Automated Leukemia Classification and Prediction Using VGG-19 on Microscopic Images

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Abstract
Within the realm of illness diagnostics, one of the most significant challenges is the early detection and diagnosis of leukemia. In order to successfully overcome this obstacle, it is necessary to accurately differentiate between healthy and malignant leukocytes during the early stages of the disease while simultaneously minimizing costs. Leukemia is a disease that affects a large number of people, yet there are only a few flow cytometers available, and the diagnostic processes that are carried out in laboratories are time-consuming. This is accomplished by contrasting three models, notably the regular CNN model and the deep CNN model (Alex Net and the VGG-16 Net model). As indicated by the C-NMC 2019 dataset, a total of 11,154 blood microscopic images were gathered for the aim of analyzing the approach that we have proposed. It has been observed, on the basis of the findings of our research, that the performance of a VGG-19 Net model is superior to that of other two models, such as the Traditional CNN model and the Alex Net model. By employing the VGG-19 Net model as a feature extractor and Soft-max as the classifier, the model is able to attain the highest possible level of performance. With this arrangement, the accuracy is 97.44, the precision is 97.5, the recall is 97.5, and the F1-score is 97.5.

Keywords: Alex Net model, blood microscopic images, deep learning, , disease prediction, leukemia disease and VGG-19 Net model

1. Introduction

Cancer is a huge public health problem that affects people all over the world and, in many cases, is the primary reason for a person's passing away. It is a disease that spreads from generation to generation. The progression of blood cancer to the point where it poses a serious hazard to the patient is one of the most severe forms of the disease [1,2]. One of the most serious types of the disease is blood cancer. The development of aberrant blast cells is one way that leukemia, a form of blood cancer, impairs the body's capacity to make healthy blood cells. These blast cells cause major health issues by interfering with the production of red blood cells (RBCs) and white

blood cells (WBCs). Leukemia is thought to be caused by a combination of environmental and genetic factors, though the precise cause is still unknown..

An estimated 67,410 new leukemia cases were diagnosed in the US in 2020 [3]. An estimated 9,500 new cases are reported annually in the UK [4]. In a similar vein, India records about 10,000 pediatric leukemia cases every year. According to the Indian Association of Blood Cancer and Allied Diseases, leukemia, a cancer that affects white blood cells, is responsible for one-third of all severe pediatric cancer cases with a high risk of death [5]. This is a fact that is mentioned by the organization. Leukemia blood cells are distinguished from normal blood cells by the morphological changes that are depicted in Figure 1. The fact that leukemia blood cells are not normal cells is brought into sharper focus by means of these alterations.

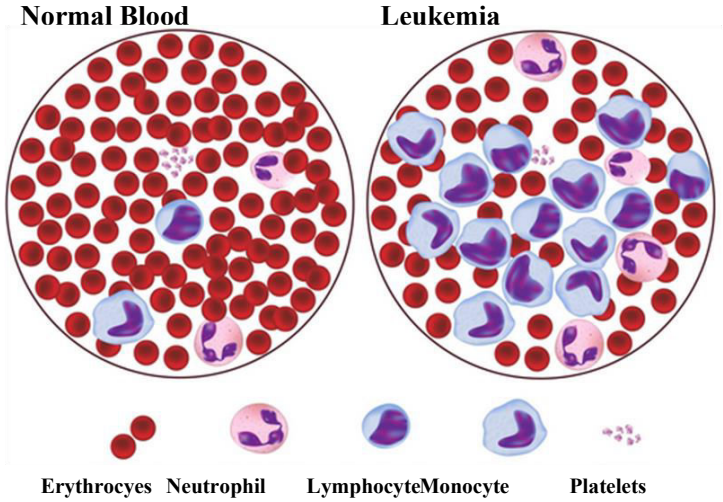

Fig. 1. Blood Cells Details

Leukemia was traditionally classified based on the type of cells involved and the rate at which it progressed. The primary method of classifying leukemia is based on how the disease develops, and it divides the disease into two subtypes: acute and chronic leukemia [6]. A hallmark of acute leukemia is the rapid proliferation of abnormal blood cells, also known as immature blood cells, which are incapable of performing their normal functions. Those chronic leukemias that cause an unusually high cell count or an abnormally low cell count are the two most common types. Chronic leukemia, in contrast to its acute counterpart, targets mature blood cells. Leukemia type 2 is known as lymphocytic leukemia; subtypes of this disease include myelogenousleukaemia and lymphocytic leukaemia, which are based on the affected white blood cell type. One form of leukemia that targets the bone marrow's lymphocytes is lymphoblastic leukaemia, which is also called lymphhocyticleukaemia. One kind of cancer that attacks white blood cells is myelogenousleukaemia, which is also called myeloid leukemia [7]. The creation of RBCs, WBCs, and platelets is carried out by myeloid cells. Table 1 shows that there are four main subtypes of leukaemia, which are defined by the type of infected cells and the severity of the disease: acute lymphoblastic leukemia

(ALL), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), and chronic myeloid leukemia (CML) are the four primary forms of leukemia [8].

Table I: Types of Leukemia

	Lymphocytic	Myelogenous
Level 1	ALL	AML
Level 2	CLL	CML

A reliable way to detect and diagnose leukaemia is to look at blood cells under a microscope [9]. The challenge of making an early diagnosis of leukemia has long perplexed researchers, doctors, and haematologists. Even while swelling of the lymph nodes, pale skin, fever, and loss of weight are all indications of leukemia, they can also be caused by other diseases [10]. Enlargement of the lymph nodes is one sign of leukemia. When leukemia occurs in its early stages, the symptoms are often minor, making a proper diagnosis difficult. The most popular way to diagnose leukaemia is by microscopical examination of PBS, although the gold standard involves studying bone marrow samples [11]. To overcome these challenges, several approaches have been developed by combining traditional image processing methods with machine learning procedures. Regardless, their learning procedures failed to achieve accuracy, effectiveness, or precision [12].

The following section will involve a literature review on the topic of automated detection techniques for leukemia diagnosis and classification. In section 3, we will delve into similar endeavors, with an emphasis on systems that forecast and classify leukemia diseases. Section 4 presents the current state of research on deep learning techniques; Section 5 discusses the study's conclusions and possible future applications; and Section 4 discusses the process of gathering datasets and evaluating performance measures.

2. Literarture Survey

Many researchers have developed machine learning-based leukaemia disease classification and detection systems within the previous several decades. The utilization of microscopic images is central to these techniques. As an example, Paswan et al.[13] achieved an 83% success rate in identifying and classifying k-Nearest Neighbor (k-NN) and Support Vector Machine (SVM) have been used to categorize AML leukemia types. With a 93% classifier success rate, Patel et al. [14] also used SVM to correctly diagnose ALL leukemia. Karthikeyan et al. [15] used SVM in conjunction with c-mean clustering to eliminate WBCs from the background with 90% accuracy.

The goal of a technique put forth in [16] was to identify the health or illness of lymphoblast cells. There were two steps in the procedure: first, white blood cells were separated from other blood components, and then lymphocytes were eliminated. The algorithm classified the extracted feature map using Support SVM and used the Grey Level Co-occurrence Matrix (GLCM) to identify hemorrhological diseases. A Random Forest Algorithm (RFA) was also presented by Dasariraju et al. [17] for the classification and identification of leukemia. To successfully segment the nucleus and cytoplasm, they used morphological processing, multi-Otsu thresholding, and image format conversion.

Hegde et al. [18] proposed an automated decision-support system for leukemia diagnosis based on photos of peripheral blood smears used for diagnosis. The inexplicable abnormality of white blood cells is the hallmark of leukemia. The researchers extracted 1159 images from peripheral blood smears stained with Leishman, each of which displayed a unique range of color tones and brightness levels. The abnormal white blood cells (WBCs) are effectively classified as leukemic using a support vector machine (SVM) classifier. By combining NN and SVM classifiers, the total classification accuracy is increased to 88.8 percent [19].

Feature weight adaptive K-means clustering was developed by other researchers [20] as a mechanism of white blood cell sorting. This approach blended traditional methods with machine learning techniques. Next, we partitioned the color space and found the initial clustering center using the histogram distribution. For our second point, we used a combination of K-mean clustering and color space decomposition to successfully segment the image. From that point on, the watershed approach became the de facto standard for identifying various white blood cell kinds. Afterwards, the white blood cells were sorted into their various categories using a convolutional neural network.

Label augmented and weighted majority voting (LAWMV) is a mechanism proposed by manikandan et al. [21] to enable crowdsourcing. This model outperformed other state-of-the-art models by achieving an accuracy of 82.89%. A simple and effective method of integration is voting by the majority. The m6A-Neural Tool was created by Rehman et al. to help with m6A location prediction and identification. The three sub-architectures of the model were all decided by a simple majority vote. Using a succession of convolutional layers, these systems retrieved the input data that was most pertinent to their purposes. With this model, we were able to achieve a degree of accuracy that no other model had before. Its accuracy in identifying species of A. thaliana was 83.9%, that of M. musculus was 91.5%, and that of H. sapiens was 92%. A hybrid categorization strategy was introduced by Singh et al. in their studyto analyze pictures of skin lesions. The model's performance was evaluated in relation to alternative approaches. The hybrid model achieved an accuracy of 89.80 percent with the support of principal component analysis, factor analysis, and majority voting.

The most common drawback that has been noted in numerous surveys and studies conducted by various academics is the issue of over-segmentation approaches and machine learning models failing to gain adequate accuracy in their results. It takes a long time and doesn't always yield reliable results to manually diagnose leukemia. In order to build an automated system for classifying and detecting leukemia illnesses, we need to employ a deep learning model. This will allow us to handle the concerns.

I. Proposed Systems

When it comes to the classification and prediction of leukemia disease in blood microscopic images, Investigating the viability of applying the VGG-19 transfer learning model is the aim of this work. The deep convolutional neural network (CNN) architecture known as VGG-19 was developed by Oxford University's Visual Geometry Group (VGG). The 2014 ImageNet Large Scale Visual Recognition Challenge (ILSVRC) garnered significant attention and impressed the judges with its exceptional performance in computer vision tasks, especially in the area of image categorization. The structure of the VGG-19 Net is comprised of a number of layers, which can be represented in the following manner, as illustrated in Figure 2:

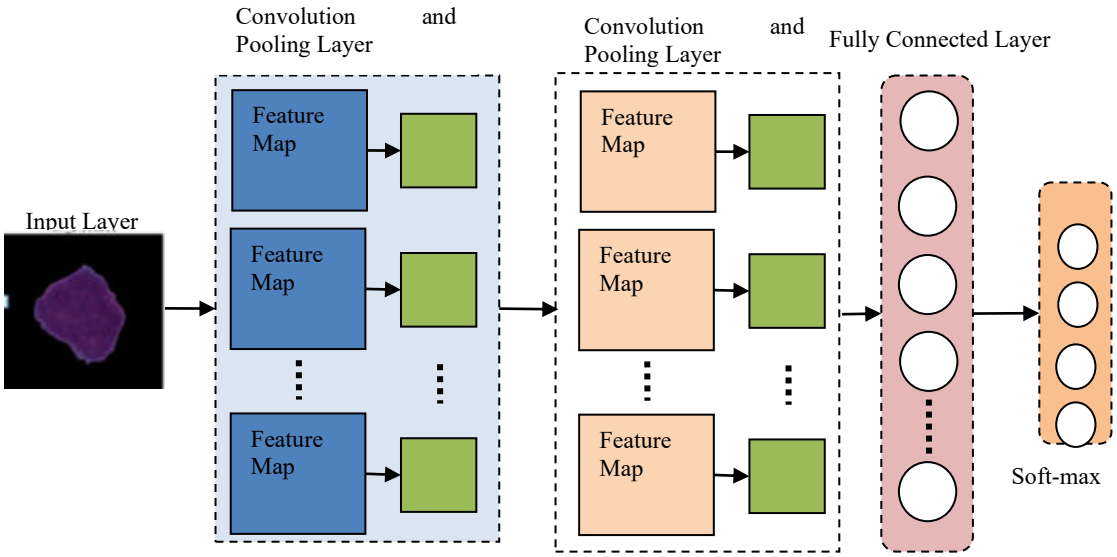

Fig. 2. Architecture of leukemia disease Prediction and Classification Systems

From the above representation following features are adopted,

- The incorporation of input images for the purposes of both training and testing.
- The extraction of features through the convolutional layer.
- The utilization of a non-linearity function to enhance the capacity of the model.
- The reduction of features through the down-sampling layer.
- The flattening of the data and the utilization of fully connected layers.
- The usage of soft-max classifiers for classification tasks.

Input Layer: The VGG-19 network begins with an input layer that is capable of accepting images of a standard size, which is typically 224 pixels by 224 pixels.

Convolutional Layers: The VGG-19 model is made up of a stack of convolutional layers. Small 3x3 convolutional filters with a stride of 1 are utilized in these layers. A reduction in the spatial dimensions is achieved by interspersing the convolutional layers with max-pooling layers that make use of 2x2 windows and a stride of 2.

Layer Depth: The total number of layers in VGG-19 is 19, with sixteen of those layers being convolutional layers. The convolutional layers are intended to extract features that are progressively more complicated as one moves deeper into the network.
Filter Sizes and Strides: 64 filters are used in the first layer, followed by 128 filters, 256 filters, and 512 filters in the following layers. In order for VGG-19 to be able to capture fine details while yet maintaining a relatively modest receptive field, the 3x3 filter size is an important architectural choice.

Activation Function: Non-linearity is introduced via ReLU, which also speeds up the training process.

Fully Connected Layers: VGG-19 culminates with three fully connected layers, each comprising 4,096 neurons, followed by the output layer. These layers integrate high-level features from the convolutional layers and map them to the number of output classes (e.g., 1,000 for ImageNet classification).

Dropout: In order to prevent overfitting, dropout layers are sometimes inserted before the first two layers that are fully coupled.

Output Layer: The last layer is often a softmax layer, which generates class probabilities for the purpose of image classification.

Training and Optimization: In order to train and optimize VGG-19, it is trained on large labeled datasets like ImageNet. Optimization techniques like as stochastic gradient descent (SGD) with weight decay are utilized throughout the training process.

Transfer Learning: The VGG-19 architecture has presented itself as a very helpful tool for transfer learning. It can be adjusted for a range of image identification applications since it utilizes pre-trained weights that have been learned from ImageNet data. VGG-19 has had a significant impact on the field of computer vision because it combines performance and ease of use. VGG-19 is frequently used by researchers and practitioners in the field of visual recognition as a benchmark model and as a

foundation for a variety of specialized applications. Its outstanding capabilities in image classification and feature extraction have made it a crucial part of deep learning.

II. Experimental Results and Discussions

This section provides a discussion of the outcomes that the developed model produced in various experimental settings. Arguments and comparisons are then presented after these findings. Additionally, Python and the Keras deep learning framework were used in the development of the previously mentioned model. A 12GB NVIDIA Tesla K80 GPU was used to run each and every simulation on Google Colab. Additionally, Python was used to generate the model. There are two datasets that make up the experimental design, and each dataset's performance is examined alone as well as in conjunction with the other dataset respectively. All of the parameters are defined through the process of trial and error, and the findings are summarized with the values that are considered to be ideal for the parameters.

A. Dataset

A total of 15,114 lymphocyte images belonging to 118 different participants are included in the C-NMC 2019 dataset. There are three distinct folders that contain these images: "CNMC test preliminary phase data," which comprises 1,867 cells; "C-NMC test final phase data," which comprises 2,586 unlabeled cells from 17 subjects; and "C-NMC training data," which comprises 10,661 cells, comprising 7,272 malignant cells from 47 subjects and 3,389 healthy cells from 26 subjects. Every one of these folders represents a distinct kind of cell. Single-cell images of lymphocytes that have been classified as benign or malignant by oncologists with previous experience in the field are included in the files. The subset of the dataset that is displayed in Figure 3 is indicative of the whole.

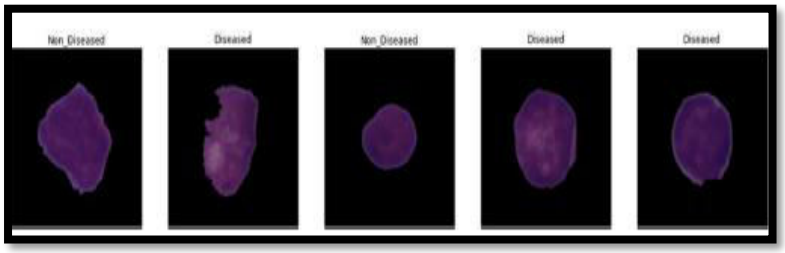

Fig. 3. Sample Dataset images Healthy and Disease affected images

B. Performance Metrics

The following metrics will be utilized in the process of developing the criteria that will be utilized in the assessment of the model's performance that was initially suggested:

Factor 1 - Accuracy: Out of all the categories, this statistic displays the total number of classes that the trained model accurately predicted, such as Acute Lymphoblastic Leukemia (ALL) and not Acute Lymphoblastic Leukemia (ALL). Both the percentage of patients with a leukemia diagnosis and the percentage of patients without a diagnosis

are displayed by this metric. The model will be more accurate the higher the accuracy value used. The following equation displays the accuracy equating formula:

Accuracy=(True_PT+True_NT)/(True_PT+True_NT+False_PT+False_NT) (1)

Factor 2 - Precision: This statistic calculates the proportion of true positives to all positive events. In the context of the disease, the model's capacity to precisely identify leukemia patients is essential.. The following equation is used to formally define the concept in question mathematically:

Precision=True_PT/(True_PT+False_PT) (2)

Factor 3 - Recall: This statistic measures the proportion of true positive results out of all positive events [72]. The model's ability to accurately detect individuals with leukemia is crucial in the setting of this disease. The concept in question is precisely defined mathematically through the utilization of the following equation:

Recall=True_PT/(True_PT+False_NT) (3)

Factor 4- F1 Score: This statistic assesses the overall efficiency of the model by combining the values of both recall and accuracy in order to determine the overall efficiency.

$$F1 = 2.\frac{\text{Precision.Recall}}{\text{Precision + Recall}}. \quad (4)$$

C. **Results and Discussions**

To categorize and predict leukemia disease in Blood Microscopic Images, we trained and evaluated two separate models of convolutional neural networks (CNNs). The standard CNN and the Alex Net model are the two CNN models. We have concluded that the Alex Net model achieved the highest level of accuracy based on the data displayed in Table 2 and Figure 4.

models of convolutional neural networks (CNNs). The standard CNN and the Alex Net model are the two CNN models. We have concluded that the Alex Net model achieved the highest level of accuracy based on the data displayed in Table 2 and Figure 4. possible and was the most effective method. Conversely, the CNN model achieved an accuracy rate of only 91.65%.

Table II. Performance Comparison of Base Models

S. No.	Representation	F1_Accuracy	F2_Precision	F3_Recall	F4_F1-Score
1.	Traditional CNN	91.15	91.45	91.3	91.25
2.	Alex Net Model	93.65	93.15	93.25	93.15
3.	VGG-19 Net Model	97.44	97.5	97.5	97.5

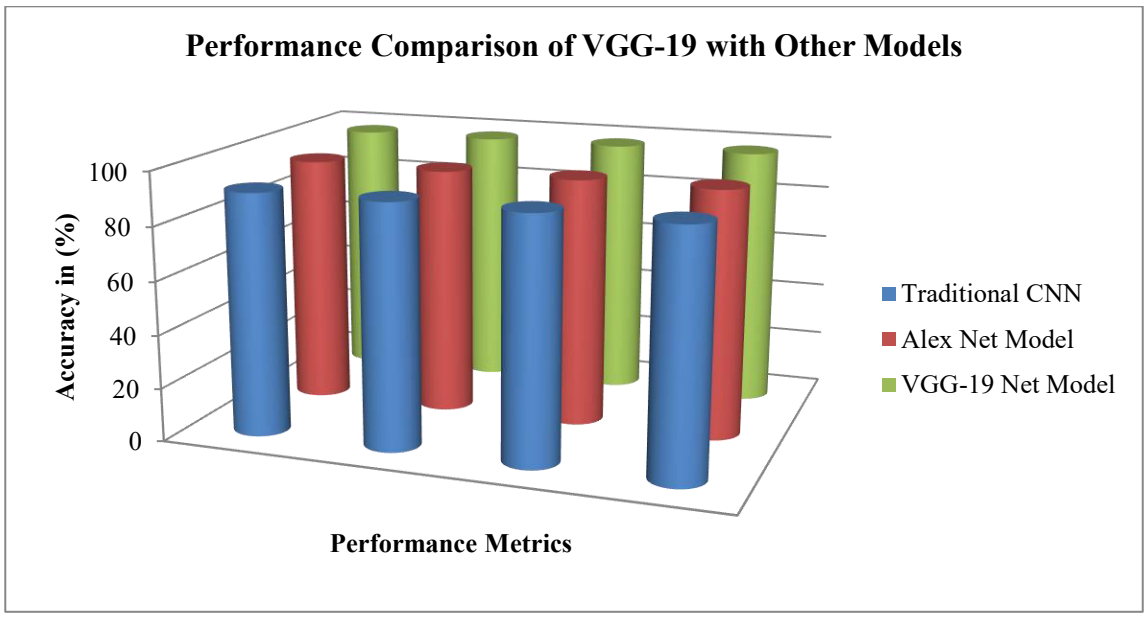

Fig.4. Performance analysis of proposed LD model

The VGG-19 Net model is a further level deep CNN model that we have implemented to attain an even higher level of prediction accuracy. There are more trainable parameters in the VGG-19 Net model than in the traditional CNN and Alex Net models. Because the VGG-19 Net achieved the highest level of accuracy (97.44%), we were able to determine that it was the most successful approach. As a result of the findings that are presented in Table 2 and Figure 7, we were able to determine that this was the most efficient strategy. The confusion matrix was utilized in the process of calculating a number of different performance evaluation measures, all of which are presented in Figure 5.

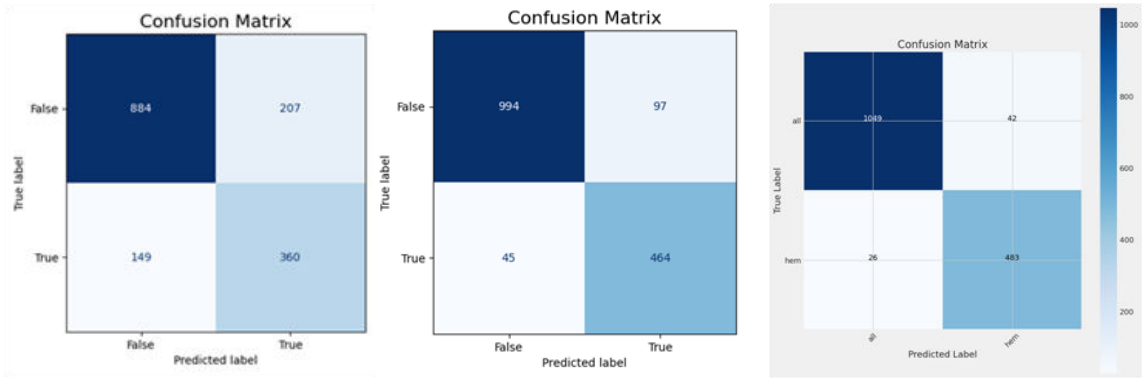

Fig.5. Representation Model - Confusion Matrix Results

The results of comparing the VGG-19 Net model to the base models, which are the standard CNN and the Alex Net model, are shown in Figure 6 to Figure 8. Common measures, such as trained and validated accuracy, as well as trained and validated loss, formed the basis of the evaluation. With the use of dropout, the analysis was carried out over 15 epochs, and the model that was produced is a VGG-19 Net. These

parameters are calculated to get an estimate of the trained models using SGD optimization and a learning rate of 0.00001. These parameters are calculated to give an assessment of how much the training models have been overfitted.

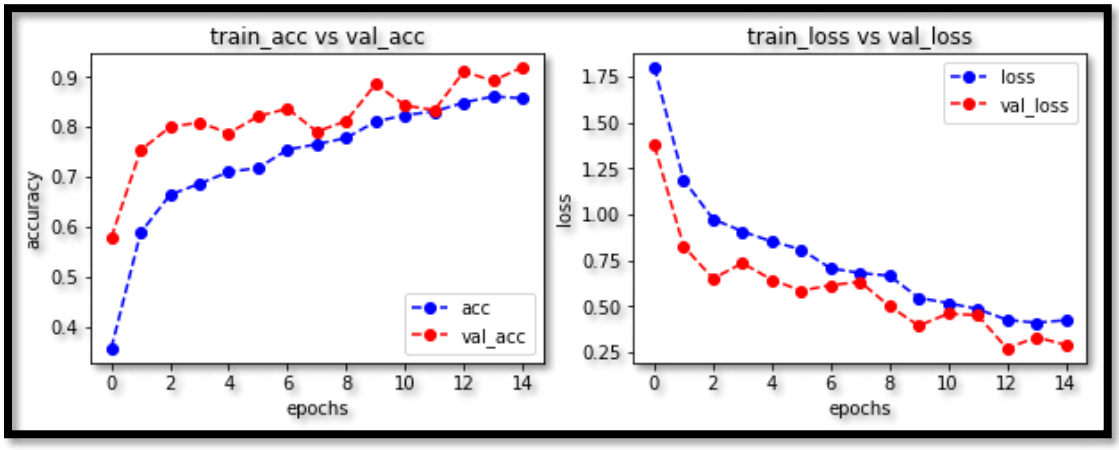

Fig.6. CNN Model Results

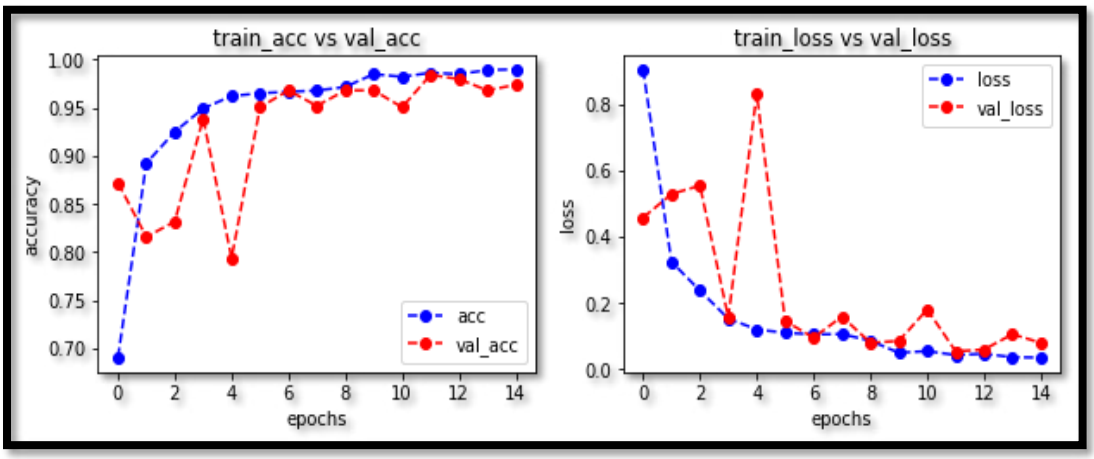

Fig.7. Alex Net Model Results

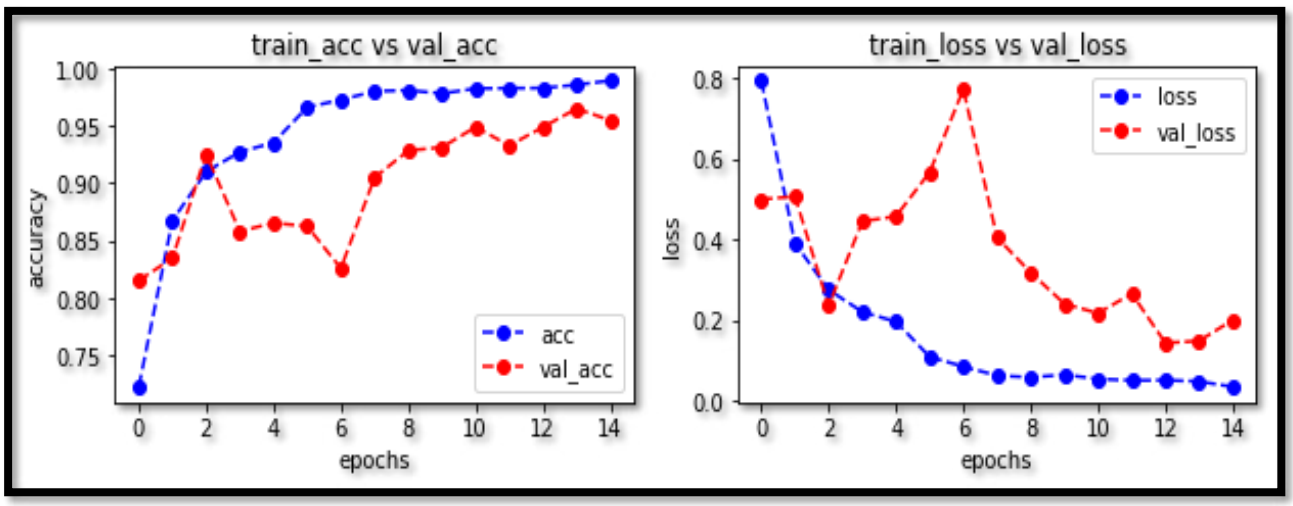

Fig.8. VGG-19 Results

III. **Conclusions and Future Enhancements**

The low-cost, precise differentiation of malignant leukocytes is a hallmark of leukemia in its early stages. Despite the high incidence of leukemia, laboratory diagnostic centers lack the necessary flow cytometer equipment and labor-intensive procedures. Early detection of leukemia increases the likelihood that treatment efforts will be successful. This study presents a novel classification model for blood microscopic images that can differentiate between images of leukemia patients and healthy individuals. The primary elements of the methodology presented in this work are image preprocessing, feature extraction, and classification. An image's classification as "normal" or "abnormal" is determined using a Deep convolutional neural network (VGG-19 Net model). According to our analysis, the VGG-19 Net model performed better than two other models: the Traditional CNN and the Alex Net. The model performs at its peak when the VGG-19 Net model is used as the feature extractor and Soft-max as the classifier. The aforementioned configuration shows a 97.44% accuracy, 97.5% precision, 97.5% recall, and 97.5% F1-score. Accuracy may be improved in the future by combining various deep learning and machine learning algorithms. Moreover, a hybrid dataset can be produced and applied to studies.

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