in

Prof. Amit Mishra
dept. Electronics and Telecommunication.
Sandip Institute of Engineering and Management
Nashik, India
amit.mishra@siem.org.in

Nikita Arun Thorat
dept. Electronics and Telecommunication.
Sandip Institute of Engineering and Management
Nashik, India
thoratnthorat@gmail.com

Kaushal Sachin Lahamge
dept. Electronics and Telecommunication.
Sandip Institute of Engineering and Management
Nashik, India
kaushalslahamge26@gmail.com

Vishal Raghunath Chaudhari
dept. Electronics and Telecommunication.
Sandip Institute of Engineering And Management
Nashik, India
vishalchaudhri4530@gmail.com

Abstract: The use of machine learning (ML) and image processing models has improved prediction and classification accuracy, which has been beneficial to medical imagery investigations. The immune system needs white blood cells (WBCs) to combat infections caused by bacteria, fungus, and viruses. There are five subtypes of white blood cells: monocytes, lymphocytes, eosinophils, basophils, and neutrophils. White blood cell types must be identified and measured in order to diagnose and treat a wide range of illnesses, including leukemia, autoimmune diseases, infections, and immunological deficiencies. A rapid and accurate technique is required to classify WBCs. This paper offers a comprehensive review of the state-of-the-art techniques for classifying white blood cells in medical image processing.

There are numerous commercially accessible technologies for counting blood components, but the expensive clinical equipment these technologies require is out of reach for the majority of developing nations. This paper proposes a low-cost classification technique to calculate differentiated white blood cell counts using digital image processing and machine learning. White blood cells (WBCs) are part of the human immune system; they protect the body against foreign substances and halt infections. They are composed of neutrophils, eosinophils, basophils, monocytes, and lymphocytes, each of which constitutes a unique component and performs a unique role. A complete blood count (CBC), which aids in patient tracking, has historically required the clinical laboratory technique for counting different types of white blood cells. To address these issues, this work proposes an automated method for identifying white blood cells using machine learning and image processing methods. The proposed method first preprocesses microscopic pictures of blood samples in order to minimize noise and enhance contrast. Then, from the preprocessed images, the form, texture, and intensity parameters of each unique WBC are retrieved together with other relevant features. These characteristics are used as input by the machine learning model, which is trained using a dataset of tagged images of white blood cells.

I. Keywords: Autoimmune diseases, image analyses, classification, feature extraction, machine learning (ML), subtypes of white blood cells, convolutional neural networks (CNN), and classification.

II. INTRODUCTION

White blood cells are a vital component of the immune system in humans. An essential component of the human immune system are white blood cells. Granulocytes and agranulocytes are two subtypes of WBCs. Monocytes (2–10%) and lymphocytes (20–45%) make up agranulocytes, while basophils (0–1%), eosinophils (1–5%), and neutrophils (50–70%) make up granulocytes. Figure 1 shows several occurrences of WBC images. There are three methods available for classifying white blood cells: manual inspection, automatic classification using a haematology analyzer, and machine learning. The manual examination approach is regarded as the most effective. Differentiation of WBC [9, 10]. This strategy, however, is ineffectual and depends on the understanding and proficiency of hematopathologists. A deficiency or excess of white blood cells (WBCs) can cause a number of illnesses [7, 8]. Correctly classifying the many types of white blood cells is essential. Leukocytes, or white blood cells, are the cells that make up blood components. The immune system's ability to protect the body against infectious diseases depends on these cells. White blood cells are colorless, have a nucleus, can diapede—pass through capillary walls—and can carry amoebas. A normal adult human blood drop has less than one liter and between 4x109 and 11x109 cells, or approximately 7000–25,000 cells per drop. Classifying white blood cells is essential for the early diagnosis and management of several illnesses. WBC classification is useful in the diagnosis and treatment of a broad variety of medical conditions. Leukocytes, or white blood cells, are produced by the lymphoid organs and bone marrow of the immune system. The body uses these cells to fight against infections from bacteria, viruses, and fungi. In this work, we combine image processing and machine learning models to provide a novel approach for categorizing white blood cells. Our process entails several crucial steps:

Image Acquisition: Digital images of blood smears are obtained by means of defined protocols and microscopy apparatus.

Preprocessing: Various processing techniques, such as noise reduction, contrast enhancement, and segmentation, are used to captured pictures to improve the quality and clarity of cell borders.

Feature extraction: To describe the form, size, and internal structure of each individual white blood cell, pertinent properties are extracted. These properties include morphological, textural, and statistical aspects.

Classification using Machine Learning: Using the traits that were collected, white blood cells are divided into neutrophils, lymphocytes, monocytes, eosinophils, and basophils. Support vector machines (SVM), convolutional neural networks (CNN), and random forest classifiers are used in the training of these techniques.

Evaluation of the Models: Receiver operating characteristic (ROC) curves, accuracy, sensitivity, and specificity are among the metrics used to assess how well the trained modelsclassify white blood cells.

Clinical Validation: We validate the proposed automated categorization system by comparing its results to manual microscopic inspection by skilled hematologists using clinical data from patients with known hematological diseases.

III. LITERATUREREVIEW

Altaf Khan [1]. The goal of this work was to create a single deep CNN model with strong WBC-type recognition performance and the ability to diagnose several illnesses. To achieve this, we combine multilayer convolutional features from different layers to form a new model. A variety of visual cues were employed in many deep layers to improve the accuracy of WBC categorization. High dimensional feature vectors are produced by combining these features.

Mu-chun su [2]. This paper presents a unique algorithm for distinguishing white cells from smear images. This segmentation technique locates a distinct zone of white blood cell tones in the *HSI* color space. The identified An ellipsoid in three dimensions can be used to define the discriminating region. There were twenty features proposed in total: three geometrical, three chromatic, and fourteen LDP. White blood cells were split into five groups using three neural network-based classifiers. The performance comparison between our suggested system and a trained MLP is shown in the table. The performance was measured using an open database.

AI-Dulaimia [3]. This chapter covers picture acquisition, pre-processing, segmentation, and feature extraction. This review examines various automated techniques for extracting and classifying white blood cells from 2005 to the present. Despite extensive research, white blood cell segmentation, feature extraction, and classification remain difficult, especially in low resolution and variable lighting environments.

Abdullah Elen [4]. This work extracted geometrical and statistical properties from microscopic blood pictures to create a feature vector with 35 parameters. Six machine learning techniques use this feature vector as an input parameter to classify white blood cells. To test the performance of the algorithms, five different types of data were created in alternating training and test ratios. Each data set had 100 potential combinations, which were used to examine statistical results. The leukocyte cell categorization that the MLR algorithm achieves has the highest success rate across all datasets and situations. The k-NN method has the lowest success rate and produces nearly similar outputs.

Satria Wibawa [5]. The classification of neutrophils and lymphocytes, two distinct subgroups of white blood cells, is the aim of this study. The recommended categorization method in this study was deep learning. Three traditional machine learning methods were compared to Deep Learning's performance: Multi Layer Perceptron, k-Nearest Neighbor, and Support Vector Machine. Conventional machine learning refers to methods that cannot learn from raw data. Conventional machine learning employed nine texture features. Deep Learning surpassed the three traditional machine learning algorithms with a classification accuracy of 0.995. Comparable accuracy rates during training and validation demonstrated the Deep Learning model's robustness. Future publications ought to provide additional categories for white blood cells.

[6] Siraj Khan. This investigation investigated the TML and DL techniques for recognizing leukocytes in blood smear images. We evaluated numerous TML and DL techniques for the identification of WBCs in blood smear pictures. The data came from original research publications published between 2014–2020. The study uncovered eighty primary publications (published in journals, books, conferences, and online materials) on TML and DL approaches for leucocyte categorization in blood smear images and their applications in medical diagnostics.

[7] Wang Da. In this work, a deep learning network is used to identify and count white blood cells. The results of the experiment demonstrate that the proposed system performs comparably to cutting-edge technologies. The proposed methodology makes use of the modified Faster-RCNN model. White blood cells in the dataset were effectively identified at 74.4%, 85.3%, 86.3%, 98.8%, 83.1%, and 75.5% IoU levels using image-level data.

[8] Irwan Rahadi. This research presents a system for automatically detecting and counting normal and hypochromic red blood cells using an algorithm-trained Haar Cascade classifier. The outcomes showed that the algorithm performed as expected well. Change the value for best detection. The equation. Our proposed method for cell detection is remarkably effective. Red blood cell images are all that are required to train the classifier. Explicit conclusions will be presented. Normally, everything runs smoothly. utilized in RBC detection centers or medical institutions to locate red blood cells. There will be additional research conducted.

[9] Huang Chen. This research presents an innovative deep learning method for precise white blood cell detection. Better feature representation is achieved by combining ResNet and DenseNet in our suggested approach. Furthermore, the method leverages the SCAM mechanism to enhance the model's ability to represent relevant information in WBC pictures in two distinct dimensions: space and channel, hence addressing sample similarity. various approaches for distributing spatial and channel attention will produce various categorization outputs because they fulfill distinct purposes. We use data

augmentation and transfer learning strategies to lessen the negative impact of imbalanced or insufficient training data on the performance of deep learning models.

[10] WENNA WU. This paper offers a novel deep learning approach to accurately detect white blood cells. Our proposed method combines ResNet and DenseNet to provide better feature representation. Moreover, sample similarity is addressed by the method, which makes use of the SCAM mechanism to improve the model's capacity to represent pertinent information in WBC pictures in two different dimensions: space and channel. Because they serve different functions, different strategies for allocating spatial and channel attention will result in different classification outcomes. To mitigate the detrimental effect of unbalanced or inadequate training data on the performance of deep learning models, we employ data augmentation and transfer learning techniques.

[11] Neerukattu Indrani. This technique uses convolutional neural networks and microscopic images to classify white blood cells into several groupings. network methods. This classification determines the type of ailment a patient has and divides cells. This experiment produces more accurate image identification results than traditional lab procedures. The test set has a high accuracy rate—more than 90%. To create an optimal model for medical applications and analysis about the quantity and variety of white blood cells, a highly computationally competent model can be trained.

[12] Anwar Siswanto. The classification technique test was successfully completed. It was discovered that the MLP approach had the highest accuracy for identifying white blood cells. Research indicates that the NBC strategy has an accuracy of 80% while the KNN method's accuracy is 82%. With a 92% accuracy rate, the MLP approach takes the longest (2.08 seconds). MLP was demonstrated to be the most effective classification model for recognizing white blood cells, while requiring a longer processing time. The great accuracy can be attributed to non-overlapping white blood cell cropping and proper dye absorption.

[13] Cesar Cheuque. This research proposes a hybrid multi-level technique to automatically identify and classify white blood cells from blood smear images into mononuclear (lymphocytes and monocytes) and polymorphonuclear (segmented neutrophils and eosinophils) kinds. First, the region of interest of the white blood cell is identified and mononuclear cells are distinguished from polymorphonuclear cells using a Faster R-CNN network. After they have been divided up, the subclasses are recognized using two parallel convolutional neural networks with the MobileNet structure. The model displayed good performance metrics, indicating that the proposal is a useful tool for clinical and diagnostic laboratories, with average accuracy, precision, recall, and F-score of 98.4%.

[14] Mariam Nassar. The study "Label-Free Identification of White Blood Cells Using Machine Learning" reportedly aims to develop a technique for identifying white blood cells (WBCs) without the use of fluorescent dyes or other labeling agents. This method reduces costs and sample preparation steps while streamlining and possibly even speeding up the cell identification process, making it helpful for medical diagnostics and research. Unlabeled white blood cells are likely subjected to quality assessment using machine learning approaches. These methods most likely make use of metrics discovered through imaging or other sensing techniques, such as size, shape, granularity, and optical characteristics.

Blumers AL [15]. Most likely, "GPU-accelerated Red Blood Cell Simulations with Transport Dissipative Particle Dynamics" is a scientific work that uses a computational technique called Transport Dissipative Particle Dynamics (TDPD) to explore the behavior of red blood cells (RBCs). The phrase "GPU acceleration" suggests that the simulations make use of Graphics Processing Units' (GPUs') computational power to expedite calculations.

[16] Blumers AL. "GPU-accelerated Red Blood Cell Simulations with Transport Dissipative Particle Dynamics" is most likely a scholarly publication that investigates the behavior of red blood cells (RBCs) using a computational method known as Transport Dissipative Particle Dynamics (TDPD). The term "GPU acceleration" implies that the simulations leverage the processing capability of Graphics Processing Units (GPUs) to accelerate calculations.

[17] Asghar Rabia. An extensive review of TML and DL methods for WBC categorization is provided in this article. In this case, we looked at and contrasted various approaches for WBC classification. Data from 136 source publications published between 2006 and 2023 are used in this research. These works investigate the classification of leukocytes using TML and DL approaches and their application to medical diagnosis. These studies demonstrate the significant contributions that TML and DL techniques bring to MIA. The purpose of this work is to identify and synthesize TML and DL applications in MIA, namely for the classification of leucocytes in blood smear images. The goal of this study is to shed light on the intricate characteristics of DL and TML in MIA.

[18] Blumers AL. "GPU-accelerated Red Blood Cell Simulations with Transport Dissipative Particle Dynamics" is most likely a scholarly publication that investigates the behavior of red blood cells (RBCs) using a computational method known as Transport Dissipative Particle Dynamics (TDPD). The term "GPU acceleration" implies that the simulations leverage the processing power of Graphics Processing Units (GPUs) to speed up calculations.

[19] Ritu Gupta, Deepanshi Singla, Abhilasha Singh*, Aakarsh Srivastava, and Preet Kaur Chadha. "An Image Processing-Based Automated Red Blood Cell Counting Method."

[20] Alexander Chef, Amber Eker, and Altaf Khan "Using multi-layer convolutional features with an extreme-learning machine, white blood cell type identification is achieved."

[21] SHENGWU LIAO, ZHENTAI LU, AND WENNA WU (Member, IEEE). "Image Classification of White Blood Cells Using Radiomics and Deep Learning Techniques."

IV. METHODS:

PROPOSED SYSTEM:

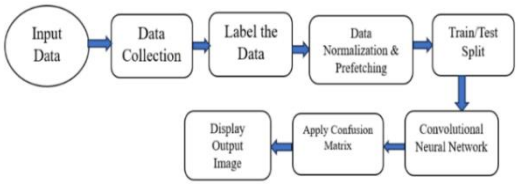


Fig: WBC Classification Diagram

Data preprocessing:
It is an essential step to prepare the dataset for training. In this project, images are loaded using OpenCV and resized to a standardized size of 128x128 pixels. Pixel intensities are then normalized to the range [0, 1], ensuring consistency and numerical stability during training. Labels are binarized using Label Binarize to convert class labels into binary vectors, enabling categorical classification. This preprocessing pipeline ensures that the input data is properly formatted and scaled, ready to be fed into the model for training.

Data Normalization:
Data normalization is a preprocessing technique used in machine learning to rescale the values of numerical features to a standard range without distorting differences in the ranges of values.
Here we used the TensorFlow's Rescaling layer for data normalization. This layer scales input values to be in a specified range, often between 0 and 1.
Rescaling layer that will scale input values by dividing them by 255, effectively bringing them into the [0,1].
Lambda function takes each sample in the training dataset, testing dataset and validation dataset and applies normalization layer. After this normalization step data will be ready to fed into a machine learning model.

Prefetching:
Prefetching is a technique used to overlap the data loading process with model training or inference. It's particularly useful when dealing with large datasets that may take significant time to load from storage into memory.

Convolutional Layer: A convolutional layer is a fundamental building block in convolutional neural networks (CNNs), commonly used in image recognition, computer vision, and other tasks involving grid-like data such as time-series analysis and natural language processing.

Model Architecture:

A Convolutional Neural Network (CNN) architecture is a popular choice for projects involving the classification of white blood cells (WBCs) utilizing machine learning and image processing due to its effectiveness in dealing with microscopic image data. Here's a simplified outline of a common CNN architecture for this task:

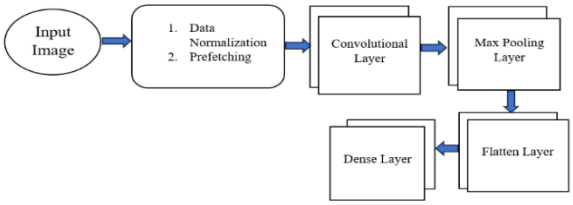


Fig: CNN Architecture Model

- Conv2d (Conv2D): A Conv2D layer in a convolutional neural network (CNN) is a two dimensional convolution layer that applies a convolution kernel in one spatial or temporal dimension to the layer input. The outputs produced by the layer are tensors. The 2D convolution layer, often known as conv2D, is the most widely used kind of convolution. To perform element-wise multiplication, a filter or kernel in a conv2D layer "slides" over the 2D input data. It will so merge the outcomes into a single output pixel.
- Max pooling2d: It also known as Max-Pooling 2D, is a pooling layer that uses a convolutional neural network (CNN) to down sample the input feature maps. A kind of spatial down sampling called MaxPooling2D helps CNNs achieve translation invariance and reduce computing complexity. By selecting the maximum value inside each pooling window, MaxPooling2D preserves the most important features while eliminating less important data.
- Conv2D_1: It is the first convolutional layer of a CNN. It extracts features from the input image. The layer is made up of several filters, each of which is a tiny weight matrix. The filters are applied to the input image, and each filter generates a feature map. The feature maps are subsequently sent to the next layer of the CNN.
- Max_pooling2d_2: The Conv2D layer slides a narrow window, referred to as a filter or kernel, over each point of the input feature map to execute a convolution operation. The filter produces a single value in the output feature map at each location by performing a dot product on the related input region.
- Flatten Layer: In a CNN for WBC classification, the Flatten layer transforms feature maps that are spatially organized into a format that can be used for fully linked layer categorization. It enables the network to generate precise predictions regarding the class labels of WBCs by utilizing the hierarchical representations of features obtained from the input images.
- Dense layer: The Dense layer serves as a powerful classifier in WBC classification models by deciphering intricate patterns and connections between recovered data and the associated white blood cell class labels. It is essential for correctly identifying the different kinds of WBCs shown in the input images.

- Dense_1: The foundational element of machine learning and image processing-based WBC classification models is the Dense layer. It is in charge of compiling data extracted from input photos and determining final classifications based on these characteristics. It is essential for converting the information that was collected into forecasts for the WBC class designations.

 # Print a summary of the model architecture
model summary ()

Model: "sequential"

Layer (type)	Output Shape	Param #
Conv2d (Conv2D)	(None, 98, 98, 64)	4864
max_pooling2d (MaxPooling2D)	(None, 49, 49, 64)	0
Conv2d_1 (Conv2D)	(None, 24, 24, 256)	147712
max_pooling_1 (MaxPooling2D)	(None, 11, 11, 256)	0
Conv2d_2 (Conv2D)	(None, 5, 5, 128)	295040
max_pooling2d_2 (Max Pooling 2D)	(None, 4, 4, 128)	0
flatten (Flatten)	(None, 2048)	0
dense (Dense)	(None, 256)	524544
dense_1 (Dense)	(None, 4)	1028

Total params: 973188 (3.71 MB)
Trainable params: 973188 (3.71 MB)
Non- trainable params: 0 (0.00 Byte)

Fig: Model architecture.

Model Training:

Train the model for a predefined number of epochs (e.g.50epochs) using the training dataset. Save the best-performing model based on validation loss at the model checkpoint.

Assessment of the Model: Utilizing the testing dataset, evaluate the trained model's performance. To evaluate the model's prediction ability and any biases, compute accuracy and generate a confusion matrix and classification report.

Testing Models: Make use of the best-performing model that was kept for instruction. Obtain an image from the test set or real data in order to create a forecast. To make sure the image meets the model's input requirements, resize and normalize it beforehand. Apply the model to predict the class label of the given image. Examine the predicted results and assess how well the model performs in real-world scenarios.

IV. EXPERIMENTAL ANALYSIS AND RESULT:

Preparing the Dataset:

Obtain a labeled photo dataset of WBC images. This collection should contain images of different WBC types, each labeled with its respective class. Getting data ready: Reduce the size of images to a consistent, model-appropriate scale. To enhance convergence during training, change the pixel values to a range (such [0, 1]).

Model Choice

Choose a Model: Select a suitable machine learning model for picture classification. Convolutional neural networks (CNNs) are a well-liked choice due to their superior image processing capabilities.

Model Training

Training Procedure: Input the model with the preprocessed training dataset. To prevent overfitting, train the model on the dataset over several epochs while monitoring its performance on the validation set.

Training Configuration: Specify the model architecture, comprising fully connected, pooling, and convolutional layers. Assemble the model using a suitable optimizer (like Adam) and loss function (such categorical cross-entropy).

Model Evaluation

Performance Metrics: Evaluate the model's effectiveness using the F1-score, accuracy, precision, and recall.

Confusion Matrix: Look over the confusion matrix to assess how well the model works with different WBC classes.

Testing Models

Phase of testing: Predict the classes of WBCs in the test dataset using the trained model. Analyze the model's performance on the test set to determine how well it can be generalized.

Adjusting and Streamlining:

Hyperparameter tuning: To optimize performance, adjust the model's hyperparameters (learning rate, batch size, etc.).

Data Augmentation: Apply data augmentation methods (e.g., rotation and flipping) to increase model resilience.

Result:

1) Test Accuracy:

Test Accuracy

```
In [25]: score = model.evaluate(test_ds, verbose = 0 )
         print("Test Score: ", score[0])
         print("Test accuracy: ", score[1])

         Test Score:  0.8360964059829712
         Test accuracy:  0.8142340183258057
```

2) Train Accuracy

Train Accuracy

```
In [26]: score = model.evaluate(train_ds, verbose = 0 )
         print("Train Score: ", score[0])
         print("Train accuracy: ", score[1])

         Train Score:  0.06280090659856796
         Train accuracy:  0.9807170629501343
```

3)Validation Accuracy

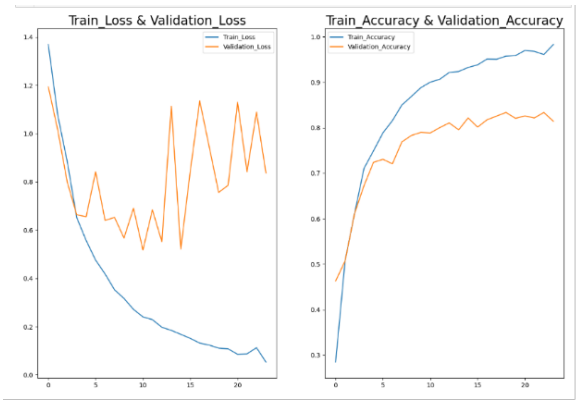
Validation Accuracy

```
In [27]: score = model.evaluate(val_ds, verbose = 0 )
         print("Validation Score: ", score[0])
         print("Validation accuracy: ", score[1])

         Validation Score:  0.61070716381073
         Validation accuracy:  0.8028169274330139
```

Sr. No	Reference Paper Name	Technique Used	Accuracy		
			Accuracy	Specificity	Sensitivity
1.	Preet Kaur Chadha, Aakarsh Srivastava, Abhilasha Singh*, Ritu Gupta, Deepanshi Singla. "An Automated Method for Counting Red Blood Cells using Image Processing."	Image Processing Technique.	90 %	87.50 %	92 %
2.	Rabia Asghar, Sanjay Kumar, Paul Hynds, Arslan Shaukat. "Classification of White Blood Cells Using Machine and Deep Learning Models."	Machine Learning and Deep Learning Models.	89 %	81.5 %	88.10 %
3.	Altaf Khan, Amber Eker, Alexander Chef "White blood cell type identification using multi-layer convolutional features with an extreme-learning machine."	Machine Learning (Multilayer CNN)	84.32 %		
4.	WENNA WU, SHENGWU LIAO, AND ZHENTAI LU, (Member, IEEE). "White Blood Cells Image Classification Based on Radiomics and Deep Learning."	Radiomics and Deep Learning Technique.	81 %		
5.	Neeru Indrani, C Srinivasa Rao. "White Blood Cell Image Classification Using Deep Learning."	Deep Learning (Image Classification Using CNN)	84 %		

4) Graphical Representation of Loss & Accuracy:



Training Accuracy and Loss:

Loss: During training, the training loss quantifies the degree to which the model's predictions agree with the actual target values. Usually, a loss function such as the mean squared error for regression or the cross-entropy loss for classification—is used to calculate it. By using methods like gradient descent and model parameter adjustments to enhance prediction accuracy, the training process aims to reduce this loss.

Accuracy: The percentage of accurate predictions the model made on the training dataset is displayed by the training accuracy. It is computed by dividing the total number of samples in the training set by the number of accurate predictions.

Validation Loss and Accuracy:

Loss: The validation loss is computed using the same loss function as the training loss on an alternative validation dataset that the model hasn't been trained on. This makes it easier to assess how well the model generalizes to new, untested data. On new data, the model is performing well when the validation loss is small.

Accuracy: The validation accuracy serves as a proxy for the model's performance on the validation dataset. Based on this unknown data, it shows the model's prediction accuracy for the target values. Similar to validation loss, a high validation accuracy indicates a strong generalization potential.

5) Confusion Matrix:

6) Output Image:

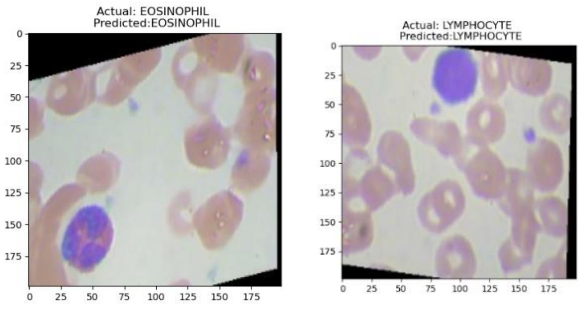


Fig: WBC Type Identification Image

Conclusion:

In this work, we used CNN algorithms to create a machine learning-based system for WBC type identification. Using data preprocessing, data normalization, and prefetching techniques of image processing on a microscopic blood smear image as an input. Subsequently, a high performance of WBC identification was achieved by applying the Convolutional Neural Network (CNN) algorithm for Machine Learning (ML), which can be used for the diagnosis of various disorders. In particular, our model outperformed previous techniques with a WBC-identification accuracy of 98.12%. To identify abnormal cells, such as those with aberrant cytoplasmic granules or the cell nucleus, deep learning may be used in future investigations.

References:

[1] Hasan Demirel c, Amber Eker b, Alexander Chefranov a, Altaf Khan a* Department of Computer Engineering, Eastern Mediterranean University, Mersin, Turkey; b Faculty of Medicine, Eastern Mediterranean University, Mersin, Turkey; c Department of Electrical & Electronics Engineering, Eastern Mediterranean University, Mersin, Turkey. [2] Abu Umer2, Oumaima Saidani1, Muniba Kiran3, Shtwai Alsubai4, Tai Hoon Kim5* & Imran Ashraf6. Nazik Altturki1, Amal Alshardan1, Muniba Kiran1. [3] Changhun Jung1, DaeHun Nyang1*, Mohammed Abuhamad2, David Mohaisen3, and Kyungja Han4. [4] Mu-Chun Su,1 Chun-Yen Cheng,1, and Pa-Chun Wang,1 National Central University, Jhongli 32001, Taiwan, Department of Computer Science & Information Engineering, 2 General Hospital, Taipei 10656, Taiwan. [5] Inmaculada Tomeo-Reyes2, Kien Nguyen1, Vinod Chandran1, Jasmine Banks1, Khamael AL-Dulaimi1, *, and 1 Queensland University of Technology, School of Electrical Engineering and Computer Science, QLD, Australia Telecom and Electrical Engineering School No. 2. [6] M. Kamil Turan 2 1 Karabük University, Department of Computer Science, Vocational School of T.O.B.B. Technical Science, 78050 Karabük, Turkey; Abdullah Elen *1. 2 Karabük University, Faculty of Medicine, Department of Medical Biology, 78050 Karabük, Turkey. [7] Made Satria Wibawa Department of Information System STMIK STIKOM BALI Denpasar, Indonesia. [8] ALI SHARIQ IMRAN 2, AMIN ULLAH 3, TANVEER HUSSAIN 3, MUHAMMAD SAJJAD 1, 2, and SIRAJ KHAN 1 (all members of IEEE as students) 1Islamia College University Peshawar, Department of Computer Science, Digital Image Processing Laboratory, Peshawar 25000, Pakistan 2 Norwegian University of Science and Technology (NTNU), Gjøvik, Norway; Department of Computer Science 3 Intelligent Media Laboratory, Sejong University, Seoul 143-747, South Korea, Department of Software. [9] From the International Conference on Biomedical Engineering Innovation 2019 in Kaohsiung, Taiwan, Da Wang1TM, Maxwell Hwang1TM, Wei Cheng Jiang2re, Kefeng Ding1*, Hsiao Chien Chang3, and Kao Shing Hwang3. November 15, 19, 2019. [10] Meechoke Choodoung2, Arunsri Choodoung3, and Irwan Rahadi1 1 Statistics Department, University of Hamzanwadi, Lombok, Indonesia 2Math Department, Mahidol University, Bangkok, Thailand 3Medical Laboratory Service Center, Mahidol University, Bangkok, Thailand. [11] Dehua Cao2, Cheng Li, Baochuan Pang2, Juan Liu1*, Chunbing Hua1, Jing Feng1, and Hua Chen1. [12] (Member, IEEE) 1School of Biomedical Engineering, Southern Medical University, Guangzhou 510515, China; WENNA WU 1,2,3, SHENGWU LIAO4, AND ZHENTAI LU 1,2,3. [13] Chiraparapu Srinivasa Rao2, Neerukattu Indrani1, 1PG Scholar, Dr. K S Raju Arts & Science College, Penugonda, W.G.Dt., A.P., India; Department of Computer Science, SVKP. 2Dr. K S Raju Arts & Science College, Penugonda, W.G.Dt., A.P., India; Associate Professor of Computer Science, SVKP. [14] Anwar Siswanto 1, Abdul Fadlil 2, Anton Yudhana 3 1 Department of Electrical Engineering, Universitas Ahmad Dahlan, Yogyakarta, Indonesia 23 Informatics Engineering Master Program. [15] Rodrigo Salas 3,4, *; César Cheuque 1, Marvin Querales 2, Roberto León 1, and Romina Torres 1, 4, *. [16] Mariam Nassar,1* Minh Doan,2 Andrew Filby,3 Olaf Wolkenhauer,1,4 Darin K. Fogg,5 Justyna Piasecka,6 Catherine A. Thornton,6 Anne E. Carpenter,2 Huw D. Summers,6 Paul Rees,6 Holger Hennig1. [17] Muhammad Yildirim*, Çrat University, Elazığ, 23100, Turkey; Ahmet Çinar Computer Engineering Department. [18] Arslan Shaukat, Paul Hynds, Sanjay Kumar, and Rabia Asghar Rabia Asghar works as a Lecturer at the University of Lahore (UoL), in Pakistan, in the Department of Computer Engineering. [19]] W. Stock, R. Hoffman, White blood cells 1: non malignant disorders, The Lancet 355 (2000) 1351–1357, https://doi.org/10.1016/S0140-6736(00)02125-5. [20] B.J. Bain, Diagnosis from the blood smear, N Engl J Med 353 (2005) 498–507, https://doi.org/10.1056/NEJMra043442. [20] Meiyu Li1,8, Cong Lin2,8, PengGe1, Lei Li3, Shuang Song1, Hanshan Zhang4, Lu Lu5, Xiaoxiang Liu2, Fang Zheng6, Shijie Zhang7* & Xuguo Sun6*.