Blood Cells Cancer Detection Based on Deep Learning

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Abstract: Acute Lymphocytic Leukemia (ALL) is a form of cancer characterized by the abnormal production of white blood cells in the bone marrow. These cells do not function properly, leading to the overcrowding of healthy cells and weakening the body's immune system, making it more susceptible to infections. ALL progresses rapidly in children, and without timely treatment, it can be fatal. However, manually detecting this disease is a time-consuming and laborious task. In contrast, machine learning and deep learning techniques offer faster and more accurate detection methods. This study proposes a deep feature selection approach for identifying Acute Lymphocytic Leukemia in images of peripheral blood specimens. The approach utilizes the MobileNetV2 model to extract deep features from a dataset of peripheral blood specimen images, which are then used to train the model. By leveraging the base structure of MobileNetV2, the model demonstrates a high level of accuracy. Furthermore, by incorporating activation functions and additional layers into the model, the accuracy is significantly improved.

Keywords: Blood cell, Cancer, CNN, deep learning, MobileNetV2.

1. Introduction

Cancer is a devastating disease with significant global implications, and among its various types, blood cancer is particularly dangerous in advanced stages. Leukemia, a form of cancer that affects white blood cells or leukocytes, constitutes one percent of the total blood volume and plays a crucial role in the body's immune function. In addition to leukocytes, blood also contains red blood cells (RBCs) and platelets, which collectively contribute to the body's defense mechanisms [1]. Leukemia compromises the immune system by producing an excessive number of immature leukocytes, primarily affecting the bone marrow. The disease is classified into two main types: chronic and acute. Acute leukemia progresses rapidly, while chronic leukemia advances more gradually. The symptoms associated with acute leukemia are significantly more severe compared to the chronic form. Acute Lymphocytic Leukemia (ALL) is a specific subtype of white blood cell cancer characterized by the uncontrolled proliferation of immature leukocytes within the bone marrow. Remarkably, ALL is predominantly found in children, accounting for approximately 25% of all childhood cancers [2]. Diagnosing ALL poses challenges due to its flu-like symptoms, such as weakness, joint pain, and fatigue. Manual detection of this cancer requires the expertise of doctors or physicians for early and accurate diagnosis. The examination of blood smear images has become common for ALL detection. However, manual

detection has limitations, including issues with noise, blurriness, weak edges, and the complex nature of blood cells. Additionally, it is reliant on human interpretation. Machine learning (ML) and deep learning (DL) advancements have the potential to improve the accuracy of disease detection and assist doctors in proper diagnosis and treatment [3]. The proposed approach involves preprocessing the images, extracting features, selecting relevant features, and performing classification. Convolutional Neural Networks (CNNs) are a well-known technique frequently used for classification purposes, including medical image datasets. ML techniques have shown great potential in enhancing the accuracy and efficiency of leukemia diagnosis, classification, and predicting treatment outcomes [4]. This study presents an innovative approach for the detection and classification of blood cancer using machine learning techniques. The MobileNetV2 architecture implemented in Python is employed, achieving remarkable accuracy results.

2. Convolution Neural Network

Convolutional Neural Networks) belong to a class of Neural Networks that have demonstrated remarkable effectiveness in various domains, particularly in image recognition and classification tasks. CNNs have been widely successful in identifying faces, objects, and traffic signs, while also playing a crucial role in enabling vision in robots and self-driving cars. Within the realm of Neural Networks, Convolutional Neural Networks (CNNs) are specifically designed for image recognition and classification, making them a prominent choice in these areas [5, 6]. They have found extensive application in object detection, face recognition, and similar domains. A notable advantage of CNNs is that they eliminate the need for manual feature extraction. Instead, the system learns to automatically extract relevant features. The fundamental concept of CNNs revolves around performing convolutions on images using filters to generate invariant features, which are then passed to subsequent layers. A Convolutional Neural Network typically comprises one or more convolutional layers, often accompanied by a subsampling step, followed by one or more fully connected layers, resembling a standard multilayer neural network. The architecture of CNNs is specifically designed to leverage the two-dimensional structure of input images (or other 2D inputs like speech signals) [7, 8]. This is achieved through local connections and shared weights, which are then followed by some form of pooling operation to generate translation-invariant features. Additionally, CNNs offer the advantage of being easier to train and containing significantly fewer parameters compared to other neural network architectures. Layers of CNN structure:

2.1. Convolutional Layer

The primary goal of the convolutional operation is to capture essential image characteristics, including color, edges, gradients, and orientations, from the input image. Feature maps are employed to extract these significant image features. The convolutional operation involves the multiplication of the feature map matrix with the input image, resulting in a reduction in the dimensionality of the input image [9]. Fig. 1 illustrates the convolution operation.

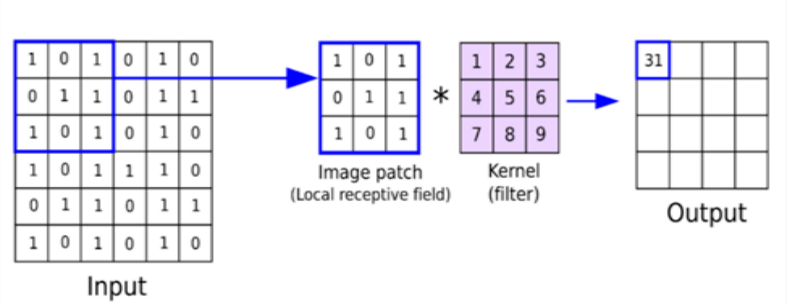

Fig. 1. Convolution operation.

2.2. Pooling Layer

Just like the convolutional layer, the pooling layer serves the purpose of reducing the dimensionality of the convolved feature. Its main function is to extract prominent features that possess rotational and positional invariance, which contributes to the effective training of the model. Pooling can be performed in two ways: Max pooling and Average pooling. In Max pooling, the highest value within the kernel matrix's covered portion of the image is selected. On the other hand, Average pooling calculates the average of all the values within the kernel's coverage area. Fig. 2 depicts the pooling operation [10].

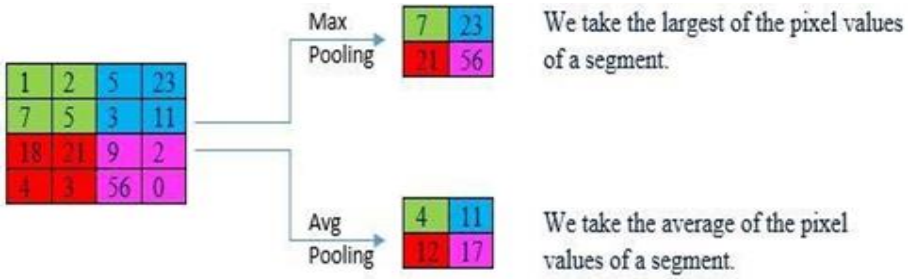

Fig. 2. Max & Avg Pooling.

2.3. Flattening

Flattening layer reduces the three- dimensional matrix into one dimensional matrix so that it can be easily given as an input to the next layer [11]. The flattening operation is shown in the Fig. 3.

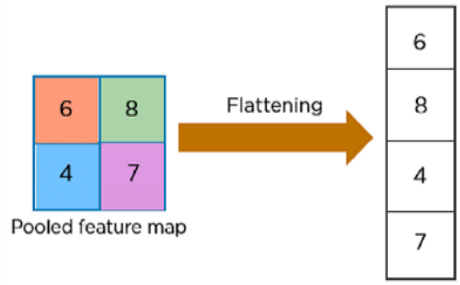

Fig. 3. Flattening operation.

2.4. Fully Connected Layer

In neural networks, fully connected layers refer to those layers where every input from one layer is connected to each activation unit of the subsequent layer. Typically, in many well-known machine learning models, the final layers consist of fully connected layers that combine the data extracted by preceding layers to generate the ultimate output. Among the network layers, fully connected layers rank as the second most time-consuming layer, following the Convolutional Layer [12]. Fig. 4 illustrates the structure of a fully connected layer.

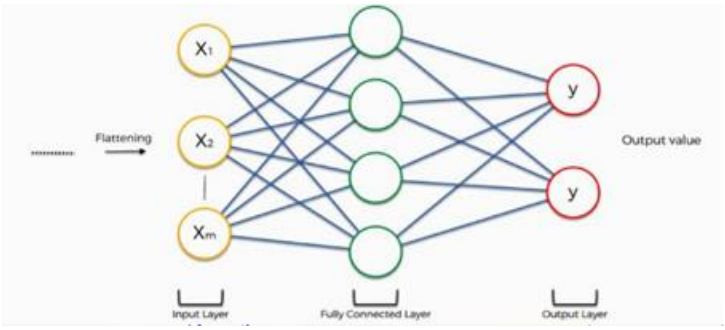

Fig. 4. Fully connected layer.

3. Transfer Learning

Transfer learning is a field of study within Deep Learning (DL) that centers around the idea of utilizing knowledge acquired during the training of one model and applying it to another model. It involves retraining a model, previously trained for one specific task, to perform a different but related task. The diagram depicted in Fig. 5 illustrates the distinction between transfer learning and traditional learning approaches [13].

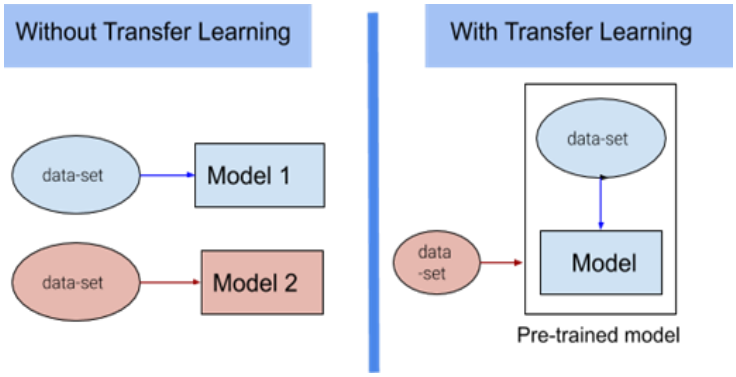

Fig. 5. Traditional learning vs transfer learning.

In the diagram above, looking at the traditional approach that is without transfer learning, both models, which are meant for different tasks are trained from scratch. On the other hand, when using transfer learning, we use our data-set to train a pre-trained model that performs a different task. Here are some of the pre-trained models can use for computer vision: MobileNetV2, VGG-19, Inception V3, XCeption, ResNet-50 [14, 15].

The architecture of MobileNetV2 is a convolutional neural network (CNN) that incorporates depthwise separable convolution, an approach that divides the standard convolution operation into two parts: depthwise convolution and pointwise convolution. In the depthwise convolution, a single filter is applied independently to each input channel, resulting in reduced computational costs. Subsequently, pointwise convolutions employ a 1x1 convolution to merge the output of depthwise convolutions across channels, facilitating more comprehensive feature interactions. The model also employs inverted residuals with linear bottlenecks, which expand the number of channels in the bottleneck layer and utilize a depthwise separable convolution. These features collectively enhance the efficiency of the MobileNetV2 model. Figure 6 illustrates the architecture of MobileNetV2 [16, 17].

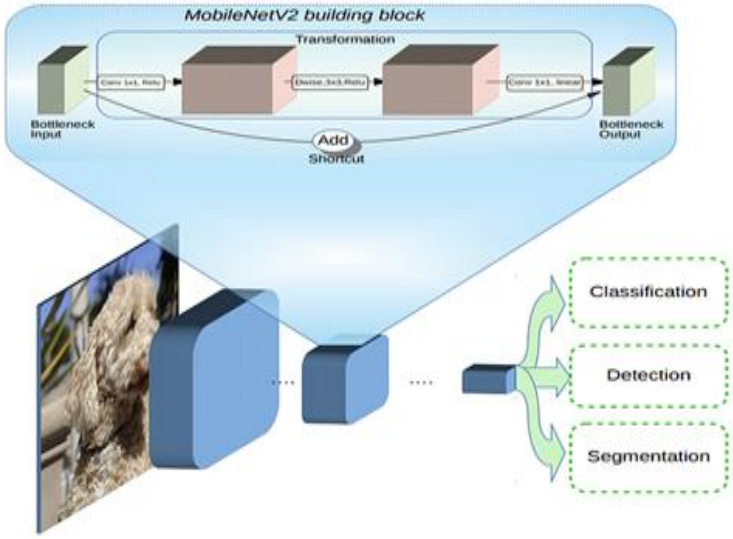

Fig. 6. The architecture of MobileNetV2.

4. System Implementation

Blood cell cancer identification and diagnosis are critical in early intervention and treatment planning, and have a substantial impact on patient outcomes. Advances in DL and computer vision techniques have paved the path for more accurate and efficient tumor detection systems in recent years. In this chapter, pre-trained model which is MobileNetV2 will be used to build a blood cell cancer detection system [18–28].

4.1. Dataset Preparation

In this paper, the Blood Cells Cancer (ALL) Dataset has been utilized from the Kaggle platform [29]. This dataset were prepared in the bone marrow laboratory of Taleqani Hospital (Iran). This dataset consisted of 3242 PBS images from 89 patients suspected of ALL, whose blood samples were prepared and stained by skilled laboratory staff. This dataset is divided into two classes benign and malignant. The former comprises hematogenous, and the latter is the ALL group with three subtypes of malignant lymphoblasts: Early Pre-B, Pre-B, and Pro-B ALL. Early Pre-B, Pre-B, and Pro-B cells are different stages of B-cell development in the bone marrow [30].

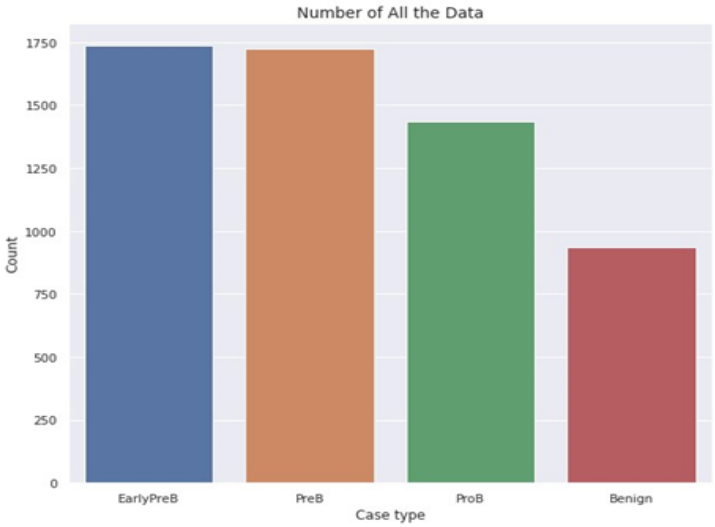

Fig. 7. Distribution of the utilized dataset.

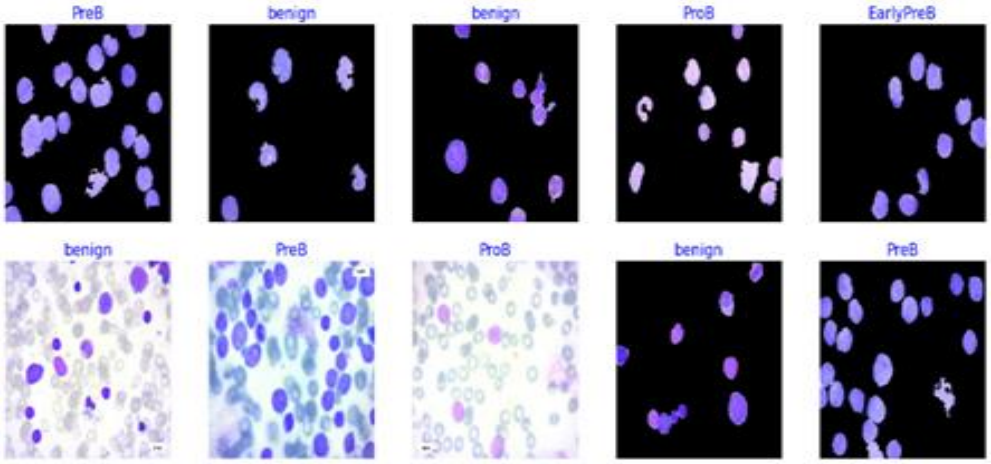

Fig. 8. Sample of the dataset.

4.2. Training Phase

This phase consists of four stages which are: preprocessing, data splitting, shuffling, training process, saving the model.

Pre-processing

Pre-processing consists of two steps which are: shuffling and image segmentation.

***Shuffling*:** The data is mixed up to improve a neural network's performance and generalization, starting with the shuffling technique. This procedure merely rearranges the data. To improve testing accuracy, all training and testing data should be randomly shuffled [31–35]. The dataset has been randomly shuffled in this step.

Image segmentation: Image segmentation refers to the process of dividing a digital image into multiple segments or pieces. The objective is to group pixels together based on their similarity, which can be evaluated using factors such as color, intensity, texture, or other distinctive features. Machine learning techniques for image semantic segmentation have wide-ranging applications, including object recognition and medical image analysis. Various methods can be employed for deep learning-based image segmentation, such as clustering, region expansion, and thresholding algorithms [36]. Fig. 9 provides a visual representation of image.

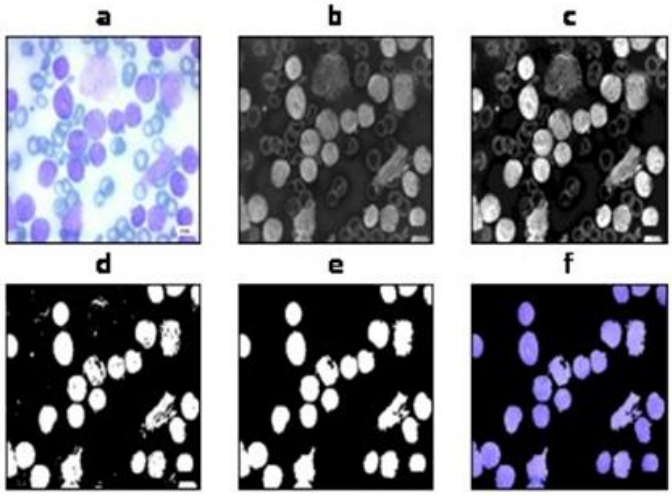

Fig. 9. Image segmentation.

Data Splitting

Following data pre-processing, the second step is to partition the dataset, the dataset needed for the DL model is divided into two parts: the training set and the test set. This division implies that 90.0% of the data was allocated for training purposes, while the remaining 10.0% was used for testing.

Training process

On the Kaggle platform, transfer learning was applied to the pre-trained MobileNetV2 model. Researchers have utilized the ImageNet dataset to train, MobileNetV2 model. This dataset is composed of more than one million images. MobileNetV2 is a significant architecture in the MobileNets family developed by Google, with the aim of providing efficient models for mobile and embedded vision applications. The MobileNetV2 architecture builds on the original MobileNet, which used depthwise separable convolutions as efficient building blocks. MobileNetV2 introduces two new features to the architecture which are:

Inverted residuals: Traditional residual connections in architectures like ResNet have a bottleneck design where the number of channels is reduced before the convolution and then expanded afterwards. MobileNetV2 flips this design into what they call an inverted residual structure. Here, the input is first expanded to a higher dimensional space and then compressed back to a lower dimension. This technique is found to be more effective for mobile vision tasks.

Linear bottlenecks: MobileNetV2 includes what it calls linear bottlenecks between the layers. This feature

involves taking the output of the inverted residual and passing it through a linear activation function (or, equivalently, no activation function) instead of a non-linear one like Rectified Linear Unit (ReLU). This is done to preserve the full information from the previous layer, preventing the destruction of some information that could occur with a nonlinear function.

One of the key considerations in the MobileNetV2 architecture is the balance between latency and accuracy. The model has been designed to be scalable in terms of resolution, the number of channels, and the number of layers. These innovations allow MobileNetV2 to achieve higher accuracy than its predecessor, with roughly the same computational cost. Three conv2d layers were employed in this model, each followed by a Leaky ReLU activation function and GlobalAveragePooling2D layer to reduce model complexity. Batch Normalization layer is used to improve training stability and speed up the learning process. To avoid over fitting, there are Dropout layers. Model was trained for 30 epochs.

Saving the model

It is critical to store the trained models so that they can be loaded later in the testing phase without having to be trained again.

Testing phase

The aim of this stage is to test the model, it's used to assess how well a trained model performs. In this paper, all data was split, with 10.0% of this data being used for testing. It's important to use a different set of data for testing. The trained ML model that were previously saved and applied to the image are used in this stage to forecast the presence of a blood cell tumor. This stage is crucial to seeing the model' predictions. Tumor labels are linked to particular patterns discovered from a dataset of blood cell tumors. The tumor with the highest probability is chosen as the model forecast after computing a probability distribution over all tumor classifications. The forecast made by the model offers important information about the tumor's characteristics, such as its subtype or category. Medical personnel can use this information to make educated decisions about patient care, treatment planning, and diagnosis. Fig. 10 shows a sample of result of the testing phase.

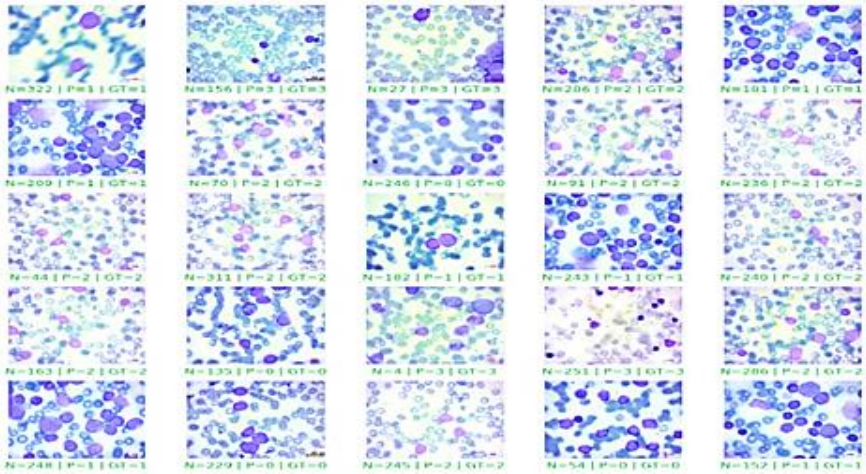

Fig. 10. Samples of tumor predictions.

5. Performance Evaluation

In this paper, various evaluation metrics were chosen which includes: confusion matrix and accuracy, and due to the dataset in this paper not balanced; model performance can be evaluated using other metrics such as F1 score, recall, and precision. These metrics are especially useful when working with imbalanced datasets because accuracy may not be enough to completely evaluate model performance.

5.1. Confusion Matrix

A confusion matrix is a technique for describing the performance of a statistical classification model. Classification accuracy alone can be misleading if the number of observations in each class is not the same (e.g., imbalanced dataset), or if the dataset has more than two classes. Calculating a confusion matrix can provide a better understanding of the classification model's correct behaviour and help to identify the errors that can be made. The number of accurate and erroneous predictions is summarized with count values and divided by class.

5.2. Accuracy

Accuracy is a popular evaluation metric in ML that assesses how well a model predicts the proper output or class labels for a given set of input data. It is a method of quantifying a model's overall performance because it indicates the model's capacity to produce the right predictions. As a percentage or decimal value between 0 and 1, where 1 indicates perfect predictions, accuracy is derived by dividing the number of correct predictions made by the model by the total number of forecasts. A higher accuracy shows that the model is producing more accurate predictions and is consequently more adept at doing the task it was taught to do. The formal equation of the accuracy equation is shown below:

$$\text{Accuracy} = \frac{(Tp+Tn)}{(Tp+Tn+Fp+Fn)} \times 100\% \quad (1)$$

where true positive (TP) and false positive (FP) are the number of samples correctly and wrongly classified as their class. Likewise, true negative (Tn) and false negative (Fn) are the number of samples correctly and wrongly classified as their classes.

5.3. Precision

Precision is calculated as the ratio of correctly categorized positive samples to all samples that were classified as positive, whether rightly or wrongly. It evaluates how accurately a sample is classified as positive by the model. The formal equation of the Precision equation is shown below:

$$\text{Precision} = \frac{Tp}{(Tp+FP)} \times 100\% \quad (2)$$

5.4. Recall

Recall, which is often referred to as sensitivity, is computed as the proportion of positively categorized samples to all positively classified samples. It gauges how well the model can identify positive samples. The formal equation of the Recall equation is shown below:

$$Recall = \frac{TP}{(Tp+Fn)} \times 100\% \quad (3)$$

5.5. F1-score

The F1 score is a measurement that combines recall and precision. As the harmonic mean of recall and precision, it is so named. The F1 score of a perfect model is 1. The formal equation of the F1-score equation is shown below:

$$F1 - score = \frac{2 \times Recall \times Precision}{Recall + Precision} \times 100\% \quad (4)$$

The model that used is the MobileNetV2 model, which was trained on the Blood cell cancer (ALL) dataset. It is composed of three conv2D layers that extract features from input images by sliding a convolution filter over the input to form a feature map. The model was trained for 30 epochs and its accuracy was assessed throughout each epoch. The model achieved a training accuracy of 98.15% at the 30th epoch using Blood cell cancer (ALL) dataset, as shown in Fig. 11. It was discovered that the accuracy increased from 30.48% in the

first epoch to 97.95% in the 30th epoch, indicating that the model is becoming more accurate as it learns.

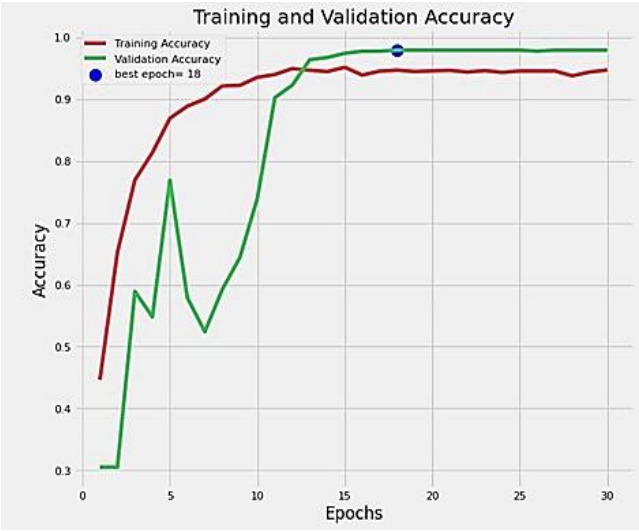

Fig. 11. The training and validation accuracy curve.

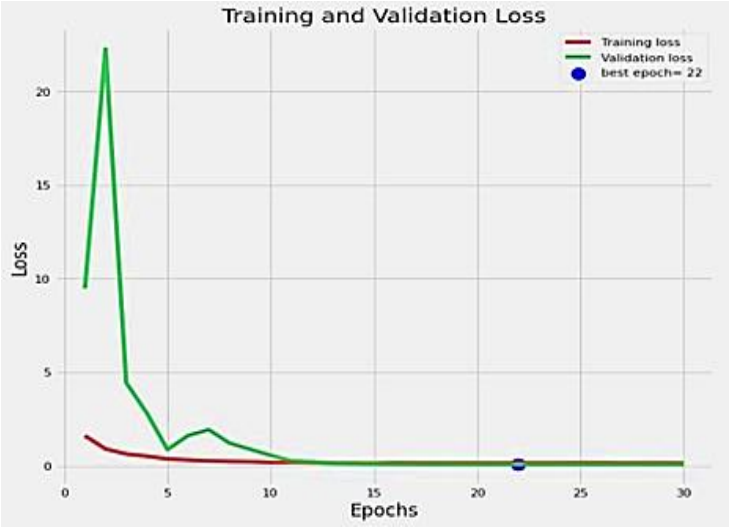

Fig. 12. The training and validation loss curve.

It was discovered that the first epoch's loss was 9.4709, indicating that the forecasts and actual values were very dissimilar. But by the 30th epoch, the loss had dropped to 0.0779, showing that the model's forecasts were now significantly more accurate. Table 1 depicts the outcomes of the other performance metrics employed in our model evaluation, namely precision, recall, and F1-score.

Table 1. The Performance Metrics of the Model

Metrics	Precision	Recall	F1-score
Early PreB	0.98	0.98	0.98
PreB	1.00	1.00	1.00
ProB	0.99	0.99	0.99
benign	0.93	0.93	0.93

The model appears to be performing fairly well, with excellent accuracy, recall, and F1-score for most classes, with the exception of the benign class it was the lowest between them. A confusion matrix is another way for describing the performance of a statistical classification model, Fig. 12 illustrates the confusion matrix.

It was discovered that the model is doing well, as most data are correctly classified, as indicated by the dark blue squares along the diagonal. Misclassifications are minimal, as shown by the lighter squares off the diagonal. In order to improve the performance of the model the Rectified Linear Unit (ReLU) activation function, Batch Normalization, and a Dropout Layer (rate: 0.3) was applied. The model after enhancing was trained for 30 epochs and its accuracy was assessed throughout each epoch. The model achieved a training accuracy of 99.69% at the 30th epoch using Blood cell cancer (ALL) dataset, as shown in Fig. 14.

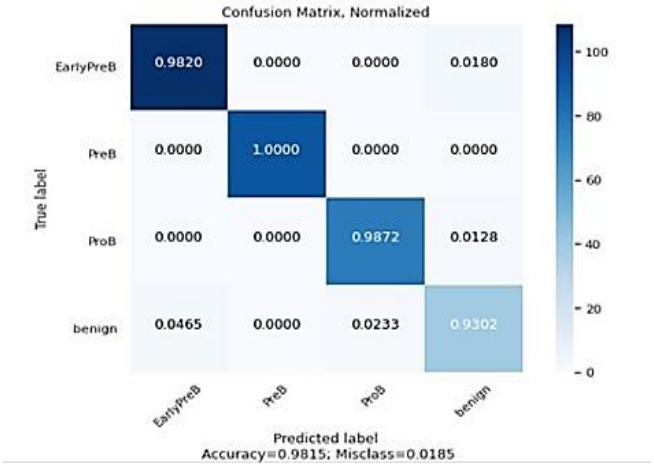

Fig. 13. The confusion matrix of the model.

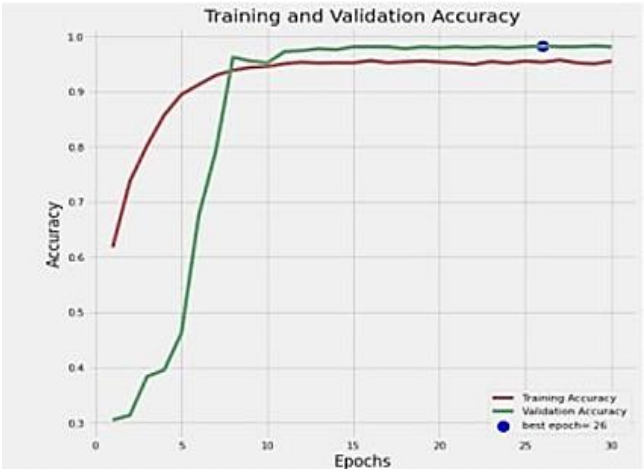

Fig. 14. The training and validation accuracy curve.

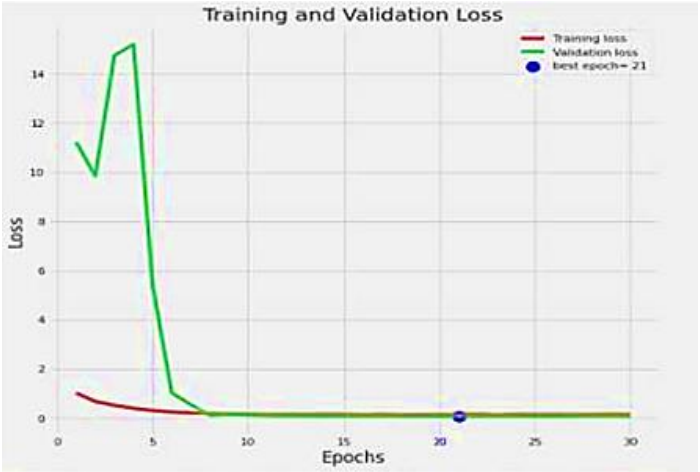

Fig. 15. The training and validation loss curve.

It was discovered that the accuracy increased from 30.48% in the first epoch to 98.12% in the 30th epoch, indicating that the model is becoming more accurate as it learns. As shown in the Fig. 15, both training and validation losses were tracked during each epoch of this paper.

It was discovered that the first epoch's loss was 11.2172, by the 30th epoch, the loss had dropped to 0.0710, showing that the model's forecasts were now significantly more accurate. Table 2 depicts the outcomes of the other performance metrics employed in our improved model evaluation, namely precision, recall, and F1-score.

Table 2. The Performance Metrics of the Improved Model

Metrics	Precision	Recall	F1-score
Early PreB	1.00	0.99	1.00
PreB	1.00	1.00	1.00
ProB	1.00	1.00	1.00
benign	1.00	1.00	1.00

The model appears to be performing fairly well, with excellent accuracy, recall, and F1-score for most classes, with the exception of the Early PreB class it was the only class with losses. Fig. 16 illustrates the confusion matrix for the previous model [37–43].

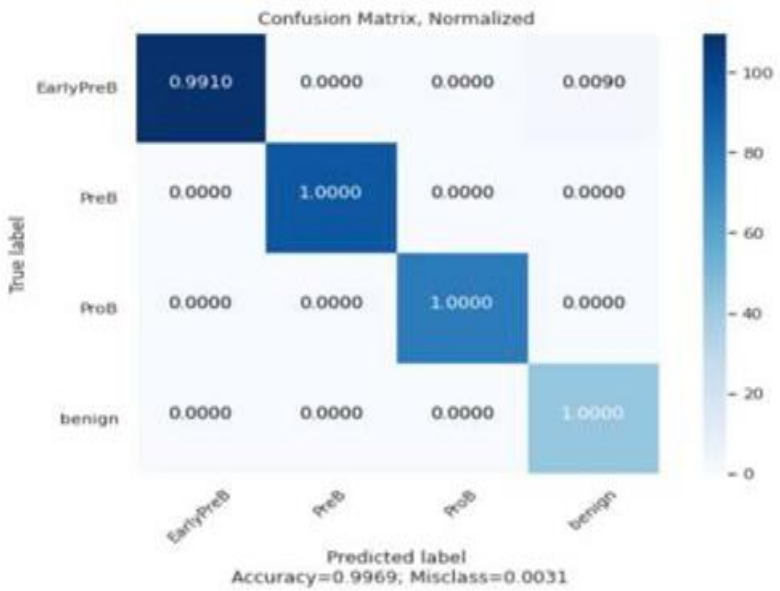

Fig. 16. The confusion matrix of the model.

It was discovered that the model performed pretty well in predicting these classes with the expiation of Early PreB that has misclassification.

6. Conclusion

Leukemia is a form of cancer that affects the blood and bone marrow. It is characterized by an abnormal increase in white blood cells, which subsequently weakens the immune system. White blood cells play a vital role in defending the body against infections and diseases. In this study, the MobileNetV2 model was utilized to detect and classify acute lymphocytic leukemias, which are a specific type of blood cancer. This study focuses on improving the performance of a machine learning model for detecting Acute Lymphoblastic Leukemia. The initial model achieved 98.15% accuracy with a 7.08% loss. To enhance its capabilities, Rectified Linear Unit (ReLU) activation, Batch Normalization, and a Dropout Layer (rate: 0.3) was applied. The updated model exhibited significant improvement, reaching an accuracy of 99.69% with a reduced loss

of 1.61%. The refined model's enhanced accuracy and reduced loss signify a notable stride towards more reliable diagnostic methodologies in the realm of medical image analysis. This advancement is particularly crucial in the early detection of Acute Lymphoblastic Leukemia. Where timely and accurate diagnosis plays a pivotal role in treatment outcomes. The integration of Rectified Linear Unit (ReLU) activation, Batch Normalization, and a Dropout Layer with a rate of 0.3 has not only fine-tuned the model but also established a robust framework for future developments in hematologic cancer detection. The paper's utilization of the MobileNetV2 model showcases the adaptability of state-of-the-art architectures in addressing complex medical challenges. This adaptability, coupled with the efficacy of advanced techniques, underlines the potential for broader applications in the field of medical image analysis. As technology continues to evolve, the collaborative synergy between machine learning models and medical diagnostics holds immense promise for enhancing patient outcomes and streamlining healthcare processes.

Conflict of Interest

The authors declare no any Conflict of Interest

Author Contributions

Ahmed J. Abougarair, M. Alshaibi Writing the manuscript and the other authors reviewing and approved

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