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Acute Lymphoblastic Leukemia Classification: Deep Learning Techniques for Blood Diseases Diagnosis

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Abstract: The most common types of blood cancer is Acute Lymphoblastic Leukemia. The procedures used to treat it is very costly and time taking. Images from peripheral blood smears serve as an early detection of acute lymphoblastic leukemia (ALL) disease for the blood sample. The manual collection of PBS images for the diagnosis of cancer contains some errors due to certain factors such as interoperability errors and human fatigue. Advanced techniques have surpassed handmade and conventional approaches for the solution of classification of images. In this paper, tuned EfficientNetB3 model used to classify ALL with its subtypes, is considered for the experiments. The model is developed using the dataset that is publicly available on Kaggle. It noticed that the observed performance through the classification on EfficientNetB3 model exceeds expectations, demonstrating an accuracy of 99.84%. One could argue that the proposed approach may assist in differentiating among various classifications of ALL and in establishing the appropriate diagnostic procedures for healthcare professionals in laboratory settings.

Keywords: Blood Diseases; NN Models; Leukemia

1. Introduction

Leukemia is a hematologic malignancy that originates in the bone marrow and disrupts normal blood cell production. The classification of leukemia cells plays very important role in the identification and treatment of blood cancer. The conventional methods for cell classification rely heavily on the manual analysis conducted by trained pathologists. The traditional approaches used before were computationally expensive and prone to error. However, recent advancements in the field of deep learning (DL) and medical image processing [15-17], are classification cells and their treatment of leukemia. Many deep learning algorithms classified the images. These algorithms use neural networks including layers to do the classification. These algorithms had remarkable success in various tasks, including classification and relationships. These models have displayed higher accuracy compared to traditional. DL image processing hold potential for advancing research in cancer diagnostics in the classification of leukemia cells.

The classification is primarily based on the 2016 World Health Organization system, factors such as the percentage of blasts of cells or leukemia cells, as well as the predominant lineage of the malignant cells. Researchers have focused on replicating the workflow of hematologists by detecting white blood cells (WBCs), excluding crushed cells, and conducting final classification steps. These studies achieved

outstanding performance in the detection and classification of WBCs associated with leukemia diagnosis, with DL techniques surpassing an accuracy rate of 82%.

Many researchers are working on the identification and classification of the leukemia cells. This will speed up the process of diagnosing the victims of cancer. Different microscopic image datasets are being used in the classification of leukemia cells according to the type of cells of this disease. Leukocytes have different types of cells. Leukemia have also different types, shown Fig. 1.

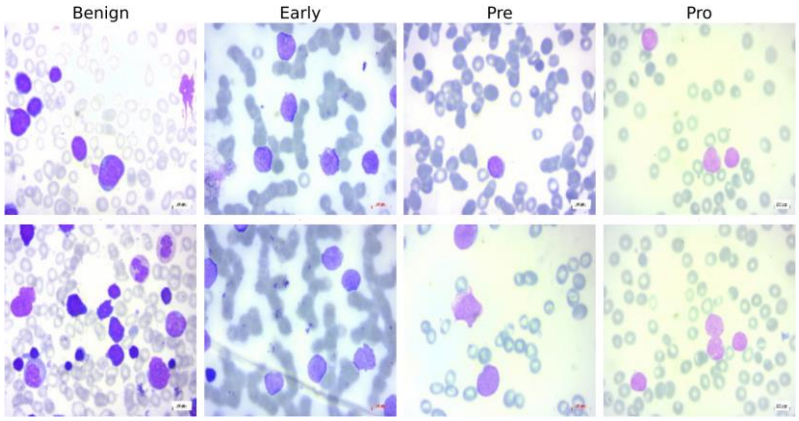


Figure 1. Some samples from ALL dataset

This study is to get maximum accuracy rate of classification of leukemia cells using a deep convolutional network [1, 2] are main objectives. There are many recent studies conducted for the classification of leukocytes using ML and DL algorithms.

The image dataset we used in the classification of leukemia cells is of acute lymphoblastic leukemia. The images within the dataset were prepared within the confines of the bone marrow laboratory located at Taleqani Hospital in Tehran, Iran, consists of 3256 PBS images that are obtained suspected 89 patients having ALL. This dataset is categorized into two classes, known as benign and malignant. The former class consists of hematogenous, latter comprises the ALL group, which is further broken down into 3 subtypes of malignant lymphoblasts: the first is Early Pre-B, second is Pre-B, and last one is Pro-B. Every image contained within the dataset was captured through a Zeiss camera, affixed to capable of 100x magnification. These images are then saved as JPG files. Different types and samples are shown Fig. 2.

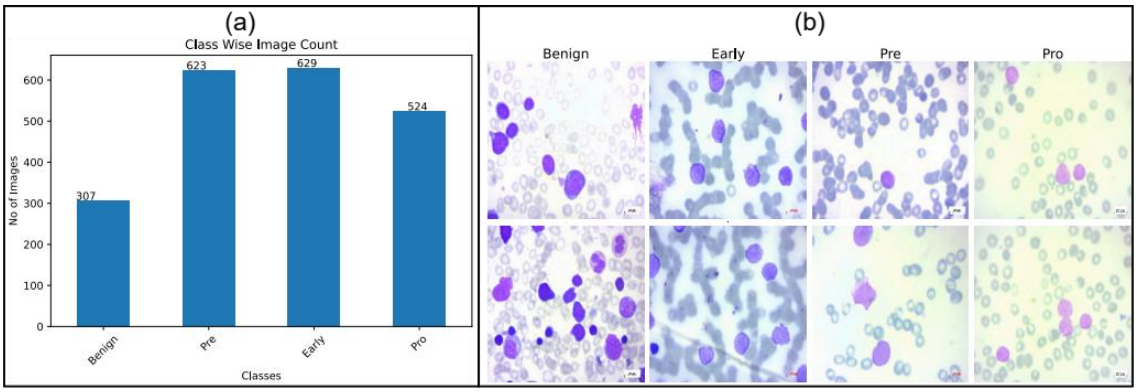


Figure 2. Class distribution and samples of datasets

2. Literature Review

In recent years, leukemia cell classification has been explored in many studies by using machine learning techniques. Different researchers have suggested different methods of diagnosis and detection of leukemia using both ML and DL approaches. These methods aimed to improve the diagnosis performance of leukemia by analyzing microscopic images of blood cells. DL and ML models, such as CNNs and SVMs, are commonly applied in many research works.

The process of leukemia classification usually involve multiple steps, including data preprocessing, segmentation, extraction of features, selection of features, and final classification. Data scientists has been working on health-related datasets for many disease. The data mostly collected by medical professionals and further analyzed by researchers. A number of works has been proposed for the classification and

identification of leukemia disease, which helps to make the diagnosis process faster. However, the results of different studies are not always comparable because of variations in techniques and datasets used.
In one study, CNN was used to identify leukemia subtypes from microscopic blood images, achieved 88.25% accuracy for leukemia datasets from normal cases and achieved 81.74% for multi-class classification of subtypes [3]. Another research focused on the diagnosis of acute lymphoblastic leukemia using an improved CNN model on peripheral blood smear images [4]. In this study, the authors used a modified ResNet50 CNN model which achieved a high accuracy of 99.65% [4]. However, researchers also proposed various techniques to standardize datasets and improve outcomes further.

Optimized CNN is discussed another study using C-NMC Leukemia to detection of leukemia. It achieved 99.99% accuracy on C-NMC-Leukemia, to detect normal or affected cells, it was a binary classification [5]. This study [6], used understand convergence of training DNN for its classification. In the classification of 72 leukemia patients of bone marrow gene expressions. In this research, the two types of leukemia were classified, DNN model achieved 98.2%, 96.59% of sensitivity, and 97.9% of specificity. The authors in [7], they performed classification of acute type leukemia using automation techniques on multiple dataset. The dataset was used for binary automated classification of leukemia, which is considered as the main task of their research work. The proposed method acquire an accuracy of 97% using VGG 16 and 98% for DenseNet121 along SVM. In three class classification, an accuracy of 95% was acquired for ResNet50 along SVM [7]. DL Method for automated Leukemia Detection in real images was proposed using three different methodologies [8]. Researchers used transfer learning approach for three models to classify Images. Models includes CNN accuracy rate of 95.3%, MobileNetv2 accuracy rate of 97.6%, and Alex's Net accuracy rate of 81.6% [8].

The authors [9] introduce a method for segmenting and classifying white blood cells (WBCs) was suggested to help in detecting acute leukemia. This approach combines Otsu's automatic threshold with image enhancement and some arithmetic operations to segment WBCs. The classification of blast cells from normal lymphocytes was performed by using a K-Nearest Neighbors (KNN) classifier, are discussed in study [9]. The study [9] was tested on a set of 108 images from a public leukemia dataset, and it reached an accuracy of about 93%. In another work [10], WBC classification was performed using a technique based on Entropy-Controlled Deep Feature Optimization. This method was evaluated on a dataset that includes 5000 synthetic images representing five types of WBCs. The results showed a really high accuracy of 99.9%, which is quite impressive [10]. The study [11] was also a deep learning-based approach proposed specifically for classifying ALL. According to the experiments, the CNN-based model achieved around 97.78% accuracy. Similarly, another study [12] explored leukemia detecting and classifying using smear blood images.

3. Materials and Methods

Aim of proposed study is to classification of ALL using peripheral blood smear microscopic images. These images of blood smears is playing an important role in the early screening process, especially for detecting non-cancerous cases. The researchers give an idea towards the advancement of ML techniques in medical science field. The methodologies which were used in the research have following steps.

3.1. Data collection and image acquisition

The image dataset for the classification of leukemia cells belongs to acute lymphoblastic leukemia cases were used in study. The images in this dataset was prepared in the bone marrow laboratory at Taleqani Hospital, located in Tehran, Iran. There are total 3256 peripheral blood smear (PBS) images collected from 89 patients who were suspected to have Acute Lymphoblastic Leukemia. This dataset is divided into two classes: benign and malignant. The benign class contains hematogenous samples, while the malignant class includes ALL group, which is further divided into three subtypes of malignant lymphoblasts. These are named as Early Pre-B, Pre-B, and Pro-B ALL. Each image in dataset was captured using a Zeiss camera that was attached with microscope under 100x magnification. After capturing, saved in JPG.

3.2. Data Preprocessing

Data preprocessing is the step where data is cleaned and transformed so that it become usable for applying machine learning mode. First, the collected data checked for the missing labels and noise. Then, data paths with labels are then generated. Concatenation is performed of data paths with labels into a

DataFrame. Data loaders objects are created from the dataFrame to load the images in the dataset. At last, a batch display of 16 images to verify the dataset is prepared for the ML model.

3.3. Model Structuring and Training

Following are the steps of Model Structuring and Training:

3.3.1. Data Loaders

Data loaders ('dls') are used to load and preprocess data for model training. In machine learning, data divided into two parts; training and validation. Data loaders handle tasks such as loading images, applying transformations (like resizing or augmentations), and creating mini-batches for training. In experiments, 'dls' is previously defined as a loaded. For example, it could be created using 'ImageDataLoaders.from folder'from the fastai library, specifying the path to the data, train/validation folders, and any necessary transformations.

3.3.2. *Modified Deep Learning Model*

We used a model EfficientNetB3,with learner object learn created with the specified architecture (EfficientNetB3), data loaders dls, and metrics. fp16() is used to enable mixed-precision training, which can speed up training by using half-precision floating-point numbers. EfficientNet-B3 is a cost-effective model that utilizes three parameters to adjust depth, width, and resolution. The architecture of EfficientNetB3 shown Fig 3.

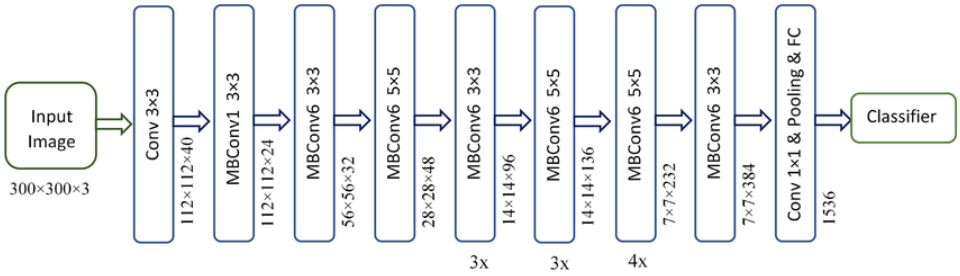


Figure 3. Architecture of EfficientNetB3 [13]

3.3.3. *Learning Rate Finder*

The lr find () method explored to find a best learning rate for training the proposed model. It increases the learning rate while monitoring the loss, helping to identify a range of learning rates where the model is learning effectively, is shown in Fig 4. Model being trained for fine tuning has 12278312 total parameters among which 1669376 are trainable parameters and 10608936 are non-trainable parameters which confirm that 13.60% of the parameters are being trained.

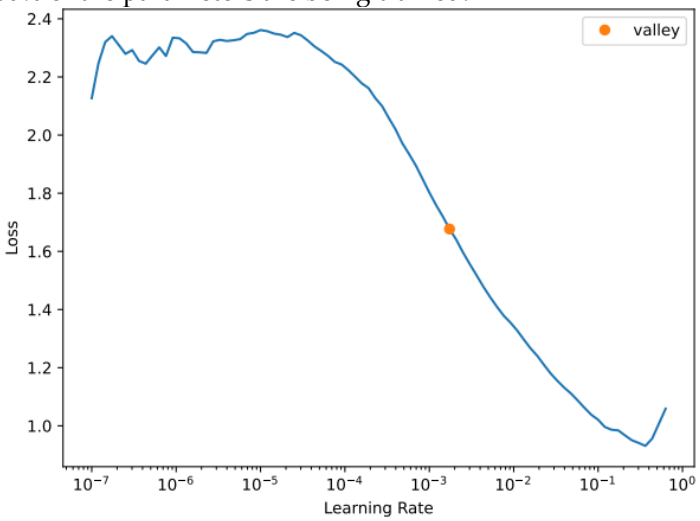


Figure 4. Learn Rate Tuner

3.3.4. Model Training (fit one cycle):

The fit one cycle method is used to train the model. This method uses the one-cycle policy. This policy involves updating the learning rate for the first half of training, then gradually down it to second half. It helps prevent over-fitting and under-fitting. A learning rate range was specified by parameters lr max=slice (1e-2, 1e-1).

3.3.5. Model Export (export)

Export method is used to save the trained model. It exports the model, which can be loaded later for further analysis. The line learn.export('/kaggle/working/leukemia model.pkl') exports the trained model to the specified path in the Kaggle working directory.

3.4. Model Evaluation Metrics

To check how well the proposed model performs, various evaluation metrics has been used in this study. These metrics help in understanding the accuracy and robustness of classification results from different perspectives.

- Accuracy – It measures how correctly the model predicted overall.
- Precision – This shows precision.
- Recall – It tells how many actual positive cases were identified by the model.
- F1-score – It is average of precision and recall, giving balance between the two.
- ROC Curve – It helps to visualize the trade-off rate between true positive and false positive.
- Confusion Matrix – It gives a summary view of prediction results for classification.
- Precision-Recall Curve – This curve shows how precision and recall change over different thresholds.
- Cohen's Kappa – It measures how much agreement there is between predicted and actual labels, beyond chance level.
- Matthews Correlation Coefficient (MCC) – It gives a balanced evaluation, especially helpful when classes are not balanced.
- F2 Score – Similar to F1-score, but gives more weight on recall side.

4. Results

Classification Experiment is performed on acute lymphoblastic leukemia stages, the EfficientNetB3 was utilized to achieve an impressive overall accuracy of 99.84% after 20 epochs.

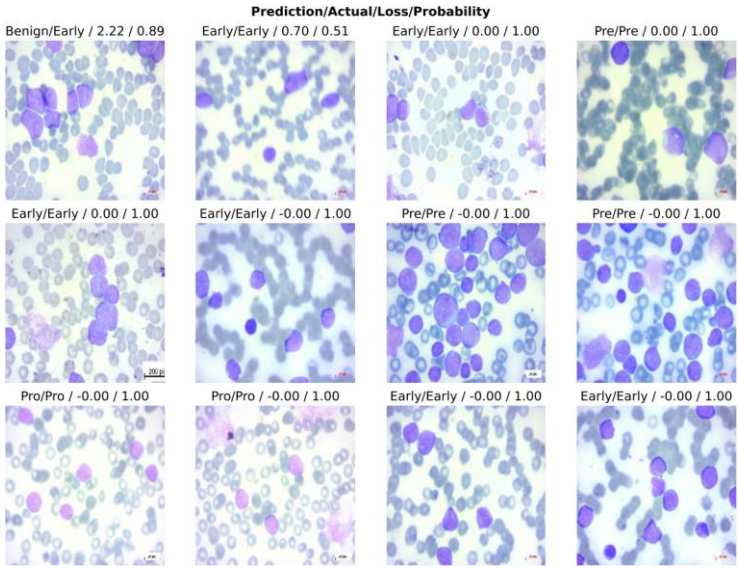


Figure 5. Predictions Results

The utilization of deep learning techniques, specifically Efficient-NetB3, showcased significant advancements ALL automated diagnosis, surpassing manual diagnostic efficiency and reducing the risks associated with late or inaccurate Diagnoses. Some predictions results are shown in Fig 5.

4.1. Evaluation Results

Following are the evaluation results of EfficientNetB3 on the dataset with a learning rate range specified by lr max=slice (1e-2, 1e-1). The highest accuracy rate of 99.84% achieved in the classification of ALL. Results Comparison are shown in table 1 below and Fig. 6 shown training and validation results.

Figure 7 shows the results using confusion matrix which is a table that shows how well a classification model is performing. Each row of the matrix shown the actual class of an item, and each column represents the class that the model predicted the item belonged to. Following is the confusion matrix of the Leukemia ALL dataset classification:

The graph plot provides a visual for outcomes obtained from an experiment, helping in the assessment of the efficiency of the model used in experiment. Following Figure 9, shows the graph plot of Leukemia ALL classification subtypes include error rate and accuracy achieved in the experiment. The multi-class ROC (Receiver Operating Characteristic) analysis shown in Figure 8 reveals exceptional performance by the classifier across all classes in the dataset. The ROC curves for each class are plotted, and all exhibit an AUC (Area Under the Curve) of 1.0, which is the highest possible value. This indicates that the model perfectly distinguishes each class from all others with no overlap between the positive class (the class in focus) and the negative classes (all other classes). An AUC of 1.0 means that for each class, model achieved 100% sensitivity and 0% False Positive Rate at some threshold, effectively making no errors in classification. This outcome suggests that the model is perfectly calibrated and has learned to separate the classes with complete accuracy. Such a result is often rare and may indicate either a well performing model on a well-separated dataset or potential overfitting. The model performs exceptionally on the training and validation sets but to maintain accuracy on out-of-sample data may fails.

Table 1. Evaluation Results Comparison of w.r.t Previous Studies

Model Used	Problem	Accuracy %
CNN [3]	Multiclass Classification of Leukemia Subtypes	81.74
Optimized ResNet50 [4]	Multiclass Classification of Leukemia ALL Types	99.65
OCNN [5]	Binary Classification of Leukemia (Present or Not)	99.99
DNN [6]	Classification of Bone Marrow Gene Expression	98.2
ResNet50, SVM [7]	Three-class classification of Leukemia	95
CNN,MbileNetv2, Alex's Net [8]	Automated Detection of Leukemia	95.3,97.6, 81.6
KNN [9]	Detect Acute Leukemia	85
Entropy-Controlled [10]	White Blood Cells Classification	99.9
CNN [11]	Classification of ALL	97.78
NN-SVM [14]	Automated Detection of Leukemia	98.8
KNN- Na¨ıve Bayes [15]	Automated Detection of Acute Leukemia	92.8
SVM-KMeans [1]	Acute Leukemia Classification	92
Proposed Method	Multiclass Classification of acute lymphoblastic leukemia subtypes	99.84

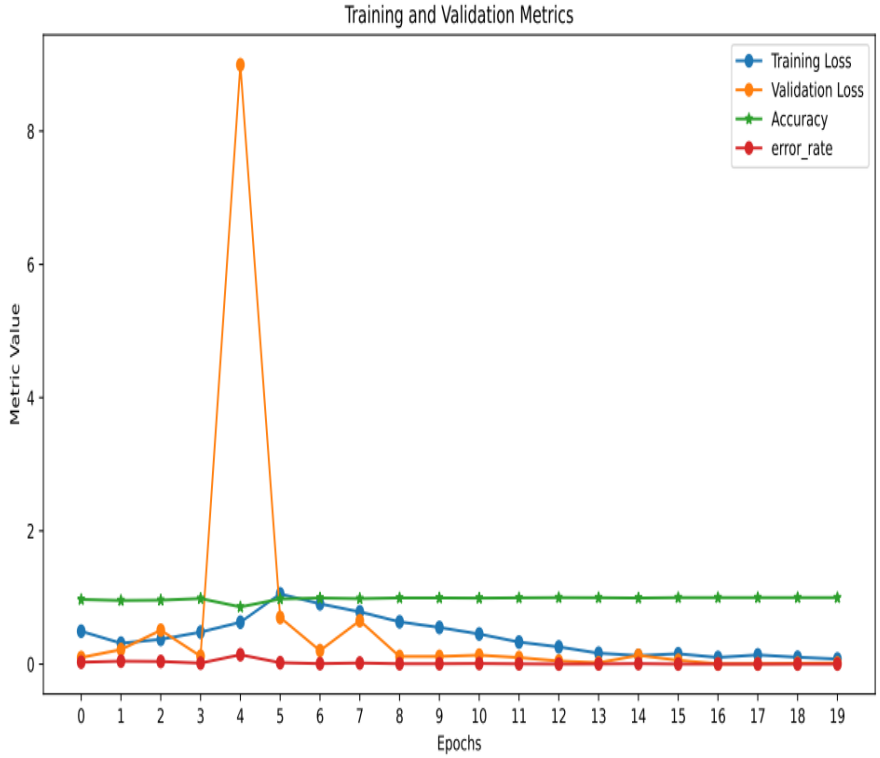


Figure 6. Training and validation results

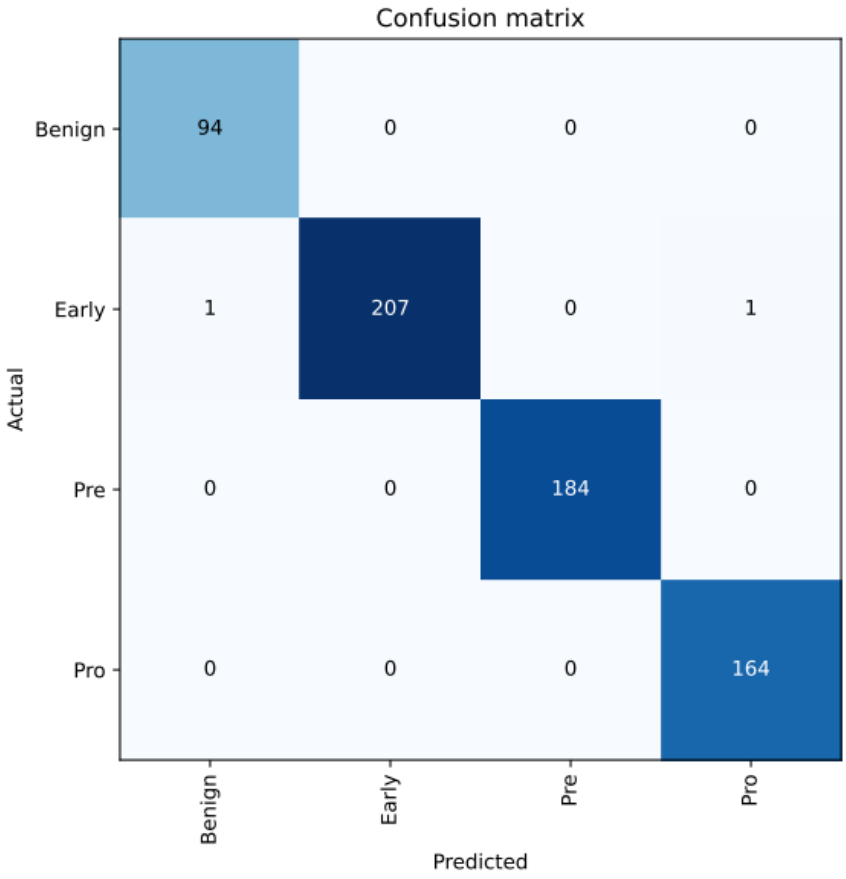


Figure 7. Confusion Matrix of ALL Subtypes

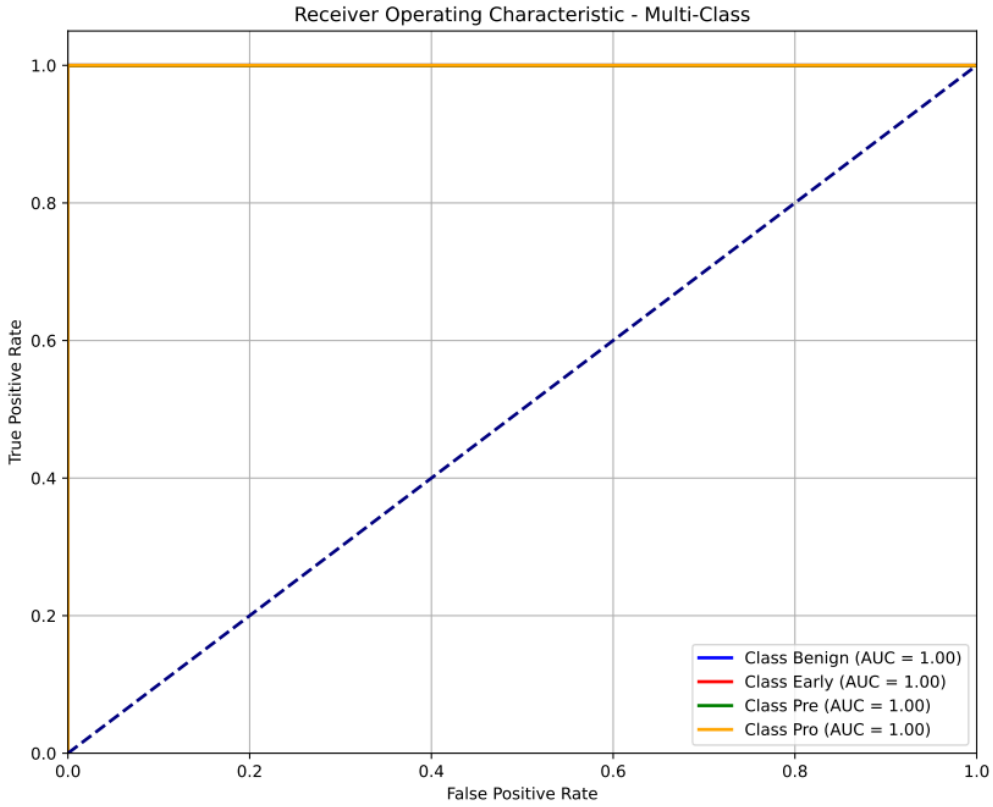


Figure 8. Classification ROC

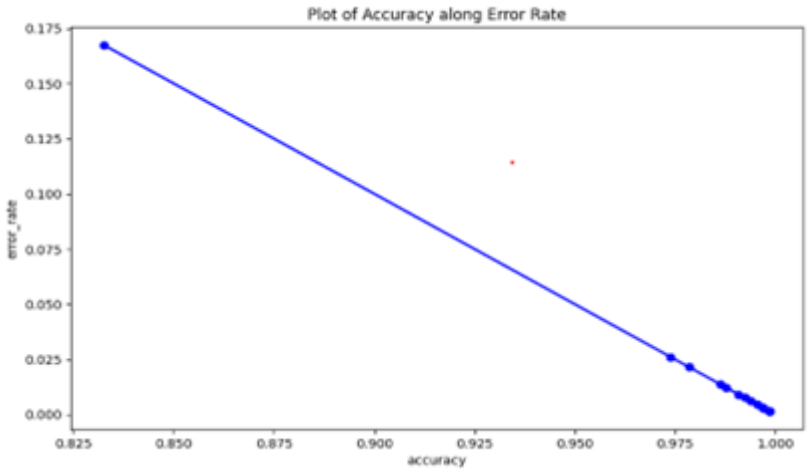


Figure 9. Accuracy v/s Leukemia Classification Error Rate

5. Conclusion and Future Works

The challenges in disease diagnosis is the early detection and accurate identification of leukemia, especially the ability to distinguish cancerous white blood cells precisely while keeping the costs low during the initial stages of the illness. Leukemia affects a large number of individuals, yet access to flow cytometry remains insufficient, and the laboratory techniques currently used are often time-consuming. Early detection greatly improves the chances for successful treatment of leukemia. In this study, a new classification system has been developed for microscopic blood images, which can separate images without leukemia from those affected by the disease. The overall method proposed in this paper includes three main steps: (i) Data Preprocessing, (ii) Model Structuring and Training, and (iii) Classification. For classification of Acute Lymphoblastic Leukemia subtypes, EfficientNetB3 was employed. The results showed that EfficientNetB3 performed best, especially after optimizing the learning rate hyperparameters during training. For future work, the classification can be extended to cover all four types of leukemia and their subtypes, with improvements in both models and datasets.

References

1. Laosai, J. & Chamnongthai, K. Acute leukemia classification by using svm and k-means clustering, 1–4 (IEEE, 2014).
2. Madhukar, M., Agaian, S. & Chronopoulos, A. T. Deterministic model for acute myelogenous leukemia classification, 433–438 (IEEE, 2012).
3. Ahmed, N., Yigit, A., Isik, Z. & Alpkocak, A. Identification of leukemia subtypes from microscopic images using convolutional neural network. Diagnostics 9, 104 (2019).
4. Ozbay, E., ¨Ozbay, F. A. & Gharehchopogh, F. S. Peripheral blood smear images classification for acute lymphoblastic leukemia diagnosis with an improved convolutional neural network. Journal of Bionic Engineering 1–17 (2023).
5. Talaat, F. M. & Gamel, S. A. Machine learning in detection and classification of leukemia using c-nmc leukemia. Multimedia Tools and Applications 83, 8063–8076 (2024).
6. Mallick, P. K., Mohapatra, S. K., Chae, G.-S. & Mohanty, M. N. Convergent learning–based model for leukemia classification from gene expression. Personal and Ubiquitous Computing 27, 1103–1110 (2023).
7. Abhishek, A., Jha, R. K., Sinha, R. & Jha, K. Automated classification of acute leukemia on a heterogeneous dataset using machine learning and deep learning techniques. Biomedical Signal Processing and Control 72, 103341 (2022).
8. Muhamad, H. A., Kareem, S. W. & Mohammed, A. S. A deep learning method for detecting leukemia in real images. NeuroQuantology 20, 2358 (2022).
9. Joshi, M. D., Karode, A. H. & Suralkar, S. White blood cells segmentation and classification to detect acute leukemia. International Journal of Emerging Trends & Technology in Computer Science (IJETTCS) 2, 147–151 (2013).
10. Ahmad, R., Awais, M., Kausar, N. & Akram, T. White blood cells classification using entropy-controlled deep features optimization. Diagnostics 13, 352 (2023).
11. Rehman, A. et al. Classification of acute lymphoblastic leukemia using deep learning. Microscopy Research and Technique 81, 1310–1317 (2018).
12. Ghaderzadeh, M. et al. Machine learning in detection and classification of leukemia using smear blood images: a systematic review. Scientific Programming 2021, 9933481 (2021).
13. Soleimanipour, A., Azadbakht, M. & Rezaei Asl, A. Cultivar identification of pistachio nuts in bulk mode through efficientnet deep learning model. Journal of Food Measurement and Characterization 16, 2545–2555 (2022).12
14. Hegde, R. B., Prasad, K., Hebbar, H., Singh, B. M. K. & Sandhya, I. Automated decision support system for detection of leukemia from peripheral blood smear images. Journal of digital imaging 33, 361–374 (2020).
15. Kumar, S., Mishra, S., Asthana, P. & Pragya Automated detection of acute leukemia using k-mean clustering algorithm, 655–670 (Springer, 2018).