Classify blood cell subtypes Using Deep Learning Techniques

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APPROVAL

This Thesis titled "Classify blood cell subtypes Using Deep Learning Techniques" submitted by Fariha Zannat Luna, ID No: 221-25-091 to the Department of Computer Science and Engineering, Daffodil International University has been accepted as satisfactory for the partial fulfillment of the requirements for the degree of M.Sc. in Computer Science and Engineering and approved as to its style and contents. The presentation has been held on 17-01-2023.

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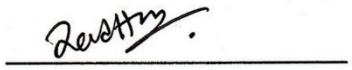

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ABSTRACT

This work describes a technique for retrieving White blood cells (WBCs) employing blood microscopic images, identifying them, variety of WBC. A new challenge in the medical sector is diagnosing by comparing the number of WBCs with a normal number of them. A new problem in medical science is diagnosing by comparing the number of white blood cells (WBCs) to what is considered normal, and this topic has been studied. Image processing techniques are used in this study as promising modalities for diagnosing various types of blood malignant development in an effort to prevent these problems. Deciding the goal of the project is to employ image-processing methods to detect and classification of blood cell subtypes at an early stage. The proposed methodology is to detect and classify blood cell subtypes by implementing a TensorFlow library from the microscopic pictures of human blood cells using Convolutional Neural Network (CNN) architecture deep learning. After utilizing the TensorFlow framework and VGG16 architecture in our proposed methodology, we got 98.21% accuracy in training and 91.08% in validation individually. The TensorFlow model beat the Keras model with additional productive and precise outcomes.

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CHAPTER 1
Introduction

1.1 Introduction

Differentiating and describing patient blood tests are typically included in the investigation of blood-based infections. Clinical applications for automated methods to identify and arrange platelet subtypes are many. The blood's nucleated cells, including neutrophils, lymphocytes, monocytes, and eosinophils, are referred to as "white cells" or "leucocytes." This enormous number of cells contributes to the host's defense against contamination and other insults.

Platelets, red platelets, and white platelets are among the blood's cell types. Each one is continuously produced in the bone marrow and transported conveniently through the circulatory system. The rapid production of unusual blood cells impairs normal platelet development[7]. Malignant growth arises when the body's normal regulatory system breaks down. All things considered, old cells don't die; instead, they proliferate, resulting in the development of weird, new cells. Characterizing white blood cells (WBCs) is a major step because it is able to aid hematologists in the diagnosis of a few. Due to the unwanted cells' involvement in RBC space, there are three basic types of blood that can have an iron deficiency (low red blood count) [1]. Thrombocytopenia, which is caused by several myelomas, is responsible for decreased platelet counts in the blood. Additionally, it results in bone sores that are visible on CT scans, which are the breakdown of bones. About 1500 people passed away as a result of this illness in 2019, which accounts for 0.2% of all deaths brought on by malignant growth alone. In the US, over 20,000 people have myeloma which has been regularly diagnosed. Age, kind, speed of illness progression, contaminated areas, and other factors all affect how blood diseases are treated. Blood contains dangerous white platelets, or lymphoblasts, that travel to various organs like the cerebrums, livers, and kidneys before spreading to emergency bodily tissues. Because of the vague notion of the side symptoms, leukemia diagnosis is challenging in the early stages. The smallest evaluation of PBS is the most common leukemia analysis technique, however, the only

effective way to detect leukemia is by collecting and evaluating bone marrow tests [3]. One of the key factors in classifying the many types of blood diseases is the blood count. It should be physically and naturally possible to count. On the off chance that it is carried out by a skilled individual, the manual technique offers a 100% recognition rate, but it is also a time-consuming cycle [4]. However, although programmed counting is a speedier interaction, there is a greater chance that the count will be off. Both methods so have advantages and disadvantages.

This article provides a diagram of the automated process for determining the type of white blood disorder. The mechanical arranging technology is economical and perhaps can be swiftly provided in both urban and rural regions. The problems that are addressed by the suggested framework include errors brought on by manual characterization, the need for a skilled expert, errors produced by cells that are not clearly defined when viewed up close, and so on. Since they derive benefits from the basic facts themselves, Deep learning substructured strategies can assist in resolving each of the identified issues. Convolution Brain Organizations (CNNs) combine several multi-facet perceptrons and, with a little pre-handling, produce useful results. As each convolution layer of the organization learns a new element that is present in the images and afterward produces a high enactment, CNNs operate as component extractors [6]. A strong and overpowering mechanized order strategy for the specific type of white blood malignant growth using Convolution Brain Organizations is introduced in the proposed review. Thus, the study evaluates the proposed deep learning model's presentation using the criteria of accuracy, precision, recall, sensitivity, and specificity. In order to present a subjective also quantitative assessment, precise results, and quick handling, it is crucial to create a programmed framework that integrates image handling, signal handling, design acknowledgment, or deep learning procedures. Deep Learning is recognized to perform better than trained AI when managing a large number of images.

1.2 Problem Statement

The ability to detect infections by seeing and counting white platelets is one of the current challenges in clinical science. Neutrophils and Eosinophils belong to the primary whole gathering, whereas Lymphocytes and Monocytes belong to the subsequent entire gathering. White platelets are divided into two primary groups (Granulocytes and A granulocytes) and five final groups [7]. According to the World Health Organization's (WHO) malignant growth measurements, there were 7.6 billion people worldwide in 2021, with 18 million cases of chronic disease and 9.5 million deaths. In 2040, WHO prophesy that the amount of expected disease occurrences will depend on a staggering figure of 29.5 million people. Blood cancer is a generic word that covers a variety of blood tumors, and it accounts for 8–10% of all malignant tumors worldwide that are typically referred to as cancerous growths Every year, 900,000 or more people are diagnosed with blood diseases worldwide, but the majority of those affected continue to exist unaware of this common state because the sign looks like typical fever and weariness and don't actually manifest in the early stages. Nearly 140 different types of blood malignant development exist, with leukemia, lymphoma, and multiple myeloma constituting the major subtypes[1].

1.3 Research Objectives

a) To look into the gaps in knowledge that prevent current machine vision-based classification systems from accurately classifying various types of blood cells into the appropriate groups.
b) To employ a simple machine vision-based strategy to increase the precision of classifying them.

1.4 Research Questions

a) How can we look at the flaws in the currently available machine vision-based systems that correctly classify various types of blood cells?
b) How can we improve the accuracy of classifying various blood cell types correctly using a machine vision-based approach?

1.5 Report Layout

Chapter 1 Includes an introduction to the research goals and main research topics..

Chapter 2 A review of the relevant literature is highlighted.

Chapter 3 Outlines in detail the proposed methodology.

Chapter 4 provides an explanation of the result analyzation of existing output.

Chapter 5 concludes the current research and outlines a future research direction.

CHAPTER 2
Literature Review

2.1 Related works

The method for extricating white blood cells (WBCs) from blood microscopic pictures, identifying them, and counting each type of WBC is provided in the work. After reviewing the techniques for separating WBCs from hematology images, we chose to classify WBCs using artificial neural networks (ANNs) due to their high applicability in this area. Complex-valued neural networks (CVNNs), which have a higher speed and more stable convergence than real neural networks, were also used for this purpose due to their superior performance. A normalized feature vector is continuously retrieved using the characteristics of the various types of globules and their coloration, and it is then fed into a complex-valued previous-propagation neural network for classification [25]. A paper was published by the authors of reference [2] who have reviewed the white blood cell types and their structure. As WBC plays a very important role in the human body, they have gone through automatically white blood cell categorizing system, adding image acquisition, preprocessing, and segmentation. They have reviewed automatic techniques to extract features of WBCs, from 2005 to state-of-the-art. One percent of all blood cells are leukocytes, which are made in the bone marrow. A study based on machine learning methods for the classification of blood cells and disease prediction was presented by Nisha Varghese [7]. The study showed that the potent machine learning algorithms efficiently identified, detected, and forecasted changes in the number, shape, texture, and color of the blood cells. Results are extremely accurate when using Support Vector Machines and Convolutional Neural Networks.

The four vital organs of blood—RBCs, WBCs, platelets, and plasma—are classified in the current work utilizing ML approaches. Due to changes in cells and haematological factors, ML may identify distorted or infected cells and subsequently forecast issues and diseases. The study showed that the potent machine learning algorithms efficiently identified, detected, and forecasted changes in the number, formation, texture, and color of the blood

cells [13]. Cecilia Di Ruberto suggested using microscopic blood images to identify and measure red and white blood cells, which is a novel and efficient method. It is nevertheless necessary to manually evaluate blood smears in order to check the counter results and to keep track of the patients getting therapy. It is based on the cutting-edge region proposal methodology known as Edge Boxes. By using Edge Boxes to introduce knowledge-based limits into the detection process, they swiftly and efficiently locate cell proposals. Excellent experimental outcomes in both cases—beating the state-of-the-art on ALL-IDB and establishing a solid baseline on MP-IDB—show that the suggested approach may be applied to a variety of datasets and image types [14]. Digital image processing is an essential component in the research areas of medical image processing, object detection, biometrics, information concealment, and picture compression. The study compares the color-k-means clustering segmentation method, which is the most popular segmentation technique, with a segmentation technique created for separating WBCs from microscopic blood images using a thresholding segmentation approach[17].

The study attempts to more accurately detect and categorize WBCs in a microscopic picture into four groups. The two main elements of the suggested approach are a shallow tuning pre-trained model and a traditional ML classifier. Six different types of machine learning are used in this study's ten different pre-trained models. Additionally, for comparison, a standard classifier known as the fully connected network (FCN) of pre-trained models is used. [24].

This study presents an effective deep learning-based method for certifying white blood cells automatically in images of bone marrow and peripheral blood, which will save hematologists from onerous clinical responsibilities. Before implementing a deep neural network model tailored to cell localization and segmentation, input picture pre-processing was first suggested. The segmentation quality was enhanced by the use of a novel method that makes use of the interaction between model outcomes and geographical information[26].

2.2 Scope of the Problem

Counting and organizing WBC should be possible using both automated and manual methods in the inquiry technique. There are many clinical issues associated with the manual categorization of WBC, including recalling errors for the accuracy of results due to testing errors, likelihood, unfortunate awareness, particularity, and prescient features. It takes a lot of time as well [9]. Additionally, several programmed methods have been used at research institutions to identify and characterize WBC using tools like stream cytometry and programmed counting machines. These tools don't use image processing methods, and they are quantitatively and not arbitrarily ordered and count WBCs. [10] Researchers worked on trained AI, but they didn't get better performance. Some researchers tried to detect and classify blood cells with numeric datasets, but the accuracy level was low [11].

2.3 Challenges

There are some investigated difficulties zeroed in on this study which are the following:

a) **WBCs's Structure:** Monocytes, lymphocytes, neutrophils, and eosinophils are examples of WBCs with diverse designs that are depicted in minute detail. These characteristics are very helpful for describing WBCs in the most usual fashion, but they make it difficult to divide cells accurately and separate out their constituent parts.

b) **Change of Size:** The WBC core may appear in different images at different sizes, and it may also be positioned differently inside the cells. While some WBC cores may be thin and distant from the cell wall, others may be broad and engulf the entire cell.

c) **Image Rotation:** In WBC images, cells can be observed from any random angle, and their appearance can change according on the angle from which they are seen. To express this, a framework for order is necessary.

d) **Image Quality:** Image noise and contrast changes are caused by poor picture quality and using different cameras or imaging systems.

e) **Choosing Machine Learning method**: Scientists used various ML techniques to complete the tasks quickly. In this manner, the perfect ML method that can precisely order diverse WBC classifications is determined.

f) **Improvement of Accuracy/ Precision:** Improving the accuracy of the Machine Learning model is also a huge challenge.

CHAPTER 3
Materials and Methods

3.1 Automated Processes of White Blood Cell Classification

The entire process is separated into Six steps. These are listed below:

a) Image Collection/Data Preparation
b) Image Preprocessing
c) Image Split
d) Transfer Learning Model
e) Blood Cell Classification
f) Result Survey

The complete working process, Figure 1 illustrates this process, which is thoroughly detailed in the areas following, before concluding with a result analysis.

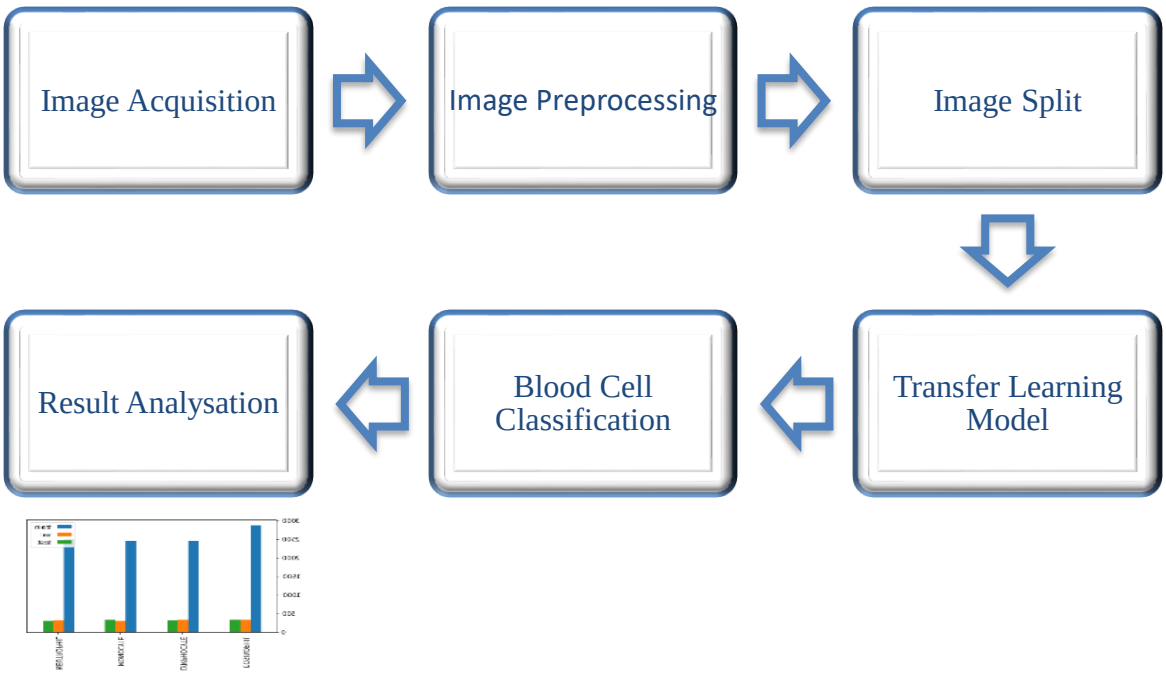


Figure 1: The CNN model's operational method

3.2 Dataset Preparation

In this study, we use secondary datasets which are collected from the internet. The dataset is containing 12,444 images of 4 subtypes of blood cells. Among them, 3,121 are Eosinophils, 3103 are Lymphocytes, 3,101 are Monocytes, and 3119 are Neutrophils.

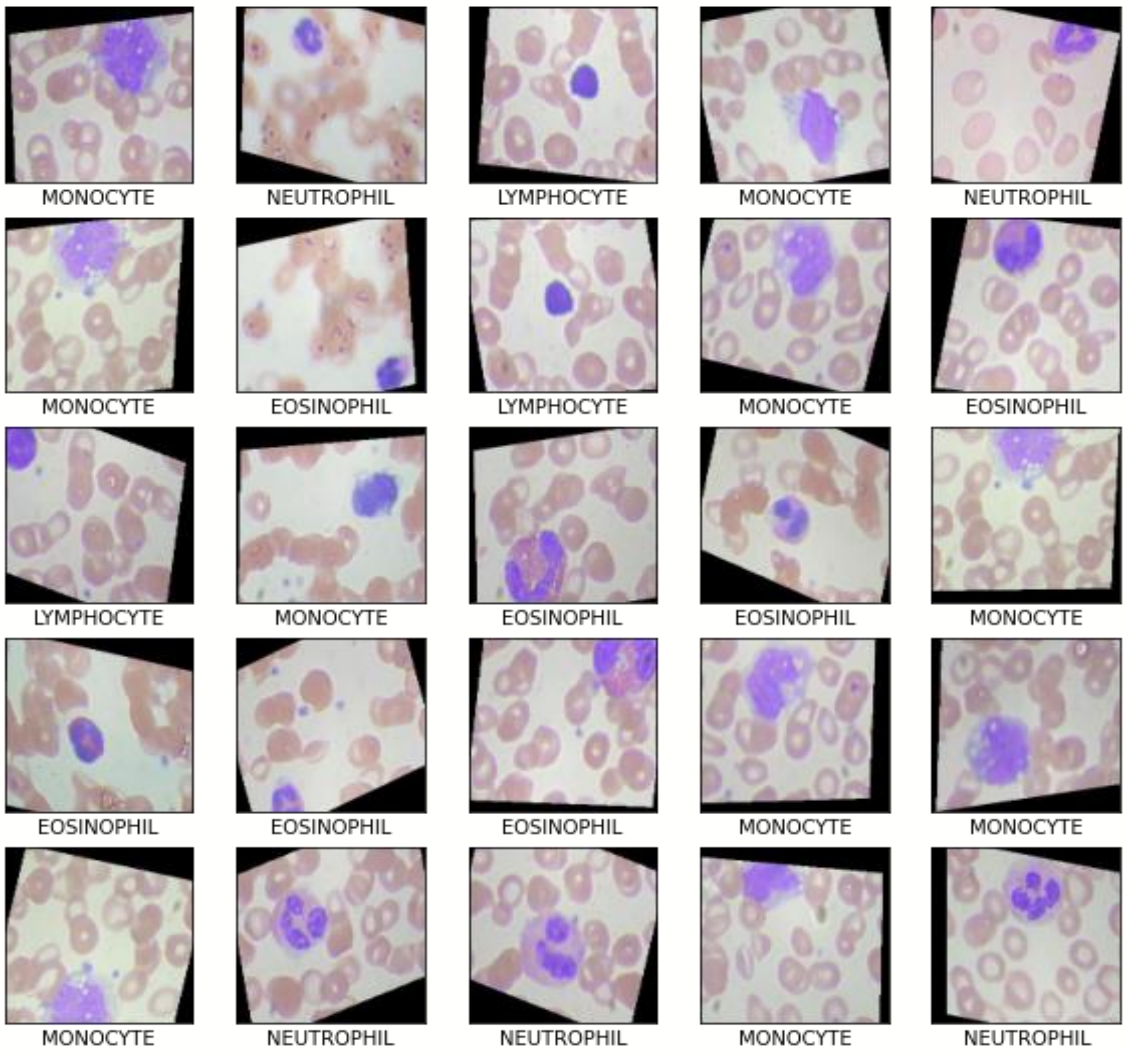


Figure 2: Example of images in the Dataset.

The gathered images lack diversity and size, and some are noisy. A sizable portion of the dataset was anticipated to be used to create the model. There are training and testing sets of the rearranged photos. Because the object of interest should be present in various sizes, locations, and lighting conditions, there should be a lot of information accessible for the model to perform properly during the evaluation (testing) stage.

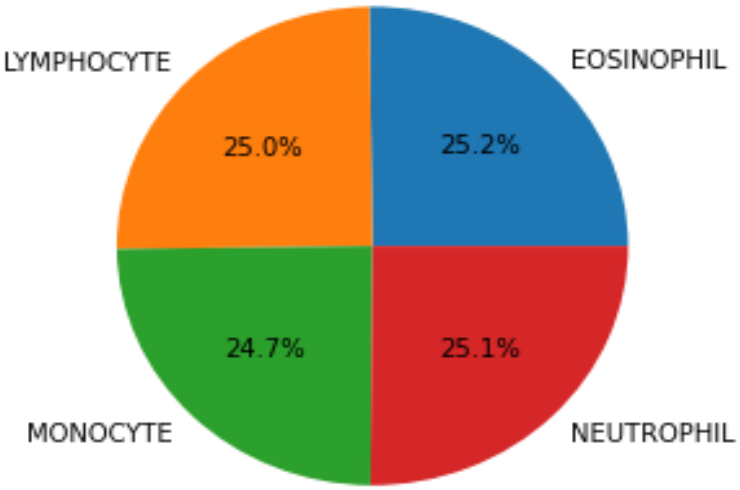


Figure 3: Proportion of Dataset

3.3 Image Pre-processing

Pre-Processing includes dealing with incorrect properties, one-hot encoding, standardization, scaling the data, reordering the data, and so on. Three different RGB components were used to address the images. Red, green, and blue variation part photos were initially explored. Pictures are being pre-handled to produce better grouping outcomes[13]. This work performed image pre-handling through image reading, image resizing, image dimming, noise reduction (Denoise), and morphology (smoothing edges). Tiny photos that are obtained have turmoil because of extravagant stains and manual mediation [14]. The majority of the bustle here is caused by shadows of cores.

Our area of interest is the platelet core, thus we filter images to remove distracting movements and recover important ones [15]. In the suggested review, the modified data obtained through highlight selection is first standardized, and after rearranging it, It is separated into sets for testing and preparation. The dataset is divided into 20% for model testing and 80% for model preparation [16].

3.3.1 Image Enhancement Technique

One of the primary strategies in image research is regarded to be picture upgrading. The prime goal of image enhancement is to improve the image's quality and aesthetic appeal or to offer a superior transform representation for automated future image management. It improves the clarity of images for human evaluation by removing noise and concealing, enhancing distinctiveness, and spotting subtleties. Because of its high effectiveness and straightforwardness, histogram equalization out is a typical differentiation improvement procedure in picture handling [18]. It is one of the more complicated strategies for changing a picture's dynamic reach and difference by changing it to such an extent that its power histogram takes on the ideal shape. A nonlinear cycle known as histogram equalization out is designed to showcase picture brilliance in a way that is particularly suitable for human visual inspection.[19,20]. Histogram balance anticipates altering an image to produce one with a compliment histogram, in which all levels are conceivable. In this procedure, an image is divided into smaller images, and histogram equalization is done for each smaller image and square independently. By that time, isolating or bilinear interference has limited the hindering artifacts among surrounding blocks[22].

3.3.2 Contrast Limited Adaptive Histogram Equalization

Development of the adaptive histogram equation (AHE), contrast limited adaptive histogram equalization (CLAHE) contributes to upgrading contrast in the image by broadening the image's forcefulness range or implementing a stretching out mechanism at the image's greatest frequent potency efficacy.

Compared to AHE, CLAHE was an improvement. Using the CLAHE method, a picture is divided into tiles, or logical sections. Each logical area's histogram is created, and cutting is carried out at predetermined esteem. The histogram containers are divided up again according to the cut sum. This histogram is the first histogram's modified type. This approach lessens the problem of over-improvement and addresses the edge-shadowing effect of AHE. CLAHE has demonstrated its success in improving clinical images with limited distinction. Cut histogram constraint and size of the context-oriented locale are the criteria for CLAHE that should be taken into account. The CLAHE yield may be affected by these boundaries. By rearranging the used dim characteristics, this tactic makes hidden aspects of the image more obvious[21]

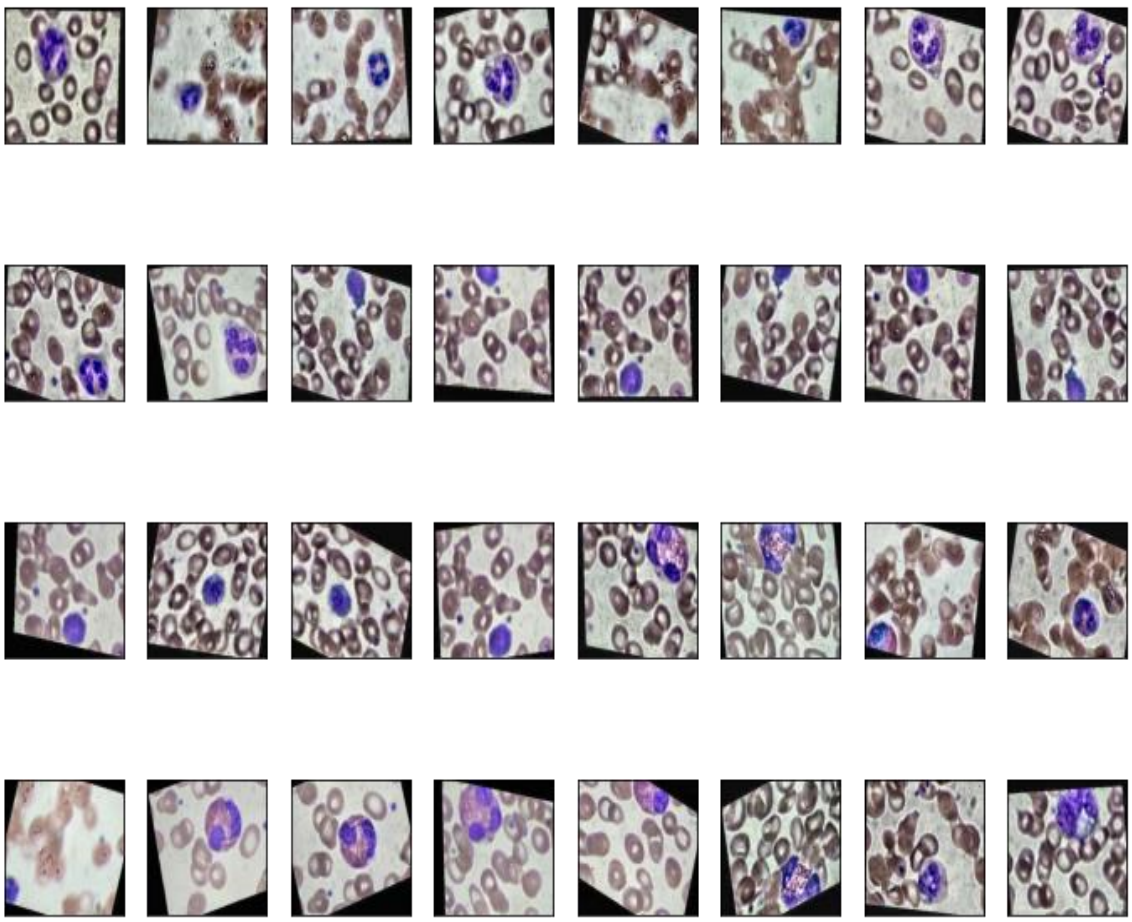


Figure 4. Example of after applying Contrast-enhanced technique CLAHE

Unsupervised learning, on the other hand, differs from prior learning in that there are no labels in the training set. The ability of the network to decrease or increase a related cost function typically determines success. In any event, it is important to remember that the majority of procedures involving image-intensive pattern recognition rely on categorization using supervised learning

3.4 Convolutional Neural Network

The initial step is to characterize CNN engineering and its preparation which normally relies upon the application and kind of information. Layers of the design are input layer that characterizes the picture size to the CNN. The upcoming layer is called the convolution layer, and it is made up of the neurons that connect different parts of the image or layers that came before it[23]. The convolutional layer advances the items localized by these areas after reviewing the image. Convolutional and ReLU layers are sandwiched with a standardization layer to speed up preparation interactions and reduce responsiveness.

To improve preparation and accelerate learning, the smaller-than-normal cluster is removed from the actuation, and the scaled-down bunch standard deviation is divided (Iqbal et al., 2018). The ReLU layer is a nonlinear initiating capability used for convolution and bunch standardization after edge activity, where every component with a value below zero is set to zero [25].

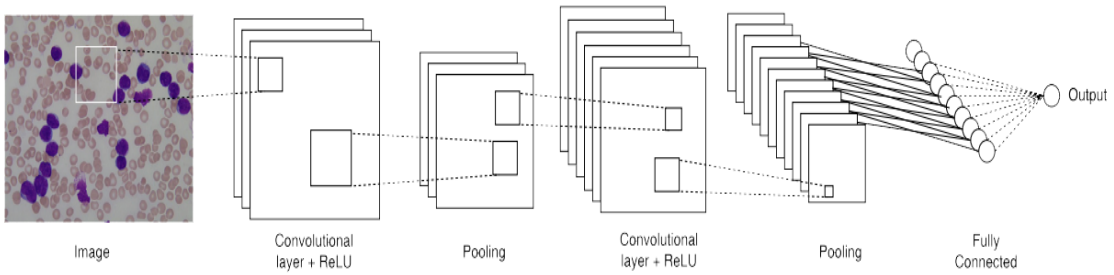


Figure 5: A simple architecture of Convolutional Neural Network.

3.4.1 Convolutional Layer

Neurons act as element-removing units in the convolution layer, the main layer responsible for handling the image. The rudimentary structural component of a CNN, the convolutional layer, is where a large portion of calculation lay hold of place. Input data, a channel, and a component map are the three components needed. We can anticipate that the information will be presented as a variety pictures, which is a 3D network of pixels. This suggests that the information will have three components that correspond to RGB in a picture: a level, a width, and a profundity. We also have a component indication, also known as a piece or a channel, which will traverse the picture's open fields and determine whether the element is there. An example of this cycle is a convolution. A two-layered (2-D) cluster of loads that addresses a portion of the image is the element finder. The responsive field's size is also determined by the channel size, which is typically a 3x3 framework, however they can vary in size [24]. A spot item between the information pixels and the channel is then established when the channel has been applied to a particular area of the image. The outcome exhibit is then handled with regard to this spot item. Once the section has cleared throughout the entire image, the channel moves by one step and repeats the cycle. A component map, initiation map, or convolved highlight is the final outcome of a series of spot items from the information and the channel. Boundary sharing, when the loads in the component locator move across the image, keeps them constant. During preparation, a few limits, including the weight values, change as a result of backpropagation and inclination plunge. However, before the brain network preparation process begins, three hyperparameters that affect the volume size of the outcome should be established. These consist of: 1. The **number of filters** influences the profundity of the result. 2. The part's **stride** is the amount of pixels it travels over the info grid. 3. **Zero-Padding** is frequently used when the channels don't match the information picture. This reduces to zero all elements that are outside of the information grid, increasing or measuring the yield [25]. There are three varieties of padding: **Valid padding, Same padding, Full padding** Two convolution layers with softmax as its actuation capabilities are available in the suggested model, and a pooling layer comes after them.

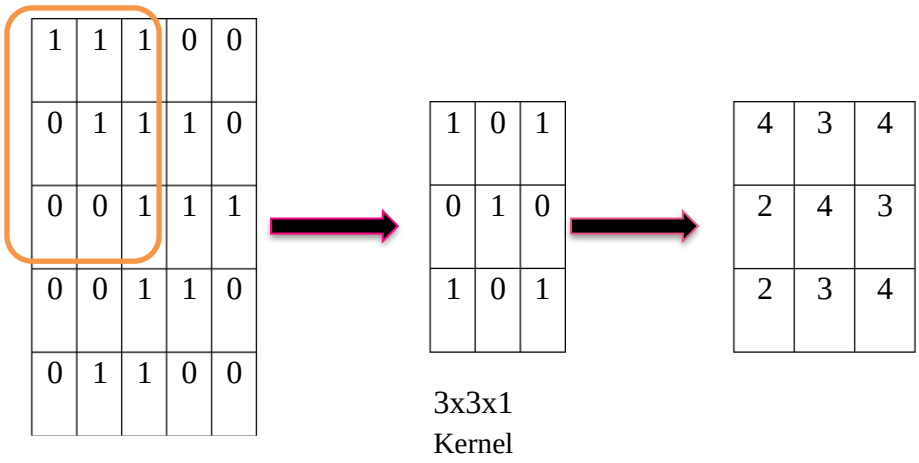


Figure 6: A 3x3x1 convolved feature resulted from the convolving of a 5x5x1 picture with a 3x3x1 kernel.

3.4.2 Maxpool Layer

The pooling layer, which frames a non-straight down-testing layer, is another important concept in CNNs. This model makes use of the maximum pooling non-straight capability, which divides the image into non-covering sections and produces the highest value for each such area. The pooling layer's main purpose is to minimize the number of boundaries., the amount of calculation carried out within the organization and overfitting [26]. The most effective CNNs start by max-pooling layers along with sections of two-dimensional (2-D) data that are spread horizontally with a step of two. This supports the profundity size to its usual size while also reducing the actuation plot depressed to 25% of the fascinating area

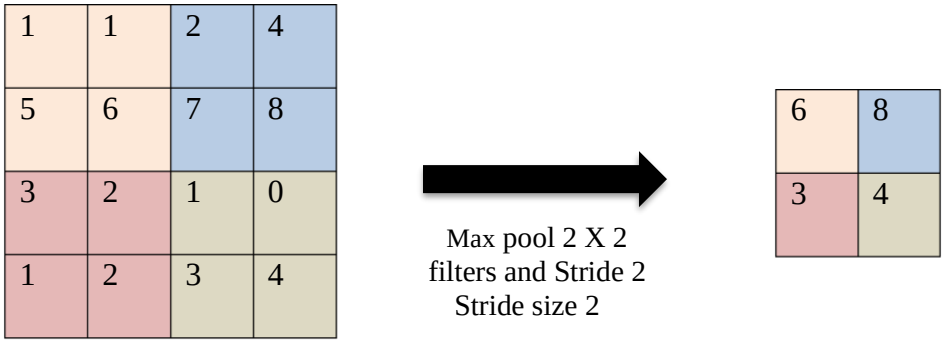


Figure 7: Max Pooling Layer Representation using Hyperparameters 2 X 2 filters and Stride size 2

There are only two often recognized methods for max-pooling because of the pooling layer's terrible behavior. The step and channels of pooling layers are often both fixed to2 × 2, allowing the layer to spread out over the entire spatial dimensions of the data. Anywhere Instead of using covered pooling, the step is corrected to 2 using a bit size fix in step 3. Consuming a portion north of 3 will often essentially diminish the presentation of the prototype due to the catastrophic manner that pooling behaves.

3.4.3 Fully Connected Layer

Full-associated layer's name accurately describes what it is. As previously mentioned, the info picture's pixel upsides are slightly associated layers and are not directly linked to the outcome layer. However, in the fully associated layer, each hub in the result layer directly associates with a hub in the previous layer. Taking into account the materials that have been removed through the previous layers and their various pathways, this layer carries out the task of characterization. While ReLu capabilities are typically used by convolutional and pooling layers, FC layers typically rely on a softmax enactment capacity to properly organize inputs and produce a likelihood ranging from 0 to 1.

3.5 Transfer Learning

With transfer learning, a model can be developed on an open, validated dataset and then applied to a related task that might contain unlabeled data.Transfer learning is typically utilized in artificial intelligence systems because designing a system to handle a different task would require a significant amount of resources.Trading this data saves having to retrain a second model to get a comparable outcome.Overall, transfer learning is used:

- To avoid having to plan numerous artificial intelligence models for the same task without any planning, saving time and resources.
- 2. As a means of reducing the amount of resources needed in computer-based intelligence tasks like image classification or conventional language processing.
- To invalidate a lack of checked, ready-to-use data that a relationship has by employing pre-planned models.

Transfer learning refers to using the pertinent components of a prepared artificial intelligence model to solve a new, conceptually similar problem. Whether or not the initiatives are identical, the need for a further model that takes new preparedness data into account may be necessary. Transfer learning is a tactic that can be used to address this problem.. The current review is utilizing vainglorious CNN models such as VGG16, Resnet50, and InceptionresnetV2 in view of deep learning. The fundamental reason for utilizing pre-prepared CNN models have the advantage of being faster and easier to prepare than CNN models created using arbitrarily presented loads Our network is trained for the CNN feature using Adam Optimizer[26].

3.5.1 VGG16

Karen Simonyan and Andrew Zisserman offered the VGG16 model at Oxford University. The convolutional brain network used in ILSVR, the Keras VGG16 as a vision model's design. The key factor with regard to VGG16 is that it will focus on the convolution layers rather than a broad border. Convolution and max pool layers, which were dependable throughout the design, are the processes it is using. It's making reference to the 16 levels that have loads in them. A staggering amount of boundaries will be present in the Keras VGG16 network, which is extraordinarily large. Python datasets are used to perform it. VGG16 has a total of 21 layers, 13 convolutional layers, 5 max pooling layers, and 3 thick layers, but only 16 of the max pool layers are weight layers, or learnable boundary layers. It makes use of the same max pool layer and cushioning of 22 channels from step 2, as well as 33 channel convolution layers from step 1 as well. Throughout the entire engineering process, it stays on this route of convolution and maximum pool layers. 64 channels make up the Conv-1 Layer, which is followed by 128 filters in Conv-2, 256 filters in Conv-3, 512 channels in Conv-4, and 512 channels in Conv-5. Three fully associated (FC) layers are present after a stack of convolutional layers; Although the third performs 1000-way ILSVRC characterization and as a result, has 1000 channels, the first two have 4096 channels apiece (one for each class). The final layer is the delicate max layer. An RGB image with a fixed size of 224 x 224 is the contribution to the Conv 1 layer.

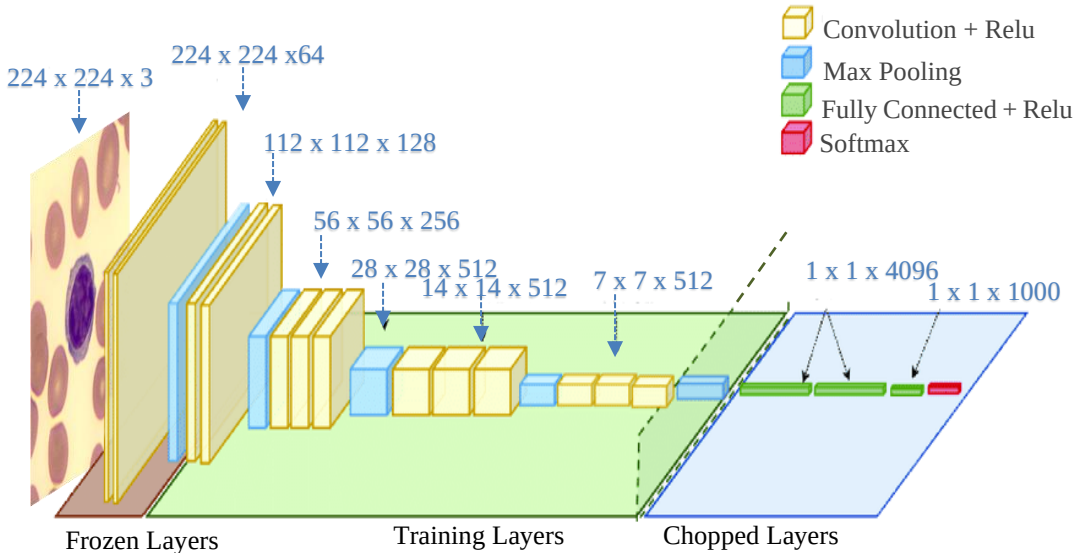


Figure 8: Architecture of VGG16

3.5.2 Resnet50

The Residual Neural Network (ResNet) by Kaiming debuted at the ILSVRC 2015 He and his collaborators created a unique architecture that uses extensive batch normalization and "skip connections." In addition to one MaxPool and one Normal Pool layer, the ResNet50 model variation has 48 Convolution layers. It consists of 3.8 x 109 Drifting focuses tasks. Each 2-layer block in the 34-layer net is shifted using a 3-layer bottleneck block, creating a 50-layer ResNet with a fixed info image size of 224 by 224 pixels.

3.5.3 InceptionResnetV2

Commencement Using more than 1,000,000 images from the ImageNet data set, ResNet-v2 is a convolutional neural network. With 164 layers of the organization, it can categorize images into 1000 different types of objects, including the console, mouse, pencil, and various animals. So, for a lot of photos, the organization has learned rich component depictions. The company's image input size is 299 by 299 pixels, and the result is a

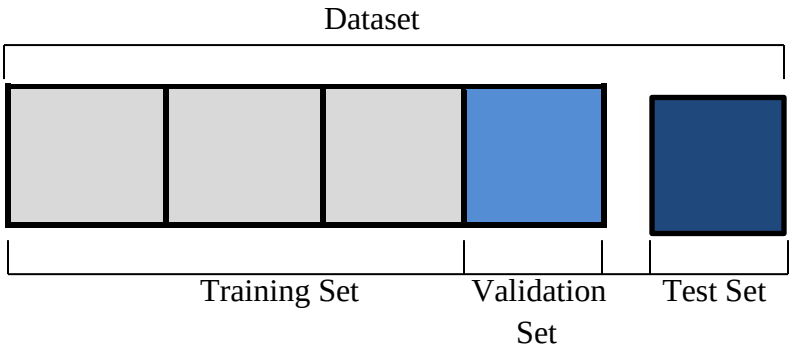
rundown of assessed class probabilities [26]. The Origin structure and the Remaining association are combined to form it. Numerous measured convolutional channels are connected with enduring relationships in the Commencement Resnet block.

Table 1. Deep learning models (Pre-trained)

Model	**Number Of layers**
VGG16	16 layers
InceptionResnetV2	164 layers
Resnet50	50 layers

3.6 Training and Testing

The information gathered for preparing should be parted into three unique sets: training, validating and test. The total dataset consists of 12,444



Training: 80 percent of the complete dataset is utilized for preparing. The model learns on the preparation set; at the end of the day, the set is utilized to dole out the loads and inclinations that go into the model. 9955 images are used for training.

Validation: 10% of the information is used during model construction to assess initial accuracy, monitor the model's evolution over time, and modify hyperparameters. The model does not use approval information, although viewing it, to determine its loads and inclinations. 1245 images used for validating.

Test: 10 percent of the information is used for definitive evaluation.Because the model has never seen this dataset, it is free of all bias. 1244 pictures used for testing.

Table 2. Distribution of the WBC Dataset

Cell Types	**Train 80%**	**Validation 10%**	**Test 10%**
Eosinophil	2496	312	311
Lymphocyte	2483	310	310
Monocyte	2479	311	311
Neutrophils	2499	310	310

CHAPTER 4
Experimental Results and Discussion

4.1 Results and Discussion

The images are collected from Kaggle and after that, we preprocessed them to remove noise, resize, and segment. For automatic detection and categorization of its subclasses, a pretrained VGG16 was used. We examined various training outcomes obtained from the data set in which the RGB-colored input image was.

We used deep learning to detect and classify WBC subtypes using CNN architecture. Additionally, the VGG16, ResNet50, and InceptionResnetV2 CNN architectures are used in this experiment. VGG16 achieved the highest accuracy (98.21%), followed by ResNet50 (80%), and InceptionResnetV2 (96.91%). To assess the test's validity, we offer many methods and confusion metrics. The confusion matrices include the grades for true positive, true negative, false positive, and false negative. To mete the accuracy of the model's prediction, the values are placed in the diagonal of the confusion matrix.

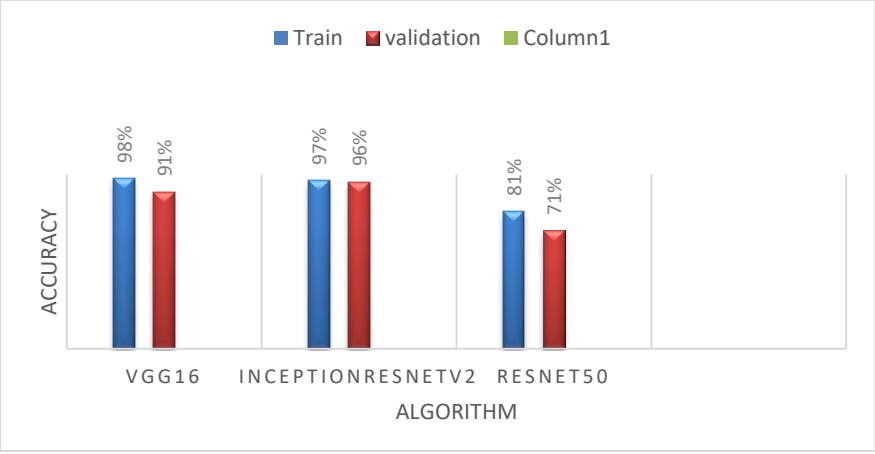


Figure 9: Train and Validation the Accuracy of different Transfer Learning Architecture

Based on the confusion matrices, the following equation is used to determine Accuracy, Recall, Precision, and the F1Score.

The following equation is used to determine F1 score based on the confusion matrix (i-iv)

$$\text{For Accuracy} = (\text{TP} + \text{TN})/(\text{TP} + \text{TN} + \text{FP} + \text{FN}) \quad \text{(i)}$$

$$\text{For Precision} = \text{TP}/(\text{TP} + \text{FP}) \quad (ii)$$

$$\text{For ecall} = \text{TP}/(\text{TP} + \text{FN}) \quad (iii)$$

$$\text{F1 Score} = 2 \times (\text{precision} \times \text{recall})/(\text{precision} + \text{recall}) \quad (iv)$$

4.2 Performance Metrics:

One of the crucial phases in creating a successful machine learning model is evaluating its performance. Performance metrics show us how well our model has done given the available data. By adjusting the hyper-parameters, we can make the model perform better. Performance metrics assist measure how well a machine learning (ML) model generalizes on new or previously unexplored data. To evaluate the performance of a classification model, different metrics are used, and some of them are as follows:

o Accuracy

o Precision o Recall

o F-Score

o AUC (Area Under the Curve)-ROC

o Confusion Matrix

4.2.1 Accuracy:

One of the simplest Classification metrics to use is accuracy, which is calculated as the proportion of accurate predictions to all other predictions.

4.2.2 Precision:

The accuracy metric's limitation is overridden by the precision metric. The fraction of positive predictions that were accurate is determined by precision. It can be measured as the True Positive, or the proportion of total positive forecasts that come true (True Positive and False Positive).

4.2.3 Recall:

It is comparable to the Precision metric and attempts to determine the percentage of actual positives that were mistakenly detected. It can be measured as a True Positive, or forecasts that actually match the overall number of positives, either correctly forecasted as positive or wrongly anticipated as negative (true Positive and false negative).

4.2.4 F1 score:

A binary classification model is evaluated using the F1 Score metric based on the predictions provided for the positive class. With the use of Precision and Recall, it is calculated. It is a particular kind of score that combines Precision and Recall. As a result, the F1 Score can be determined by taking the harmonic mean of both precision and recall and giving each variable equal weight.

TABLE 3. Matrics performance Of CNN Architecture

Architectures	Average Precision	Average Recall	Average F-1 score	Support
VGG16	0.93	0.93	0.92	1244
Resnet50	0.79	0.78	0.69	2487
InceptionResnetV2	0.90	0.90	0.89	1215

4.2.4 Confusion Matrix:

A tabular representation of the ground-truth labels and model predictions is called a confusion matrix. The instances in a predicted class are represented in each row of the confusion matrix, and the instances in actual classes are represented in each column.

Table 4: Confusion matrics

Architectures	**Predicted** **Actual**	EOSINOPHIL	LYMPHOCYTE	MONOCYTE	NEUTROPHIL
VGG16	EOSINOPHIL	278	1	0	50
	LYMPHOCYTE	0	309	4	4
	MONOCYTE	0	3	292	9
	NEUTROPHIL	20	1	2	271
	Predicted **Actual**	EOSINOPHIL	LYMPHOCYTE	MONOCYTE	NEUTROPHIL
Inceptionresnet V2	EOSINOPHIL	280	0	4	35
	LYMPHOCYTE	2	311	1	0
	MONOCYTE	0	2	289	2
	NEUTROPHIL	10	0	6	273
	Predicted **Actual**	EOSINOPHIL	LYMPHOCYTE	MONOCYTE	NEUTROPHIL
Resnet50	EOSINOPHIL	520	0	1	102
	LYMPHOCYTE	3	596	10	11
	MONOCYTE	282	11	168	159
	NEUTROPHIL	0	0	11	479

4.2.4.1 Confusion Matrix for VGG-16:

After applying the VGG16 algorithm to the dataset we find that there are 278 Eosinophils detected, 309 Lymphocytes detected, 292 Monocytes detected and 271 Neutrophil detected.

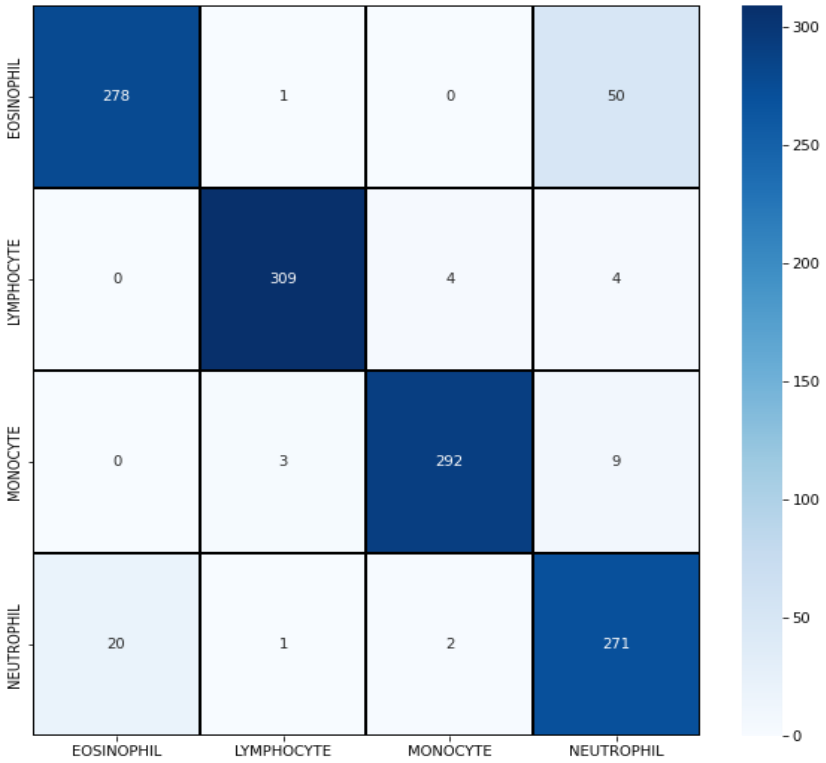


Figure 10: VGG16 (Confusion Metrics)

4.2.4.2 Confusion Matrix for InceptionResnetV2:

After applying the InceptionResnetV2 algorithm on the dataset we find that there are 280 Eosinophils detected, 311 Lymphocytes detected, 289 Monocytes detected and 273 Neutrophil detected.

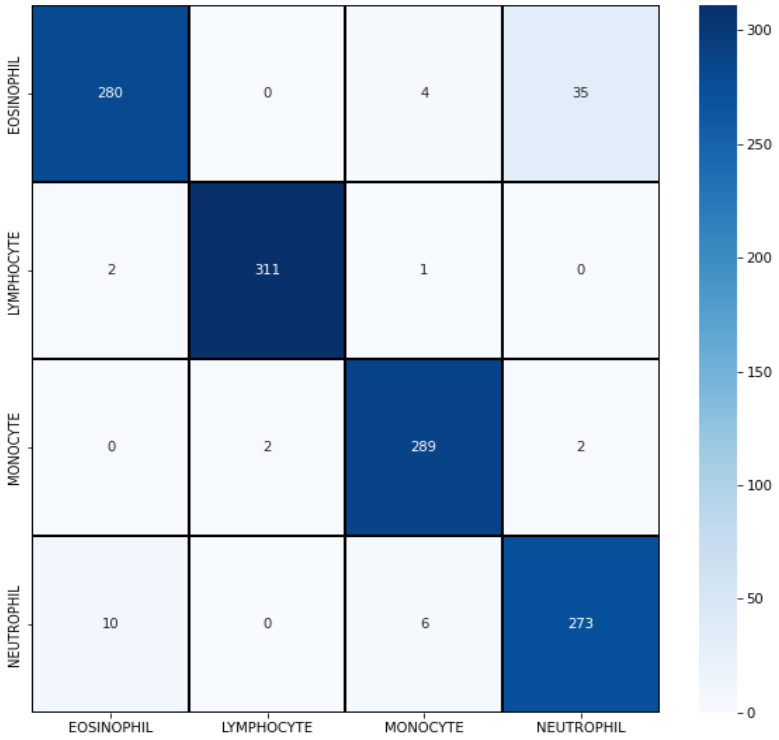


Figure 11: InceptionResNetv2 (Confusion Metrics)

4.2.4.2 ResNet34:

In this figure, we see that there are two portions of confusion metrics. One is validation confusion metrics and another is validation confusion metrics. In train confusion metrics we observed that 520 Eosinophils, 596 Lymphocytes, 168 Monocytes, and 479 Neutrophil have been detected. In train confusion metrics we observed that 2803 Eosinophils, 2035 Lymphocytes, 1421 Monocytes, and 2119 Neutrophil have been detected.

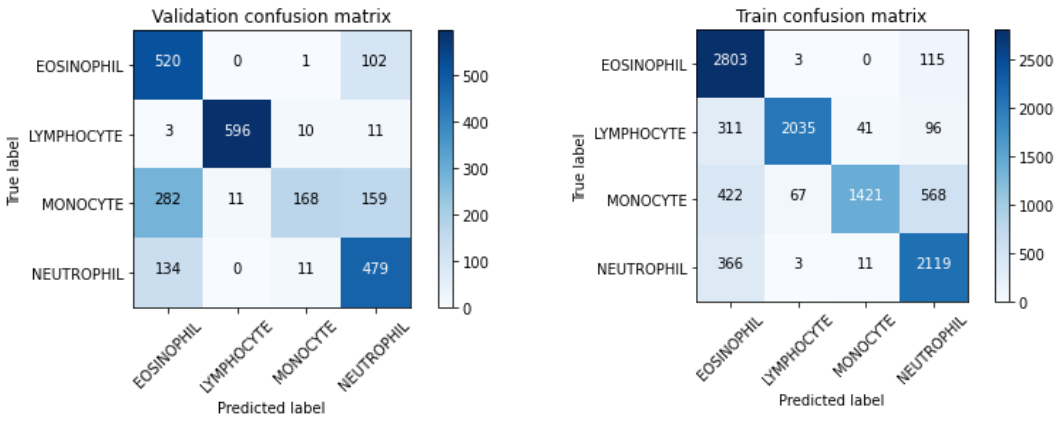


Figure 12: ResNet50 (Confusion Metrics)

4.3 Validation Accuracy:

The validation accuracy is simply the proportion of cases that are categorically accurately predicted, hence the Val acc could be higher in the case where all positive cases receive scores of 0.51 and all negative cases receive scores of 0.49, but the validation loss may be subpar in this case.

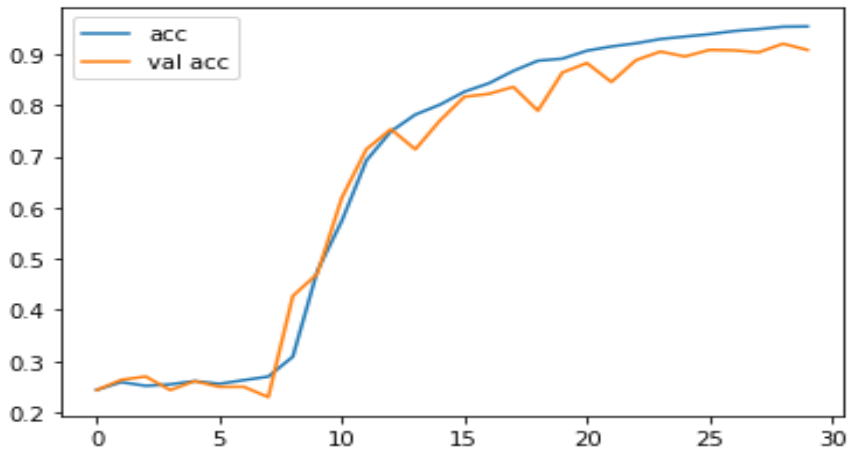


Figure 13: Validation Accuracy

4.4 Validation loss:

A deep learning model's performance on the validation set is evaluated using a statistic called validation loss. The dataset's validation set is a section set aside to check the model's efficacy. Similar to the training loss, the validation loss is determined by adding the errors for each example in the validation set.

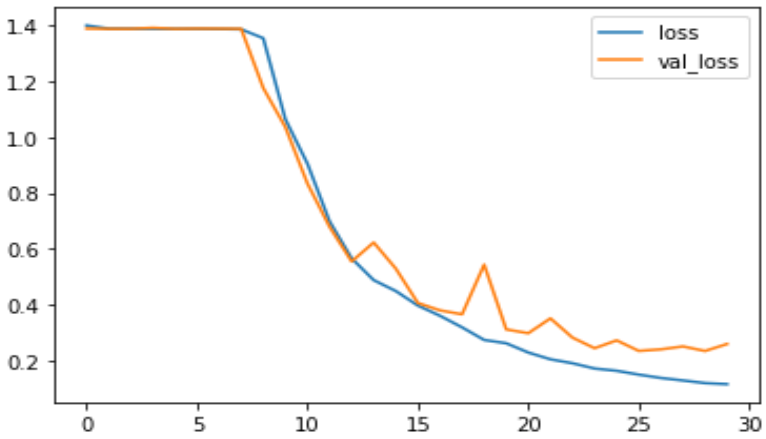


Figure 14: Validation Loss

4.5 Comparative Analysis

It is crucial to quantify the importance of the research. For this purpose, several of its mechanisms are compared to related research efforts that are visible in table 5.

For the Classification of WBCs subtypes, a variety of machine learning methods like KNN, CNN, and CNN + RNN (Recurrent Neural Network) were used. Compared to RNN (Recurrent Neural Network) achieved 90.97% [19], CNN achieved 91.01% [8] accuracy, KNN was significantly better, with 93.29% [12] accuracy. They employed machine learning after using the data and methods. Our proposed method is VGG16, which achieved 98% accuracy and the accuracy is comparatively high.

TABLE 5: COMPARATIVE ANALYSIS

Problem Space	Algorithm	Accuracy	References
classification	KNN	93.29%	[12]
classification	CNN	91.01%	[8]
classification	CNN + RNN (Recurrent Neural Network)	90.97%	[19]
classification	**VGG16**	**98%**	**Proposed Model**

CHAPTER 5
Conclusion and Future Work

5.1 Conclusion

In order to aid professionals in medical diagnosis, we proposed in this study an intelligent using deep-learning system for the automatic finding of microscopic images. The goal is to automatically identify and categorize each object in the image. To prevent the overfitting issue while lowering the training time and assisting the model's improved generalization, various regularization, transfer learning, and data augmentation strategies were used. One of the most promising deep learning techniques for real-world image classification applications is transfer learning. In this study, transfer learning is utilized to categorize images of WBCs using a variety of pre-trained models. In this article, three (VGG16, InceptionResnetV2, Resnet50) potent pre-trained models with two optimization techniques are compared. On the WBCs dataset, all three models had good classification accuracy, but the VGG16 model beat the others.

5.2 Future Work

This model will be used in more classes, including various diseases, in further research.

Additionally, greater data collection will enhance the deep learning model's training, and the outcomes provided in this research demonstrate the effectiveness of deep learning models in automatically classifying WBCs.

Some non-traditional optimization methods such as Particle swarm optimization, and genetic algorithms have recently attracted a lot of attention in the literature as ways to improve the parameters of deep learning models.

Our ongoing research will concentrate on using these optimization techniques to improve deep learning models on a bigger dataset of WBCs.

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