*2023 IEEE International Conference on Blockchain and Distributed Systems Security (ICBDS)*
*Naya Raipur, India. Oct 6-8, 2023*

# Classification of Acute Lymphoblastic Leukemia Using MobileNet and EfficientNetB3

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***Abstract*— Computer vision and deep learning are widely used in health care. Acute Lymphoblastic Leukaemia (ALL) is a severe form of malignancy that affects the body's white blood cells. An early and precise diagnosis of ALL is critical for successful therapy and improved patient outcomes. In this project, the effectiveness of deep learning techniques including MobileNet and EfficientNetB3 are explored in conjunction with data augmentation for the classification of Acute Lymphoblastic Leukemia (ALL) using C-NMC Leukemia Classification Dataset. The approach of this project involves generating augmented data using various techniques such as flipping, rotating, and zooming to remove data imbalance in a dataset. After that split the data into training and testing data and then fine-tune the MobileNet and EfficientNetB3 models on the trained data, and evaluate the performance of both models using testing data based on recall, accuracy, F1score, precision, and Area Under Curve.**

***Keywords—MobileNet, Acute Lymphoblastic Leukemia(ALL), EfficientNetB3, Deep Learning, Data Augmentation, Microscopic images.***

## I. INTRODUCTION

ALL is a type of blood and bone marrow cancer that affects both children and adults. It is defined by an overabundance of immature white blood cells known as lymphoblasts[11], which interfere with the production of regular blood cells. ALL symptoms include exhaustion, frequent infections, bone aches and pains, and easy bruising or bleeding. ALL can be lethal if not treated.

The current standard of care for ALL diagnosis consists of a battery of testing, including a physical examination, blood tests, and bone marrow assays. In the bone marrow test, a small sample of bone marrow is extracted and analysed under a microscope for the presence of abnormal cells.. This procedure, however, can be intrusive, time-consuming, and pricey. Furthermore, the accuracy of the diagnosis is dependent on the pathologist examining the samples.

In recent years, deep learning algorithms have attracted increasing attention for medical image analysis, including leukemia detection. Deep learning, a type of machine learning, searches for and recognizes patterns in data using artificial neural networks. Deep learning techniques have demonstrated promise in a variety of fields, including object recognision, image classification, and natural language processing.

Here, we propose a classification model for the classification of ALL using two popular architectures, MobileNet and EfficientNet. The MobileNet architecture is designed for efficient processing on mobile devices, making it ideal for deployment in a mobile application for rapid diagnosis. The EfficientNetB3 architecture is a deeper and more complex model that has shown strong performance in image classification tasks. To improve the performance of our models, we employ data augmentation techniques, which can be used to overcome the data imbalance in the dataset. This can aid in the prevention of overfitting and increase the model's ability to generalize to fresh data. The suggested model has the potential to considerably enhance the accuracy and efficiency of ALL diagnoses, especially in resource-constrained settings with limited access to experienced specialists. It could also provide a valuable tool for screening individuals at high risk for ALL, allowing for earlier detection and treatment.

### *A. Scope*

- The Scope of Our Project is Only for the Classification of Acute Lymphoblastic leukemia (ALL).
- To find Acute Lymphoblastic Leukemia(ALL) disease using deep learning models like efficientnetb3, mobile net, etc.

### *B. Objectives:*

The list of this project's main goals:

- To develop a classification model for the classification of Acute Lymphoblastic Leukemia(ALL) using MobileNet and EfficientNetB3 architectures.
- To compare the performance of the suggested models in detecting ALL to existing techniques.
- To employ data augmentation techniques to remove data imbalance in the dataset and improve the model's accuracy.
- Determine the best method among MobileNet and EfficientNetB3 based on accuracy, precision, Area under ROC, etc.,

## II. RELATED WORKS

This section lists the different literature reviews that are used as references. By using deep learning and image processing methods, a unique hybrid feature extraction strategy was

Developed in [1]. The suggested process entails two steps: first, a region of interest (ROI) is chosen using the Cyan, Magenta, Yellow, and Key-moment localization methodology, and then a feature fusion method based on convolutional neural networks is used to elicit Deep Learning-based features. In this work, leukocytes from Acute myeloid Leukemia patients and non-malignant controls were employed as part of the morphological dataset known as AML_Cytomorphology_LMU.18,365 images that were expertly labeled and obtained from blood samples of 100 AML patients were included in the dataset. The proposed

2023 IEEE International Conference on Blockchain and Distributed Systems Security (ICBDS) | 979-8-3503-3376-3/23/$31.00 ©2023 IEEE | DOI: 10.1109/ICBDS58040.2023.10346455

approach recognized 15 different forms of WBC, including normal and AML malignancy cells. To speed up computation and boost model precision, hybridization, and parallelization methodologies could be applied in further development of the proposed model.

The methodology used in [2] to classify ALL using Deep Convolutional Neural Networks (DNNs). The classification uses images from the American Society of Haematology's (ASH) online image repository. By using pre-trained Convolutional Neural Network AlexNet as well as LeukNet accuracy of 94.12% is reached in differentiating B-cell and Tcell ALL images. In this comparison of three distinct training algorithms' classification performances as well. The limited dataset employed in the study is one of its limitations, and to make up for it, data augmentation techniques were applied to prevent overfitting. Further research can be conducted by testing with other Leukemia patients in order to identify and classify additional types and subtypes of Leukemia. The study only sought to classify ALL.

The primary purpose of this study [3] is to create a classification model for atypical Acute Myeloid Leukaemia White Blood Cells based on their distinguishing characteristics. The augmentation model is a revolutionary strategy in the field of artificial intelligence (AI) for tackling the problem of an imbalanced number of WBC in blood samples. The hybrid models employed in this project are deep convolutional autoencoder (DCAE) and geometric transformation (GT). Furthermore, by combining White Blood Cells segmentation and this study creates a robust learning paradigm by using deep learning to extract context-free atypical WBC features. The "two-stage DCAE-CNN model" (DCAECNN) was developed as a hybrid multiclassification strategy for splitting atypical White Blood Cells into 8 separate subgroups.

The methodology used in [4] can be used to help in break-bone fever detection, It is advised that the peripheral blood smear (PBS) screening be automated to aid in dengue diagnosis. In order to identify platelets and to check whether the platelets count in blood is too low or not (thrombocytopenia).from the PBS images, an automation system was built. Moreover, a method based on machine learning is presented to identify dengue from PBS pictures based on the lymphocyte nucleus. The nucleus of both normal and dengue containment is used to extract ten features. With accuracy rates of 93.62% apiece, Decision Tree (DT) and Support Vector Machine (SVM) outperformed all other classifiers in terms of performance. The future scope might include features derived from the cytoplasm of lymphocytes in addition to nucleus features. Pre-trained CNNs will eventually be used in this study for categorization reasons.

Classifying WBCs in [5] using the traditional method, which requires visual interpretation of blood smear images, takes a long time, and is prone to errors. A better hybrid technique for accurate subtype classification of WBC is presented in this research. Deep feature extraction is performed first using enhanced and segmented data. To generate WBC images, transfer learning is used on already-trained deep neural networks like Darknet53 and DenseNet201. The Proposed method uses entropy-controlled deep feature optimization for white blood cell classification which is a novel approach and can potentially lead to improved accuracy. It is highly expensive because of its extensive feature set, it has high processing and implementation costs.

Quantifying unbalanced classification algorithms for leukaemia detection is the topic of [6]. The fine-grained diversity of the cell, including b-lymphoid progenitor cells and imbalanced data points make automatic classification problematic. They analyze several state-of-the-art (SOTA) deep learning techniques in this study to handle the imbalanced classification challenges. In order to address the problem of an imbalanced class, this experiment uses input, generative adversarial networks (GANs), and loss-based techniques. In terms of specificity, accuracy, F1 Score, and sensitivity, and the suggested method beats previous state-of-the-art methods, demonstrating its potential for usage in clinical settings. It lacks detail on the feature extraction process used for leukemia detection.

The methods utilized in [7] on Using Multiscale Information Fusion Capabilities to Aid Leukaemia Diagnosis through White Blood Cell Segmentation. Manual WBC assessment techniques are time-consuming, arbitrary, and inaccurate. To address these difficulties, They present a WBC segmentation multi-scale information fusion network (MIF-Net). MIF-Net separates and propagates boundary information on several scales in order to fuse external information. In a network, multi-scale information fusion aids in the retention of boundary information and increases segmentation performance. Multiscale information fusion techniques can help improve the accuracy of leukemia diagnosis by combining information from different sources and scales, which can improve the overall performance of the segmentation process. But its implementation can be expensive, especially if it requires specialized hardware or software.

In [8] they use the ALL_IDB2 dataset for the diagnosis of Acute Lymphocytic leukemia by extracting features through deep learning techniques. Leukemia detection decisions can benefit greatly from the use of image-based automated diagnostic tools. They classify the leukocytes for luekaemia diagnosis by developing a fine-tuned feature extractor of the VGG16 model named “LeuFeatx”, which is important for accurate leukocyte classification The learned features and filters are displayed and compared to the underlying features of VGG16 model. The use of LeuFeatx can reduce the time required for diagnosis, as it can analyze and classify images quickly. But its accuracy depends on the quality of the images used for analysis. Poor-quality images may lead to an incorrect diagnosis.

## III. MATERIALS AND METHODS

### *A. Dataset Description*

The work utilizes the C-NMC Leukemia Classification dataset from Kaggle. The "Leukemia Classification Dataset" (also known as the "C-NMC Leukemia Classification" dataset) is a collection of medical images of blood cells for the purpose of classifying Acute Lymphoblastic Leukemia (ALL) vs. normal Hematopoietic cells (HEM). A total of 10,132 blood cell images are included in the collection, of which 2,253 are labeled as HEM and 7,879 are labeled as ALL. Fig1 and Fig2 show the blood cell images of ALL-affected and healthy people, respectively.

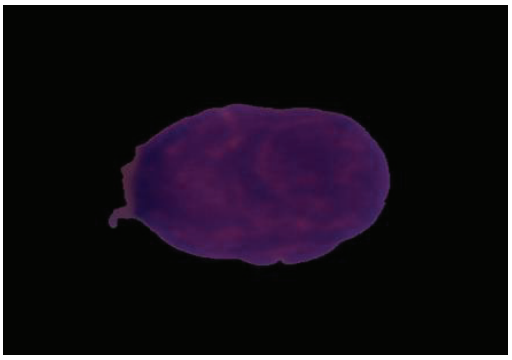

Fig. 1. Microscopic Blood image from an ALL-affected person.

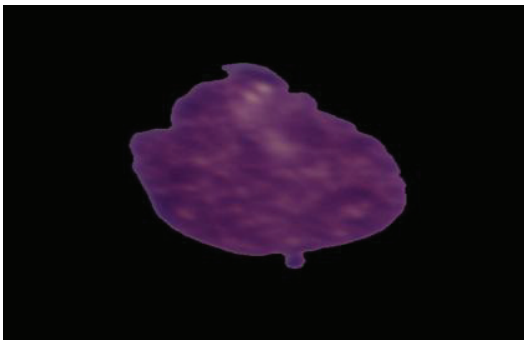

Fig. 2. Microscopic image of blood cells from a healthy person

## B. Proposed Methodology

The process flow diagram shown in figure 3 represents the overall step-by-step process of the done in the project. It involves the collection of datasets to display the end result to the user.

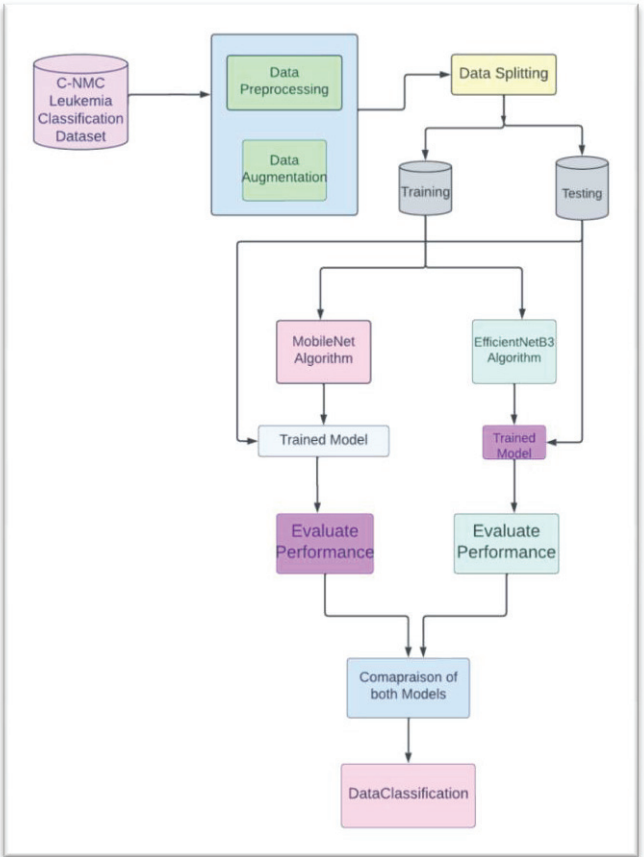


Fig. 3. Proposed System

### 1) Data Preprocessing

Data preprocessing typically involves steps such as resizing, normalizing, and standardizing the images, handling missing values, data augmentation, and performing any necessary feature engineering. Here in this Project, we use Data Augmentation as a Preprocessing method.

#### a) Data Augmentation

Data augmentation is a deep learning and machine learning technique that entails applying different changes to the current data to expand the size and diversity of a dataset. These transformations include flipping, rotation, scaling, cropping, and adding noise. Here C-NMC Leukemia Classification dataset is first augmented by rotating the image and extracting the edges to overcome the data imbalance problem in the dataset.

$$i' = (i - ci) * \cos() - (j - cj) * \sin() + ci$$

$$j' = (i - ci) * \sin() + (j - cj) * \cos() + cj$$

The coordinates of a pixel in the original image are represented by (i, j) in the preceding formulas, and the coordinates of the corresponding pixel in the rotated image are represented by (i', j'). The cos() and sin() functions compute the cosine and sine of the rotation angle. The image in the accompanying figure has been rotated by -90 degrees.

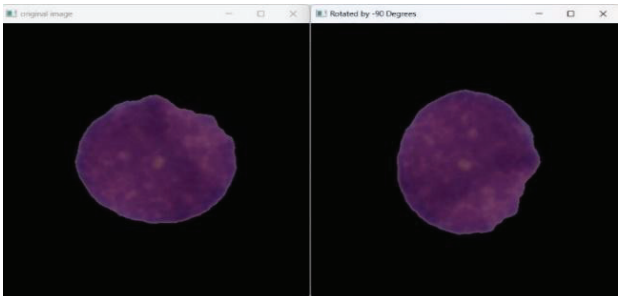

Fig. 4. Original image with Augmented image

### 2) Model Building And Training

For the Classification of Acute Lymphoblastic Leukemia, we explore two pre-trained deep-learning models.

#### a) Mobile Net Algorithm

MobileNet is an architecture shown in Figure 4 that was developed for embedded and mobile devices with constrained computing power. It achieves a good balance between accuracy and model size by using depthwise separable convolutions.

In the context of image processing, MobileNet takes an input image and extracts feature from it using a sequence of convolutional layers. Convolutional layers discover patterns in images by using filters (also known as kernels).

MobileNet's first layer is a conventional convolutional layer that applies a to generate a set of feature maps, apply a collection of filters to the input image. Each filter searches the image for a certain pattern, such as edges or corners.

MobileNet employs depthwise separable convolutions after the initial convolutional layer. A depthwise separable convolution employs two types of filters: depthwise and pointwise convolution.

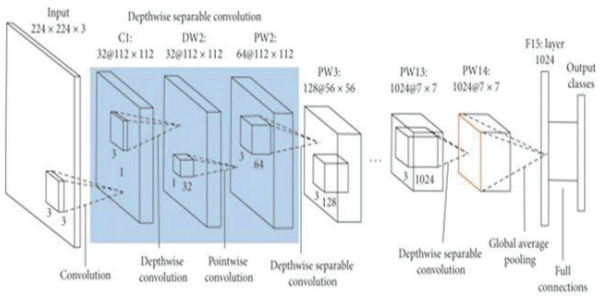


Fig. 5. MobileNet Architecture[9]

A single filter is applied to each individual input channel through the depthwise convolution method. And then the depthwise convolutions are combined by the pointwise convolutions method, which results in a set of learned weights. This approach reduces the number of model parameters while maintaining a reasonable level of accuracy.

MobileNet also uses skip connections, which allow information to flow directly from early layers to later layers. This helps to preserve low-level image features while allowing higher-level features to be learned.

Once the convolutional layers have extracted features from the image, the output is fed into a fully connected layer, which produces the final output of the network. This output can be used for a variety of tasks, such as classification or object detection.

*b) Efficientnetb3 Algorithm*

EfficientNetB3 is a specific variant of the EfficientNet family of convolutional neural network (CNN) architectures. It is known for its impressive performance in image classification tasks while maintaining high efficiency in terms of model size and computational cost.

Each image is fed as input to the EfficientNetB3 model. The size of the input image should be compatible with the input dimensions specified by the model architecture. EfficientNetB3 applies a series of convolutional and pooling layers to extract hierarchical features from the input image. These layers use filters and non-linear activation functions to capture many levels of information, beginning with low-level features like edges and textures and progressing to high-level semantic representations.

EfficientNetB3 employs depthwise separable convolutions, which divide the convolution operation into two steps: a depthwise convolution that processes each input channel individually and a pointwise convolution that combines the depthwise convolution outputs.

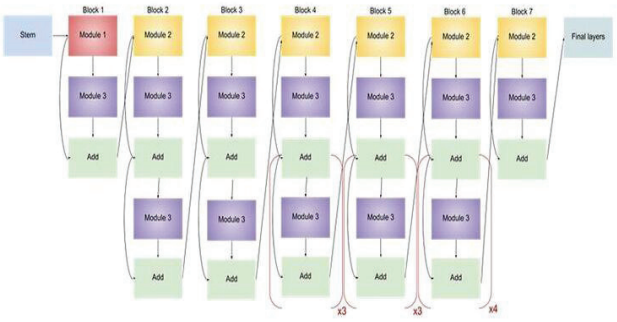


Fig. 6. EfficientNetB3 Architecture[10]

Following the convolutional layers, EfficientNetB3 employs global average pooling to compute the spatial average of each feature map, yielding a fixed-length feature vector. The feature maps' spatial dimensions are reduced while their depth is preserved by this pooling technique. These layers convert the retrieved characteristics into a classification-ready structure by learning complicated patterns and relationships between them. The final fully connected layer links the learnt features to the project's goal classes, which in this case are two:leukemia-positive and leukemia-negative

*3) Hyperparameter Tuning*

Selecting the optimal hypermeters which classify the data correctly is known as hyperparameter tuning. Hyperparameters[12] are parameters that are set before the training process and are not learned from data. They define the behavior and configuration of the learning algorithm and can have a substantial impact on the model's performance and generalization. Here we consider batch size, learning rate, and no of epochs as hyperparameters.

Batchsize=40

No of epochs=5

*4) Model Evaluation And Comparison*

Evaluate the performance of both models and Compare their results based on recall, accuracy, F1score, precision, and area under ROC

$$Pr = \frac{a}{a+b}$$
$$Rc = \frac{a}{a+c}$$

*F1SCORE=2(Pr*Rc)/(Rc+Pr)*

Where a=TruePositive

b=FalsePositive

c=FalseNegative

Pr=PRECISioN

Rc=Recall

*5) Develop A GUI*

Develop a GUI using either EfficientNetB3 or MobileNet Models. A Graphical User Interface facilitates the user to upload the microscopic image of a blood cell to know whether he/she has ALL cancer or not as shown in Figure16. If the user has a cancer then it outputs the class label as ALL otherwise it outputs as HEM.

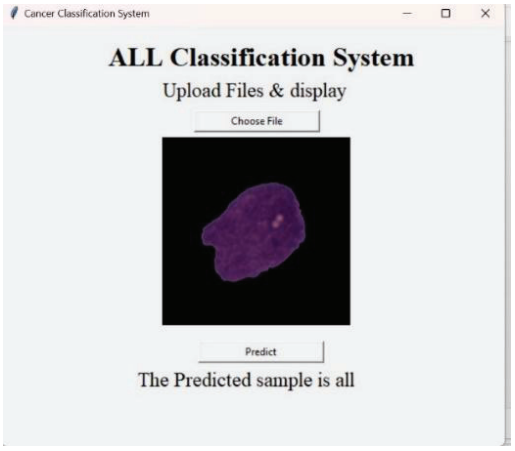


Fig. 7. GUI for ALL Classification System

## IV. RESULTS AND ANALYSIS

The Classification of Acute Lymphoblastic Leukemia Using MobileNet and EfficientNetB3 project yields several important results and analyses. Firstly, classification accuracy is the primary metric indicating the model's effectiveness in classifying whether the person has ALL. After running the MobileNet and EfficientNetB3 models for 5 epochs we got an accuracy of 93.849 and 93.835 respectively. The Confusion matrix breaks down right and incorrect classifications in great detail. MobileNet model classifies 1284 correctly and 316 wrongly. whereas the EfficientNetB3 classifies 1422 images as correct and 178 images as wrong. Comparing the algorithms EfficientNetB3 and MobileNet based on Precision, recall, and F1-Score, metrics offer insights into the model's performance on a per-class basis. we also Compare the two algorithms using Area under the ROC curve. we got 0.83 and 0.95 area under ROC for MobileNet and EfficientNetB3 respectively. During training, EfficientNetB3 takes more time than MobileNet. Evaluating the model's generalization through a separate test set ensures robustness.

### *A. Classification By Mobilenet*


Fig. 8. MobileNet accuracy-epoch during training


Fig. 9. MobileNet loss-epoch during training

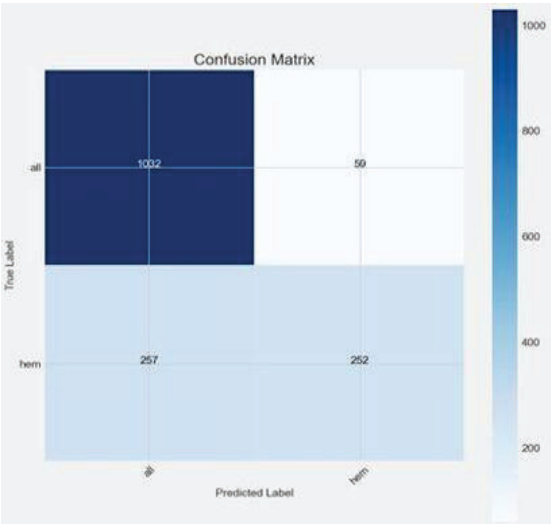


Fig. 10. Confusion matrix for MobileNet

| | precision | recall | f1-score | support |
|---|---|---|---|---|
| all | 0.80 | 0.95 | 0.87 | 1091 |
| hem | 0.81 | 0.50 | 0.61 | 509 |
| accuracy | | | 0.80 | 1600 |
| macro avg | 0.81 | 0.72 | 0.74 | 1600 |
| weighted avg | 0.80 | 0.80 | 0.79 | 1600 |

Fig. 11. Classification report for MobileNet

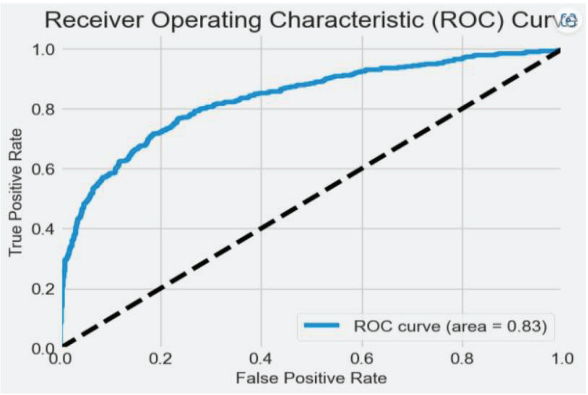


Fig. 12. ROC Curve for MobileNet

### *B. Classification By Efficientnetb3*

After training the EfficientNetB3 model up to 5 epochs the results will be shown in Table-2

TABLE I. EPOCHS OUTPUT FOR MOBILENET

| Epochs | Loss | Accuracy | Va_Loss | Va_Acc | L.R | Next L.R | Moniter | %Improve | Time |
|---|---|---|---|---|---|---|---|---|---|
| 1/5 | 5.032 | 80.126 | 4.27751 | 66.291 | 0.00100 | 0.00100 | Accuracy | 0.00 | 944.12 |
| 2/5 | 2.497 | 87.121 | 4.23228 | 54.284 | 0.00100 | 0.00100 | Accuracy | 8.73 | 1302.10 |
| 3/5 | 1.504 | 89.480 | 14.65653 | 32.270 | 0.00100 | 0.00100 | Accuracy | 2.71 | 1296.73 |
| 4/5 | 0.961 | 91.718 | 8.07500 | 68.981 | 0.00100 | 0.00050 | Val_loss | -90.80 | 1306.91 |
| 5/5 | 0.676 | 93.849 | 3.11371 | 79.612 | 0.00050 | 0.00050 | Val_loss | 26.43 | 966.68 |

TABLE II. EPOCHS OUTPUT FOR EFFICIENTNETB3

| Epochs | Loss | Accuracy | Va_loss | Va_acc | L.R | Next L.R | Moniter | %Improv | Time |
|---|---|---|---|---|---|---|---|---|---|
| 1/5 | 5.244 | 81.989 | 3.64189 | 73.671 | 0.00100 | 0.00100 | Accuracy | 0.00 | 31559.83 |
| 2/5 | 2.608 | 89.038 | 2.03579 | 85.241 | 0.00100 | 0.00100 | Accuracy | 8.60 | 6418.93 |
| 3/5 | 1.521 | 91.651 | 1.21611 | 88.618 | 0.00100 | 0.00100 | Val_loss | 40.26 | 7363.56 |
| 4/5 | 0.948 | 92.656 | 0.83599 | 87.867 | 0.00100 | 0.00100 | Val_loss | 31.26 | 6950.24 |
| 5/5 | 0.617 | 93.835 | 0.59562 | 88.180 | 0.00100 | 0.00100 | Val_loss | 28.75 | 7682.97 |


Fig. 13. EfficientNetB3 accuracy-epoch plot during training

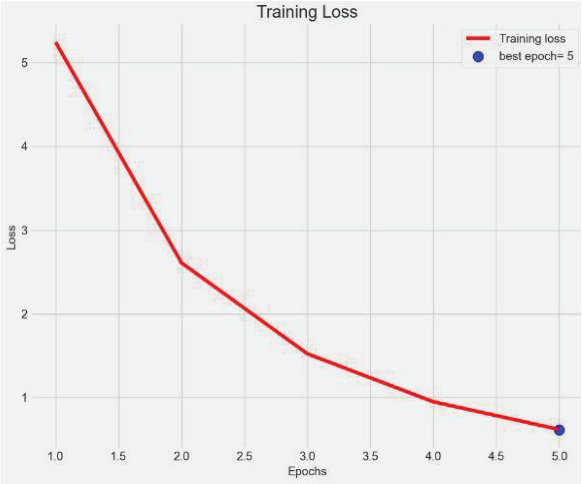


Fig. 14. EfficientNetB3 Loss-epoch plot during training

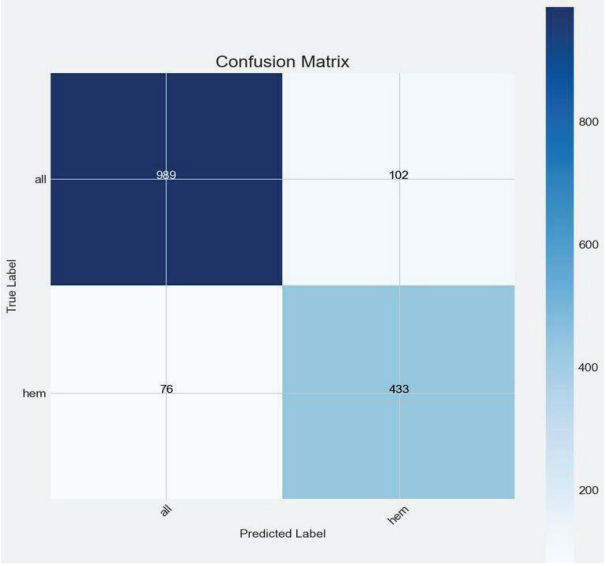


Fig. 15. Confusion Matrix for EfficientNetB3

| | precision | recall | f1-score | support |
|---|---|---|---|---|
| all | 0.93 | 0.91 | 0.92 | 1091 |
| hem | 0.81 | 0.85 | 0.83 | 509 |
| accuracy | | | 0.89 | 1600 |
| macro avg | 0.87 | 0.88 | 0.87 | 1600 |
| weighted avg | 0.89 | 0.89 | 0.89 | 1600 |

Fig. 16. Classification Report for EfficientNetB3

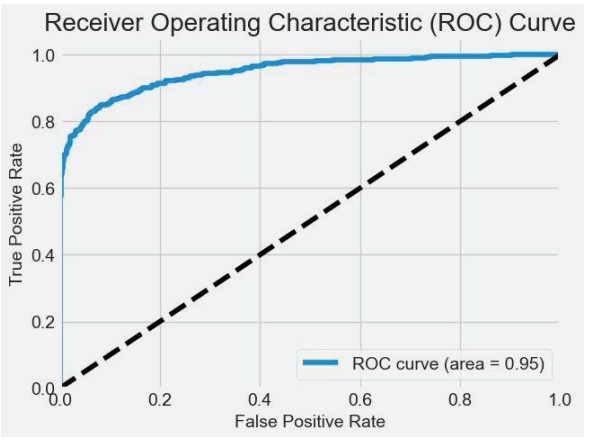


Fig. 17. ROC Curve for EfficientNetB3

## V. CONCLUSION & FUTURE WORK

The primary purpose of this project is to create Deep Learning Methods, such as MobileNet and EfficientNetB3, that will be used to classify acute lymphoblastic leukaemia (ALL) using microscopic images of blood samples. This project's methodology comprises producing Data Augmentation in order to broaden and diversify our training set.

The future scope could involve the severity of detecting ALL into normal or high and it can also be extended for the detection of other types of leukemia which includes , Chronic lymphocytic leukemia (CLL), Acute Myeloid LeukemiaChronic myelogenous leukemia (CML)

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