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Using Deep Learning Techniques to Enhance Blood Cell Detection in Patients with Leukemia

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Abstract: Medical diagnosis plays a critical role in the early detection and treatment of diseases by examining symptoms and supporting findings through advanced laboratory testing. Early and accurate diagnosis is essential for detecting medical problems and then prescribing the most effective treatment strategies, especially in life-threatening diseases such as leukemia. Leukemia, a blood malignancy, is one of the most prevalent cancer types affecting both adults and children. It is caused by the rapid and uncontrolled growth of abnormal white blood cells in the bone marrow. This accumulation interferes with the production of normal blood cells, leading to a weakened immune deficiency, anemia, and bleeding disorders. Conventional leukemia diagnostic methods are time-consuming, manually intensive, and inefficient. This research study proposes an automatic diagnostics prediction of leukemia by analyzing blood images according to the shape of the blast cells using digital image processing and machine learning. The purpose of blood cell detection is to precisely identify and classify diverse blood cells, detecting anomalies associated with blood cancers like leukemia. This supports early diagnosis and monitoring, which leads to more effective treatments and improved results for cancer patients. To accomplish this task, we use digital image processing techniques and then apply the convolutional neural network (CNN) deep learning algorithm to blood sample images. This research employs a multi-stage methodology, including data preparation, data preprocessing, feature extraction, and then classification. While our model is built on a typical CNN architecture, we make significant advances by using preprocessing techniques and hyperparameter tuning. We have modified its layers combination to include convolutional, pooling, and fully connected layers that are optimized for image characteristics. These layers are fine-tuned for better feature extraction and classification accuracy. This study showed that blood cell detection for diagnosing acute leukemia based on images had 99% accuracy and outperformed other advanced models, including DenseNet121, ResNet-50, Incep-tionv3, MobileNet, and EfficientNet. The comprehensive analysis of the results reveals the highest accuracy of leukemia detection as compared to existing studies in the relevant literature.

Keywords: cancer detection; deep learning; acute leukemia; classification; white blood cells

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1. Introduction

The healthcare sector is concerned with maintaining and improving health through medical services, research, and technology. It includes patient care, disease prevention, and

medical innovations that improve quality of life and promote better health outcomes [1]. However, the industry faces persistent challenges due to the emergence of new disease variants and evolving pathogens [2,3]. Cancer remains one of the most formidable challenges [4], accounting for a significant proportion of global morbidity and mortality [5]. The combination of genetic mutations and environmental factors, such as exposure to radiation [6], certain chemicals, and some viruses [7], can damage the DNA of blood cells [8], leading to their malignant transformation of disease [9]. Blood, a vital fluid coursing through the human body, serves as a lifeline, distributing basic nutrients and oxygen tissues while eliminating waste products [10]. Consisting of four components, comprising plasma and the liquid component, it transports hormones, proteins, and waste products from the body [11]. Red blood cells, characterized by their hemoglobin-rich composition [12], ferry oxygen from the lungs to tissues and transmit carbon dioxide back to the lungs for exhalation [13]. White blood cells, guardians of the immune system [14], mount a defense against infections, ensuring the body's resilience [15]. Platelets, tiny cell fragments, play a role in blood clotting and prevent the excessive loss of blood [16]. The intricate role of these components maintains homeostasis, protecting the body from different diseases [17].

White blood cells (WBCs), also known as leukocytes, circulate blood throughout the lymphatic system, with different types of cells functioning to anticipate the disease nature in WBCs [18]. Neutrophils are the most abundant types of WBCs that defend the human system against bacterial infections. Eosinophils, in combating parasitic infections and modulating allergic reactions, contain granules filled with enzymes and proteins that are toxic to parasites. Lymphocytes involve body immunity and can recognize and respond to specific responses by detecting infected or abnormal cells and regulating the activities of other cells. Monocyte WBCs regulate immune responses by presenting antigens to other immune cells [19]. They are also a cause factor of cancer due to genetic mutation or any tumors in WBC types.

Leukemia is classified into four types: acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), chronic lymphocytic leukemia (CLL), and chronic myeloid leukemia (CML) [20] as shown in Figure 1. ALL and AML are severe conditions that require rapid treatment. CLL and CML, which are more frequent in elderly persons, develop gradually over time. Both require immediate care to prevent their rapid course [21].

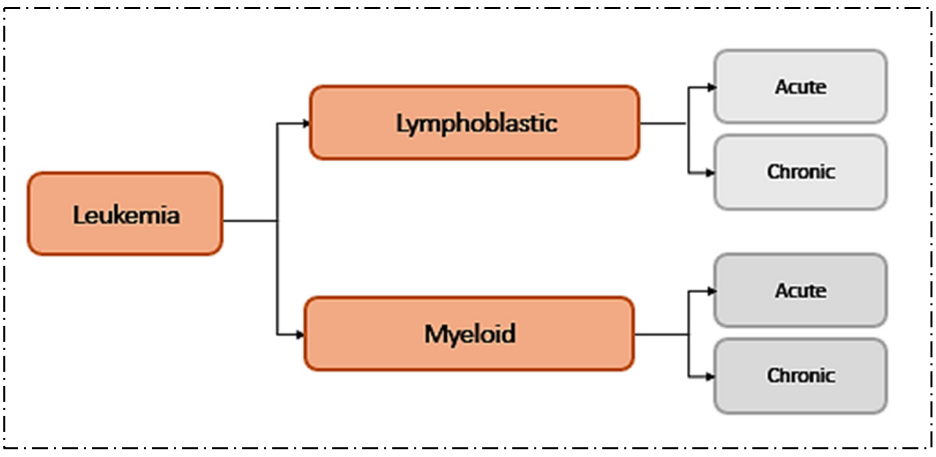


Figure 1. Types of leukemia [20].

L1, L2, and L3 leukemia are subtypes of acute lymphoblastic leukemia (ALL) identified by the appearance of leukemic cells under a microscope, as shown in Figure 2. L1 subtypes are characterized by small, uniform blast cells with minimal cytoplasm. The nuclei of these cells are typically round or slightly intended, resembling lymphoblasts at an early stage of development. L2 subtypes are larger and more varied blast cells compared to L1 [22]. These cells may exhibit irregular nuclei, more abundant cytoplasm, and occasional vacuoles. L3 subtypes are also called Burkitt leukemia, characterized by very large blast

cells with abundant cytoplasm and prominent vacuoles, associated with specific genetic abnormalities such as translocation involving the MYC gene on chromosomes [23].

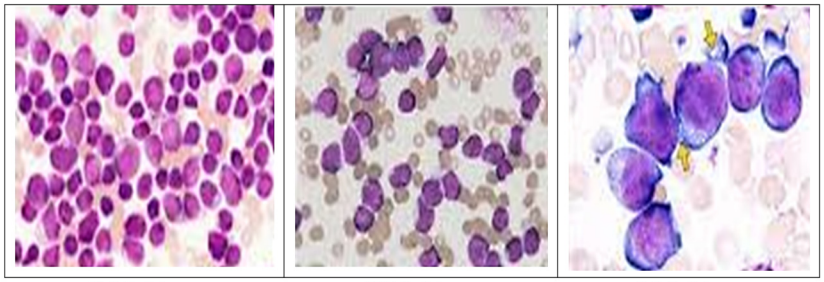


Figure 2. Stages of acute lymphoblastic leukemia [22,23].

For leukemia diagnosis, particularly ALL, hematologists face challenges in accurately detecting and classifying malignant lymphocytes through manual screening methods such as blood smear or bone marrow examination under the microscope. This process heavily depends on the expertise and involvement of pathologists. Prolonged microscopy sessions may lead to fatigue, potentially affecting diagnostic accuracy [24]. To address this challenge, researchers have turned to the detection and classification of ALL by leveraging enhancements in technology, such as image analysis algorithms and machine or deep learning techniques aimed to diagnose accuracy.

These diseases can be detected and diagnosed in their early stages, but conventional methods are manual, time-consuming, and less reliable. These issues can be resolved by improving PBS (peripheral blood smear) analysis and creating intelligent CAD systems for early leukemia prediction thanks to the development of quantitative microscopic techniques [25]. Only a suspicious and meticulous microscopic inspection of a stained blood smear can reliably identify leukemia. White blood cells are complicated; therefore, conventional examination results in heterogeneity in slide preparation, which produces a subjective, non-standardized report. Therefore, a reliable and cost-effective automated system is needed to meet the demand for accurate diagnosis without being impacted by the expertise, exhaustion, or operator fatigue of hematologists [26].

Machine learning algorithms use manual inputs to categorize output, requiring accurate training data. Deep neural networks (DNNs) are more effective than shallow learning methods. End-to-end models, created using data-driven learning techniques, are growing in popularity due to their simplicity and ability to classify leucocytes [27,28].

Our main research contributions in this research study are as follows:

- The suggested model shows best accuracy in differentiating four types of cells: monocytes, neutrophils, lymphocytes, and eosinophils, confirming CNNs' effectiveness in medical imaging applications.
- We provide a customized CNN architecture optimized for cell image categorization. The model has been fine-tuned to capture the small properties of WBCs, which improves the classification accuracy.
- Investigation of pre-trained models, including DenseNet121, ResNet-50, Inceptionv3, MobileNet, and EfficientNet.
- Conducting comprehensive empirical analysis and performance evaluation using standard metrics like accuracy, precision, recall, F1 measures, and confusion matrix on BCCD data, which is widely used in this domain.
- Achieving the highest accuracy rate of 99% using the proposed model CNN to diagnose the early stage of leukemia throughout the existing literature.

This paper is organized into different sections. Section 1 provides an introduction to leukemia and outlines the research contributions. Section 2 explores related work in the field. Section 3 presents the proposed methodology in detail. Section 4 provides an analysis

of the results and discussion. Finally, Section 5 summarizes the key findings and potential future research.

2. Related Work

A review of relevant studies has been discussed to outline various techniques for detecting WBCs using ML and DL algorithms.

Saikia R et al. [29] proposed Otsu's thresholding with GLCM characteristics carried out with CNN, YOLOv3, and KNN classifiers that were used to categorize WBCs; this method yielded a significantly higher accuracy rate of 94.25%. To increase classification accuracy, various feature extraction methods and classifiers can be used in addition to segmentation. In another study proposed by Elen A et al. [30], the k-NN algorithm yielded results that were like those of the SVM and Naive Bayes algorithms, but it had the lowest performance rate. Apart from these, the most efficient method after MLR is the Random Forest algorithm, with 95% compared to that of other approaches. Nassar M et al. [31] offered a unique label-free method for classifying live, unstained WBCs that makes use of an image flow cytometer and machine learning algorithms. It produced two kinds of WBCs, B and C, with an average F1-score of 97%. This also makes it possible for oral diagnostics, where extensive data from the shape of the cell can be used for a variety of basic blood diagnoses.

The automatic categorization model was introduced by Navya K et al. [32] to increase the precision of the evaluation procedure to classify and segment blood cells into RBCs and WBCs using a semi-automated method such as the Naive Bayes classifier, logistic regression, ANN, SVM, K-NN, decision tree, and K-means clustering. After comparing the performance metrics, it was discovered that with a 97% accuracy rate, logistic regression is the most appropriate method. Despite taking more time, MLP was shown to be the most effective classification model with the highest accuracy, at 92%, for identifying WBCs, proposed by Musliman A et al. [33]. The use of (SVM) classification methods and a feature extraction methodology with an accuracy of 88% and a required time of 3.73 s was acquired from the system's average time value and accuracy calculation. Jusman Y et al. [34] developed a white blood cell image classification system through Hu moment invariants.

Abas, S.M et al. [35] used a scaled-down blood cell detection dataset termed BCCD to accurately detect and classify WBCs into four categories. The suggested model integrates deep models for feature retrieval with traditional ML classifiers. The hybrid model outperformed the baseline FCN by 25.78% and attained 97.03% using MobileNet-224 and logistic regression for feature extraction. To classify blood cells from images, another approach was presented by Bozkurt F et al. [36] by using a model, called DCNN, with an accuracy rating of 94%, enabling the examination of a larger amount of data. Another deep learning technique for the categorization is defined by Parveen et al. [37] using the YOLO-v3 object identification methods to identify and locate WBCs using bounding box detection. The suggested work had 99.2% accuracy and was classified with 90% accuracy after a thorough experimental examination. A new semi-supervised technique for classifying white blood cells is presented by Ha et al. [38], composed of a Fine-Grained Interactive Attention (FGIA) mechanism and a Semi-Supervised Teacher–Student (SSTS) module. FGIA provides 75 labeled photos per category on the BCCD dataset, with an average accuracy of 93.2%, demonstrating good performance on the semi-supervised WBC image classification problem. Ilyas M et al. [39] introduced another approach followed by linear programming as a machine learning technique for leukemia classification, achieving an accuracy of 98%, to predict gene expression as subtypes of cancer. Bani-Hani et al. [40] used a CNN for pattern recognition to classify important characteristics that aid in class distinction. The optimized CNN attained a sensitivity of 91%. Computer-aided detection system research proposed by Abas SM et al. [41] relies entirely on deep learning using the YOLO v2 approach. This study showed that improving performance and accuracy can be achieved by breaking the addressed problem down into smaller difficulties. Additionally, the findings demonstrate that the CAD3 attained an accuracy of 94.3% in the classification of leukocytes. A study on

gene expression using image data by splitting data into 70/30 to scale the dataset followed 25 features. Data were tested on feature variations such as two, five, and seven, achieving the highest results of 96% to diagnose the bone marrow cells in DNA [42]. In this study, Toğaçar et al. [43] used image processing techniques to increase the classification accuracy of DL algorithms for WBCs' classification. The CNN was integrated with the methods of the maximal information coefficient and ridge feature selection. This study's overall accuracy rate of 97.95% showed how well CNN models classified different types of white blood cells. Researchers proposed a new Falcon optimization algorithm with a deep convolutional neural network for the leukemia detection and classification (FOADCNN-LDC) technique. This method used median filtering, the ShuffleNetv2 model, and convolutional denoising autoencoder (CDAE) models to classify and recognize leukemia. This approach achieved an accuracy of 99.62% over existing techniques [44]. This research introduced two automated classification models for detecting leukemia based on blood microscopic images, one preprocessed and the other fine-tuned. The first uses the pre-trained AlexNet for feature extraction, whereas the second employs fine-tuned AlexNet for both [45]. Experiments were carried out on a dataset of 2820 images, indicating that the second model outperforms the first due to its 100% classification accuracy [46].

3. Proposed Research Methodology

The proposed framework shows the collecting microscopic images of blood samples followed by preprocessing, feature extraction, and selection, which are the processes for the diagnosis of acute leukemia. As deep neural networks need more data for their training and higher performance, data augmentation techniques are carried out to solve the issue of limited data. Deep CNN architecture-based squeezing and excitation learning is applied to identify leukemia from the input microscopic images of blood samples. This deep learning architecture was examined on key performance metrics such as accuracy, precision, recall, and F-measure to develop an automated, dependable method for leukemia diagnosis. The basic steps of the proposed methodology are outlined below.

1. Data selection;
2. Data preprocessing;
3. Feature extraction;
4. Classification and prediction;
5. Performance metrics.

3.1. Data Selection

The data from this study are obtained from the Kaggle repository and are openly accessible [https://www.kaggle.com/code/valentinbiryukov/blood-cells-classification (Accessed on 23 April 2024)]. The image data are available with four classes: monocyte, neutrophil, lymphocyte, and eosinophil. This dataset is a variant of the BCCD dataset, which is a small-scale image set for blood cell detection [https://github.com/Shenggan/BCCD_Dataset (Accessed on 23 April 2024)]. The sample of images for each class in the dataset is shown in Figure 3.

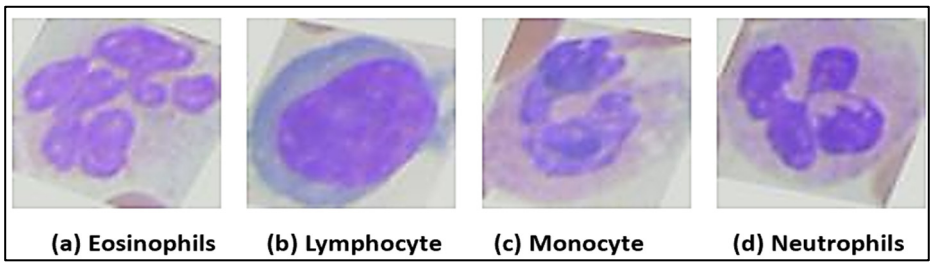


Figure 3. Sample images of each class from the dataset.

Each image is 640 × 480 in width and height, respectively, and contains RBCs, platelets, and one or more WBC types, i.e., neutrophil, eosinophil, lymphocyte, and monocyte. This dataset has 12,444 blood images as sample images of WBC components, as shown in Table 1

Table 1. Augmented dataset details.

Sr. No	Name of Class	Training	Testing
1	Neutrophil	2497	623
2	Eosinophil	2483	620
3	Monocyte	2478	620
4	Lymphocyte	2499	624

3.2. Data Preprocessing

When preparing medical images for acute leukemia analysis, a critical preprocessing step is performed to remove the noisy data that lead to the poor performance of the models. There are unwanted regions and empty spots in each image in a leukemia dataset. The selected dataset contains the original eosinophil 88 images, lymphocyte 33 images, monocyte 21 images, and neutrophil 207 images. After augmentation, which was already conducted, the number of samples included 12,444 images of classes. In this step, the same selected dataset was chosen, and the augmentation steps were performed to enhance the total samples of 10,800 images of four classes. In this study, the augmented images were kept less than the original augmented images in the available dataset.

Preprocessing is carried out following cropping and resizing, data augmentation, and image normalization steps. Cropping involves removing extraneous spaces and focusing on essential information using algorithms. For image cropping, the extreme point computation algorithm is used, and the results are shown in Figure 4. For this, the original image is further converted to grayscale, and then a threshold is applied to make it binary. Then, using the four most important contours identified from the threshold images, four distinct minimum and maximum points are computed (x, y). Finally, the information acquired from the contours and minimum and maximum points is used to crop the image.

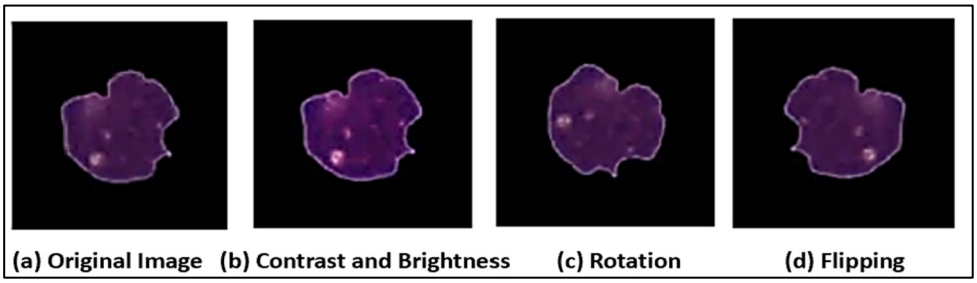


Figure 4. The outcome of using augmented data. (**a**) The original image; (**b**) modifications to contrast and brightness; (**c**) rotation; and (**d**) flipping both vertically and horizontally.

Resizing is utilized to enhance the performance of the model. It is imperative to maintain uniformity in terms of the sizes, weights, and heights of all the images inside the leukemia dataset. Resizing ensures uniformity in image sizes, set to 224 × 224 for all image classification models. This involves adjusting their dimensions to fit within a predefined range. This guarantees that all images in the context of acute leukemia are the same size. By doing this, the model will be able to constantly examine and interpret the images, producing more accurate categorization results. Medical image classification studies typically use 224 × 224 network input dimensions. The dimensions of each image are 224 × 224, with a range of 0 to 255.

To balance the dataset and prevent the unbalancing of data, overfitting, and poor generalization of the model, data augmentation is applied by rotating to a specific degree in the clockwise and anti-clockwise directions, flipping as horizontal and vertical, contrasting

the changes, and making adjustments to the brightness to enhance the quality of the dataset image and prevent it from overfitting. These changes can mimic the changes in illumination. It facilitates the identification and classification of significant structures by drawing attention to them, such as abnormal cells or cell nuclei.

Data augmentation is carried out to balance the training and validation sets because the original dataset was uneven. The test set was not subjected to this method. Every single image has its augmentation applied in real time. Each time the model receives an image, it iteratively processes the image, producing four augmented images for photos of healthy cells and two images for ALL cancer cells. This step enhances the model's ability to interpret images accurately.

Image normalization is also taken to transform the pixel values into a consistent scale, improving the accuracy of subsequent analysis methods in leukemia image studies. These preprocessing steps collectively optimize the dataset for more precise and reliable leukemia classification results.

3.3. Proposed Framework

In this study, we used five pre-trained models of Inception v3, ResNet-50, EfficientNet, MobileNet, DenseNet121, and the proposed CNN model. The model architecture is shown in Figures 5 and 6.

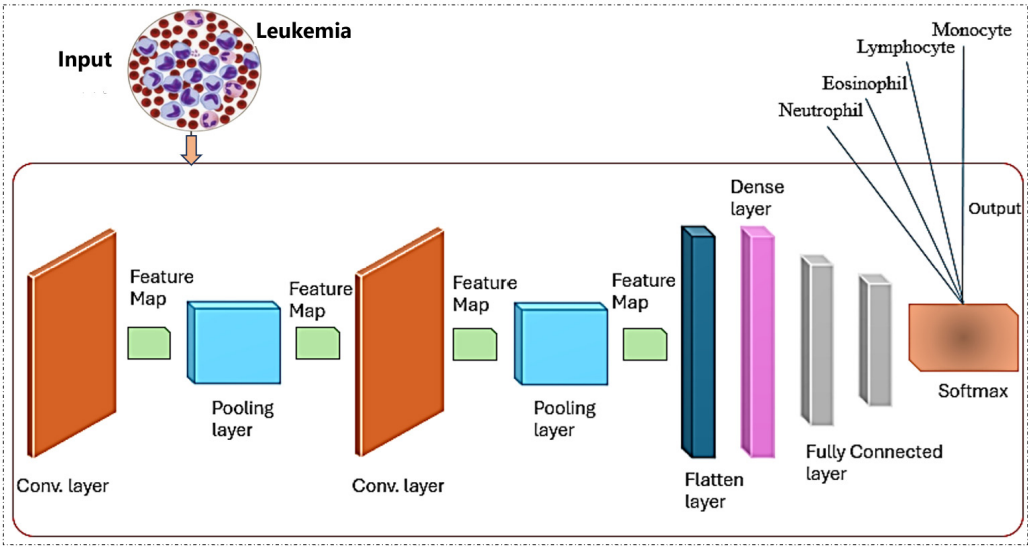


Figure 5. Proposed CNN architecture.

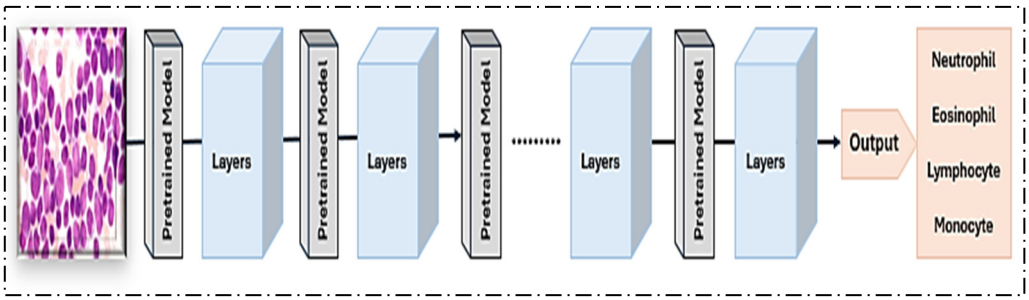


Figure 6. Pre-trained model architecture.

Table 2 shows the details of the implementation carried out using Python 3.7.0, and configuration is performed of the local system. The libraries utilized include Tensor Flow, pandas, NumPy, Matplotlib, and Scikit-learn. A computer with the following requirements was used for the experiments: Intel Core i7-9700 Processor 9th Generation, NVIDIA GeForce GTX 1660Ti 6GB GDDR6, and Windows 10 (64bit).

Table 2. Details of implementation.

Parameters	Values
Machine	i7-7700k CPU
OS	Windows 10
C U D A	10.1
Cu DNN	v7.6.5
Tensor RT	6.0.1.5
TensorFlow	2.3.1

3.4. Classification Stage

For the classification, different features and classifiers are trained and tested on the proposed dataset. The holdout method is used, and the data are divided into 80% training and 20% testing. In the training data with an 80% share of the whole data, a further 12% of the data were used for validation. The model is adapted to the dataset configuration, with the three fully connected layers, the SoftMax layer, and the fine-tuning classification layer specified with the new layers of the classifier. This approach adjusted to the specifics of the new data and the utilization of transfer learning.

After feature extraction, the optimal collection of features is then fed into a classifier, which determines each blast cell's class by analyzing its quantifiable characteristics. This is the next step in the diagnostic procedure. The training and testing of the suggested classifier are the two procedures that go into defining the classification method. The classifier's method, parameters, and feature boundaries are all optimized throughout the training phase. During the classification step, the training procedure is crucial since it aims to explain the traits of the classification groups. On the other hand, using the formerly established training and feature boundaries, the testing method is utilized to categorize examples that have not yet been seen. To prevent bias in the accuracy of the classification, testing typically calls for the use of additional independent data. Classification based on transfer learning is divided into two categories.

- Classification of pre-trained model based on transfer learning method.
- Classification of the proposed CNN model.

Transfer learning is a method of using pre-trained models to solve problems similar to detection rate problems. Pre-trained models like DenseNet121 and Inception v3 are commonly used due to their computational cost and potential to extract unique features. DenseNet121 addresses vanishing gradient problems by connecting layers directly, ensuring maximum information exchange. This design requires fewer parameters and prevents overfitting, preventing overfitting in small datasets. Concatenation is used to combine features, ensuring that each layer maintains its feed-forward character. DenseNet differs from the standard architecture in that it replaces L in the L-layer network $\frac{L(L+1)}{2}$ connections using Equation (1). The main function of Dense Net is its ability to handle vanish gradient difficulties, reuse features, lack parameter numbers, and propagate features. A dense block, which is utilized to improve the information flow across layers, is an important component of Dense Net.

$$L_l = H_l([L_0, L_1, \ldots, L_{l-1}]) \quad (1)$$

where the layers of DenseNet121 are represented by the numbers $(0, 1, \ldots, l-1)$, and the feature map derived from the layers of DenseNet121 is concatenated.

Inception-v3 is a deep neural network designed for image categorization applications, aiming to maximize computational efficiency while maintaining high accuracy. Its inception module uses different filter sizes to collect information simultaneously, improving representation learning. ResNet-50, a pre-trained 50-layer model, addresses the vanishing gradient issue by utilizing gradient descent and skip connections to accelerate training with fewer layers. Improved results are achieved with large datasets and deep CNN networks. By omitting some layers, ResNet solves this issue as gradients flow from the initial to the

last layers, and the results in terms of accuracy are shown in the figure. The ResNet model's layers can be computed mathematically following Equation (2).

$$Y = f(x) + id(x) = f(x) + x \tag{2}$$

ResNet-50 and MobileNet are lightweight convolutional network architectures, with ResNet-50 having 50 layers and MobileNet using depth wise separation convolutions. Both architectures offer competitive accuracy while reducing costs and parameters compared to conventional layers.

EfficientNet is a family of convolutional neural network architectures for balancing the model's size and complexity of task classification while maximizing accuracy. It often considers increasing dimensions simultaneously to detect the target point from the dataset.

CNN architecture classifies images based on application and data type. It uses a layered architecture with input layers, convolution layers, and a normalization layer to optimize training and sensitivity reduction. The activation is normalized by subtracting and dividing the mini-batch standard deviation to speed up training and enhance the learning rate. The activation function ReLU, is used for convolution and batch normalization. By using the threshold value, the threshold value defined for each element with a value less than zero is set to zero, as defined in Equation (3).

$$F(m) = \begin{cases} m, & m \geq 0 \\ 0, & m < 0 \end{cases} \tag{3}$$

A convolutional layer followed by the max pooling layer is followed for downsampling to minimize the connections for fully connected layers, using Equation (4). Through max pooling, values should be returned, and if the pool size is [3 × 3], it will return values of height 3 and width 3. Max pooling also helps to eliminate overfitting. To set the random values of the input elements to zero with a given probability, the dropout layer is used without learning and works as max pooling. To classify an image, all the features are combined in the last fully connected layer. The output layer is followed by SoftMax, and classification layers follow the final fully connected layer.

$$P(nr \mid m, \theta) = \frac{p(m, \theta \mid nr)\, p(nr)}{\sum_{j=1}^{k} p(m, \theta \mid nj)\, p(nj)} = \frac{\exp(qr(m, \theta))}{\sum_{j=1}^{k} \exp(qj(m, \theta))} \tag{4}$$

where $0 \leq P(nr \mid m, \theta) \leq 1$ and $\sum_{j=1}^{k} p(m, \theta \mid nj) = 1$. Moreover, qr = ln $p(m, \theta \mid nr)\, p(nr)$, $P(nr \mid m, \theta)$ is called conditional probability.

The values of the SoftMax function transfer the input to one of the K-exclusive classes using the entropy function in the classification layer in Equation (5).

$$E(\theta) = -\sum_{i=1}^{v} \sum_{j=1}^{k} tij \ln yi(mi, \theta) \tag{5}$$

3.5. Performance Evaluation

The suggested model's ability to identify lymphoblasts in a microscopic image of a blood sample was examined using the confusion matrix. The number of samples for each class that were successfully and improperly identified is shown in the performance measures. A confusion matrix with two classes (positive and negative) was used that is appropriate for a binary classification task. Five measures have been used to assess the effectiveness of the suggested method: accuracy, precision, recall, and F1-score are commonly used, as shown in Table 3.

Table 3. Equations of evaluation measures.

Sr#	Metrics	Formula
1	Accuracy	$\frac{TP+TN}{TF+FN+FP+TP}$
2	Precision	$\frac{TP}{TP+FP}$
3	Recall	$\frac{TP}{TP+FN}$
4	F1-score	$\frac{2(Precision*Recall)}{Precision+Recall}$

where TP, TN FP, and FN stand for true positive, true negative, false positive, and false negative, respectively.

4. Results Analysis and Discussion

We propose a complete approach integrating diverse DL-based models for detecting ALL diseases based on the applied algorithms. We analyzed how different computational methods, including pre-trained and proposed model CNN approaches, can effectively detect white blood cell disease with a high accuracy rate. Here is the brief methodology, along with the results of the algorithms used in this research.

4.1. Analysis of Results with Pre-Trained Models

Figure 7 depicts the training and validation accuracy of the DenseNet121 model over 100 epochs for leukemia detection, achieving 93% accuracy. While the training accuracy remains relatively stable, the validation accuracy fluctuates significantly. These sharp drops in validation accuracy suggest overfitting, where the model performs well on the training data but struggles to generalize on unseen data. Despite these fluctuations, the model achieves high final accuracy, indicating its potential, but the overfitting issue needs to be addressed with techniques like dropout, early stopping, or further data augmentation.

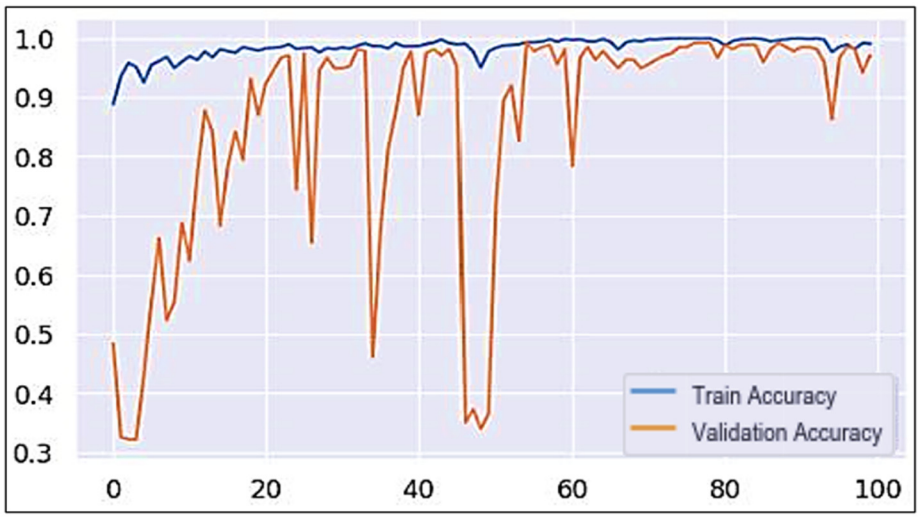


Figure 7. Training and validation accuracy of DenseNet121 model.

Figure 8 shows the accuracy of the Inception v3 model over 100 epochs, achieving 93% final accuracy in leukemia detection. The training accuracy stabilizes early, with the validation accuracy showing occasional sharp dips, but generally following the training trend. The model's precision, recall, and F1-score are all at 93%, indicating balanced performance in terms of correctly identifying leukemia cases and minimizing false positives and false negatives. However, the fluctuations in validation accuracy indicate potential overfitting, which could be mitigated with techniques like cross-validation or regularization. An auxiliary classifier activation function used in Inception v3 to solve the vanishing gradient problem and the SoftMax activation function is used to generate the final detection of accuracy with 93%, as depicted in Figure 8.

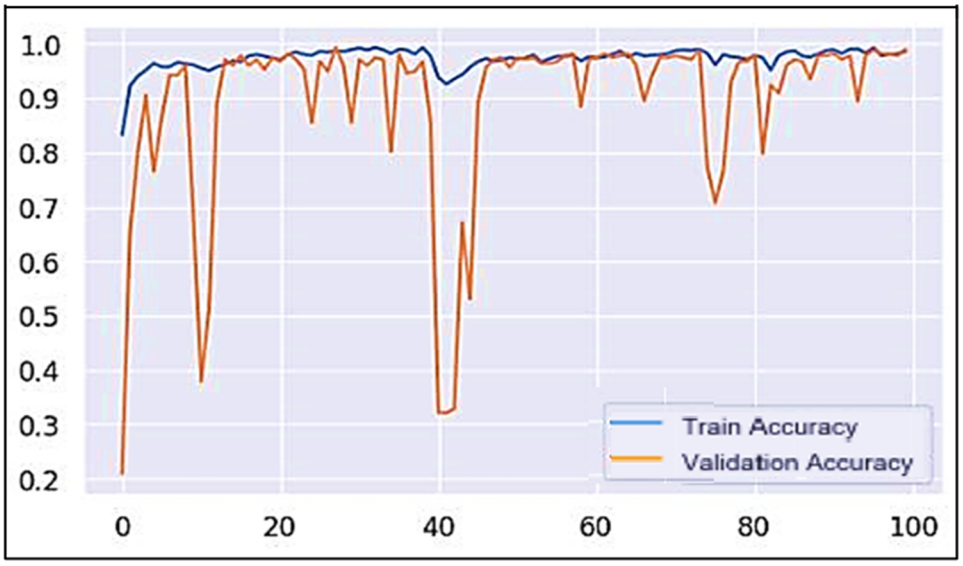


Figure 8. Training and validation accuracy of Inception v3 model.

The ResNet-50 model achieved high performance, with 95% accuracy, along with high precision (93%), recall (95%), and F1-score (95%), as shown in Figure 9, indicating its reliability in leukemia detection tasks. The accuracy curve shows quick convergence, with the training accuracy stabilizing near 100%. However, validation accuracy experiences significant dips throughout the epochs, which might be a sign of overfitting. Despite these fluctuations, the high final accuracy and consistent recall and F1-score reflect the model's ability to correctly classify leukemia cases while minimizing false negatives.

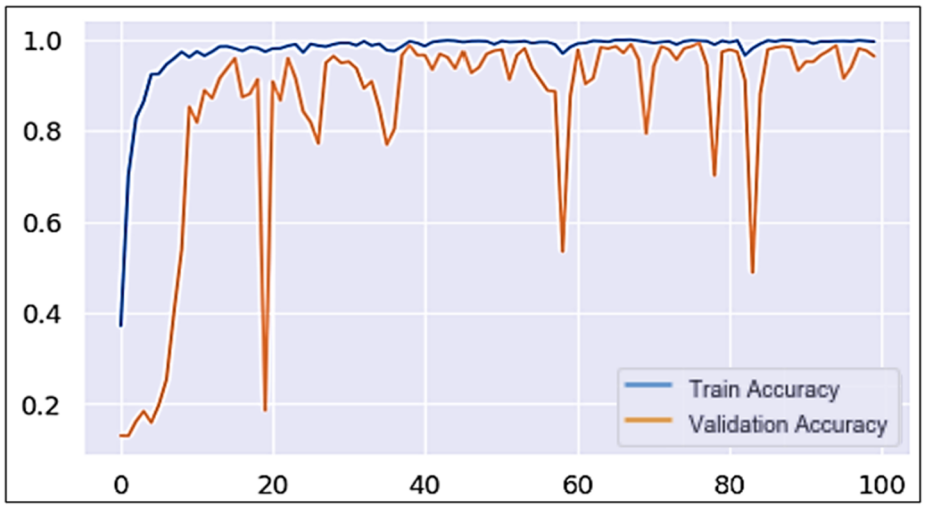


Figure 9. Training and validation accuracy of ResNet-50 model.

The performance of the MobileNet model for detecting leukemia shows strong accuracy on the training data, as shown in Figure 10, reaching 96%, which indicates that the model is highly capable of learning from the given dataset. However, the validation accuracy demonstrates considerable volatility across epochs. This suggests that the model is overfitting to the training data, struggling to generalize well to unseen data. Despite the high training accuracy, the fluctuating validation performance reveals that the model's ability to consistently detect leukemia in new, unseen cases is unstable, signaling the need for optimization or regularization techniques to improve its robustness.

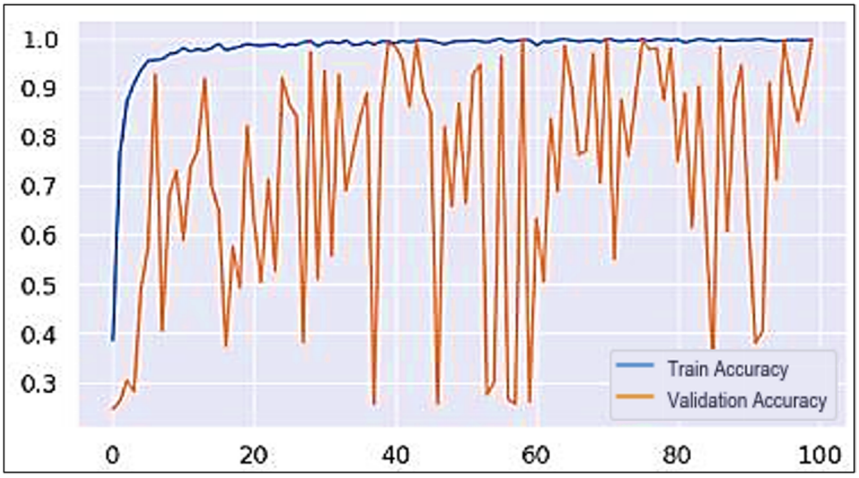


Figure 10. Training and validation accuracy of MobileNet model.

The performance of the EfficientNet model in detecting leukemia shows promising results, with a training accuracy of 92% and a validation accuracy of 90%, as shown in Figure 11. The model demonstrates strong learning capabilities on the training data while maintaining a fairly high validation accuracy. However, the validation performance still exhibits some fluctuations, which could be indicative of occasional overfitting or instability when applied to unseen data. Despite these variations, the overall performance of EfficientNet reflects a high level of reliability, with potential for improvement through fine-tuning techniques to stabilize the validation results.

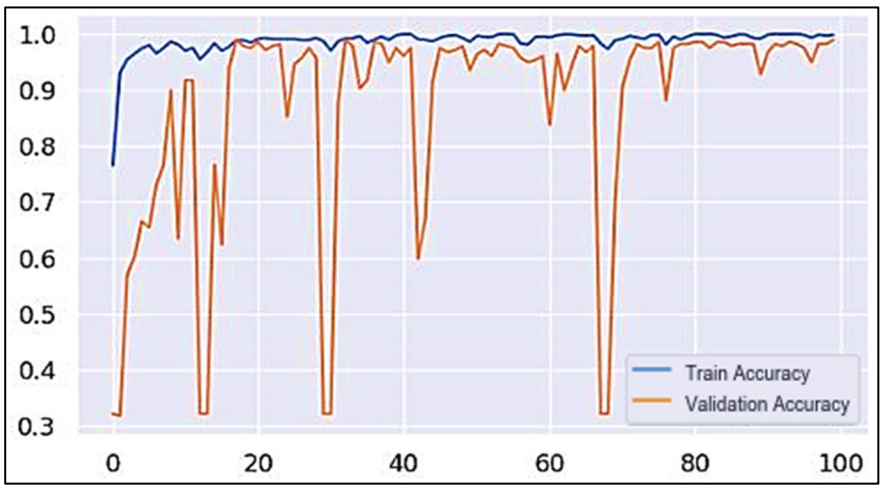


Figure 11. Training and validation accuracy of the EfficientNet model.

4.2. Analysis of Results with Proposed CNN Model

The proposed CNN model demonstrates exceptional performance in leukemia detection, achieving near-perfect accuracy with 99% for both training and validation sets, as shown in Figure 12. This consistency suggests that the model has been well optimized and is capable of generalizing effectively to unseen data. The stability of both training and validation accuracies across epochs indicates that overfitting has been minimized, and the model is highly reliable for detecting leukemia with excellent precision. These results highlight the proposed CNN as a robust and accurate tool for this medical imaging task.

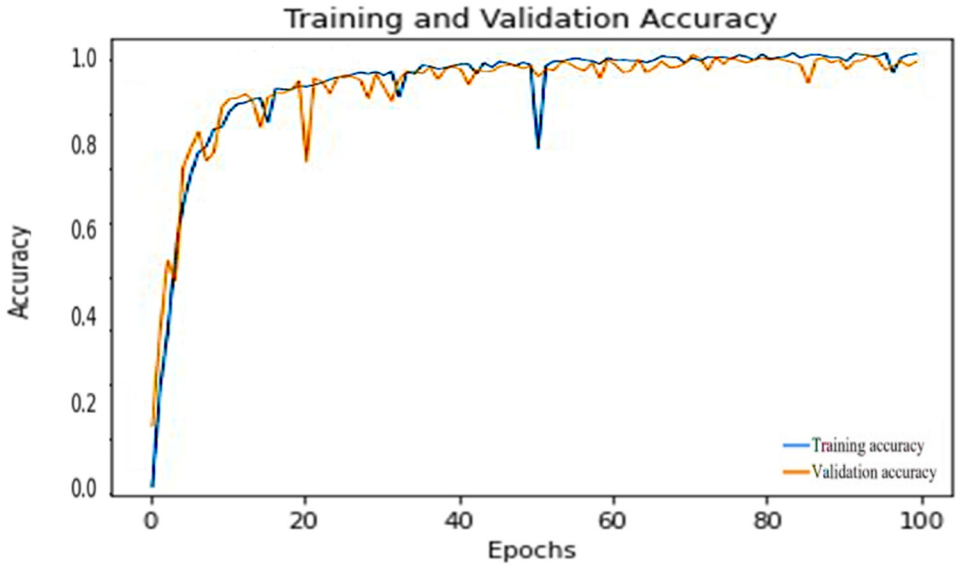


Figure 12. Training and validation accuracy of proposed model CNN.

4.3. Implementation of Models

The details of the parameters used for the experimentation are given in Table 4. The batch size sets the training batches. Throughout training, the neural network is modified iteratively depending on the mistakes made on the training dataset. It is impossible to update the weight with all the images at the same time. As a result, the batch size is a collection of images used in an iteration. Parameters are set to a multiple of 2 utilizing 32 filters at 100 batches until the training is finished with a lr of 0.01 to 0.0001 and momentum 0.9 over 100 epochs.

Table 4. Implementation parameters.

Parameters	For All Models
Batch	32
Subdivisions	4
Width	224
Height	224
Channel	3
Learning rate	0.01, 0.00001
Epochs	100
Classes	4
Filters	32

The proposed CNN achieved the highest accuracy of 99%, indicating its effectiveness in distinguishing between different types of WBCs associated with leukemia. This high accuracy suggests that the CNN architecture, with its simple yet powerful design, effectively captures the revealed features for the classification tasks in medical imaging. However, other architectures, such as DenseNet121, Inceptionv3, MobileNet, EfficientNet, and ResNet-50, also demonstrate accuracies ranging from 92% to 99%, though these are not as high as the CNN model. These results indicate their potential utility in leukemia detection. Interestingly, the EfficientNet model performed comparatively worse, achieving an accuracy of 92%. This lower accuracy might be attributed to various factors, including the specific scaling method employed to model the complexity of the leukemia detection task.

From the provided results, it is evident that the CNN model achieved the highest accuracy of 99%, indicating its effectiveness in distinguishing between the different classes of WBCs; the performance analysis is shown in Figure 13. This high accuracy suggests that the CNN model, with its ability to capture complex patterns and relationships in the

data, performed exceptionally well in this detection. The comparison in Table 5 provides a concise overview of the accuracy results for each model.

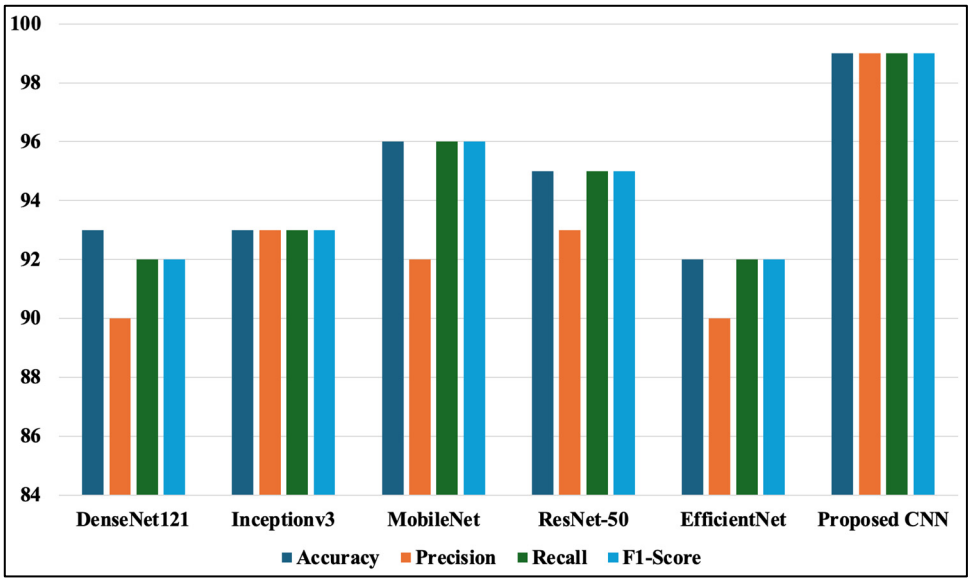


Figure 13. Comparison of pre-trained results with proposed model.

Table 5. Comparisons of pre-trained model results with proposed model (%).

Models	Accuracy	Precision	Recall	F1-Score
DenseNet121	93	90	92	92
Inceptionv3	93	93	93	93
MobileNet	96	92	96	96
ResNet-50	95	93	95	95
EfficientNet	92	90	92	92
Proposed CNN	99	99	99	99

5. Conclusions and Future Work

Diagnosis is a significant aspect of the healthcare department, serving as the foundation for the effective treatment and detection of diseases like leukemia, which is critical for improving patient outcomes, making it essential to develop highly accurate diagnostic systems. In this work, we present a novel architecture for the detection of leukemia with different variants of WBCs employing deep architecture utilizing the knowledge of five differently pre-trained models. In this study, we explored the application of deep learning architecture to improve the accuracy of leukemia detection, utilizing the BCCD dataset with four distinct classes. Implementing the CNN with knowledge of five differently pre-trained models achieved an impressive accuracy of 99%. CNN-based models, like the one used in this study to detect leukemia with 99% accuracy, show great promise for detecting early symptoms in blood cell images. This exceptional performance highlights the transformative potential of deep learning models in medical diagnostics for complex conditions. Our research led to earlier and different types of leukemia disease detection accurately. In future work, for better learning and to overcome the problem of medical imaging data, we will enhance our pre-trained models by generating more training images. We will expand our analysis to include advanced models such as Vision Transformers (ViTs), deep convolutional neural networks (DCNNs) with attention mechanisms, and hybrid models. In addition, we will investigate Self-Supervised Learning (SSL) and Advanced Generative Adversarial Networks (GANs) for data augmentation. This comparison will allow us to assess the efficacy of our method in comparison to these more advanced ones.

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