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Deep Learning Based Detection and Classification of Bone Marrow Blood Cancer Using CNN

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***Abstract*— For early diagnosis and treatment of the blood cancer affecting the bone marrow, a correct diagnosis was important. The customary diagnosis was based on peripheral blood smear image, which was examined under a microscope. However, this technique was time consuming and observer dependent. This work presented an automated framework for detection and classification of ALL using Convolutional Neural Networks (CNN). These 3,242 microscopic images were divided into the training set, validation set, and the test set. Resizing, normalizing, and other data augmentations were done on all images to prevent overfitting and improve the generalization of the model. Transfer learning was applied using the EfficientNet-B0 model, which has pre-trained weights, and additional CNN layers were appended to the EfficientNet-B0 model to better learn features specific to the morphology of nuclei structure, cell shape, and texture pattern. The metrics used to measure the performance were the standard metrics. From the experiment conducted, the proposed model has an overall accuracy of 98.56%, precision of 98.50%, recall of 98.50% and an F1 score of 99.00%. The results showed that the proposed model could be used as a computer-helped diagnosis system for the assistance of early detection and clinical decision-making.**

Keywords—Bone Marrow Blood cancer, Acute Lymphoblastic Leukemia (ALL), Convolutional Neural Network (CNN), Deep Learning, EfficientNet-B0.

I. INTRODUCTION

One of the major challenges in present day healthcwere systems was the accurate diagnosis and classification of blood cancers including Acute Lymphoblastic Leukemia (ALL), since ALL and other leukemias (uncontrolled and proliferative growth of immature and dysplastic white blood cells) affect the function of the bone marrow and hematopoiesis, leading to a variety of meaningful clinical consequences. Although early detection of the disease was important for survival time and timely clinical management, in most low resource hospitals and in remote areas, the lack of clinical expertise and clinical diagnosis often proves to be problematic. Studies have shown that the use of hybrid deep learning models could improve the accuracy and generalization of the classification in clinical settings [1]. Self-supervised learning models were investigated to reduce reliance on labeled medical images and generalize better on medical images without labels [2]. The gold standard for diagnosing leukemia was the microscopic examination of peripheral blood smears (PBS) and bone marrow. When used by an experienced physician, these methods could help in classification, but they were slow and were subject to inter-observer agreement biases since it depends on the very experience of the physician. Normal and malignant cells appear similar, especially at the beginning of leukemia, making the visual identification of leukemia by physicians difficult. Standard machine learning techniques for leukemia detection include Support Vector Machine (SVM), and different types of clustering algorithms. Classical methods include manually extracting features, as well as the inferior ability to capture discriminative, high-dimensional features from medical imaging when compared to recent developments. [3] and [4].

Recently, convolutional neural networks (CNNs) have transformed deep learning in medical image analysis. It has been shown that CNNs could extract higher level features for classifying complicated medical images in a fashion similar to the human brain. Several distinct morphological features such as morphology of cell, shape of nucleus and various texture variations, could be accurately extracted using the CNN. Experimental results for the design of CNN for detection and segmentation of leukemia were very promising. Thus, transfer learning techniques such as those used in the proposed model help reduce the model's training time

while achieving high accuracy even for datasets with limited data [6][8]. [13], [20]. However, despite the great success of deep learning in medical image analysis, the performance of existing automatic diagnostic systems was still limited in many situations because of imbalanced class distributions, variations in imaging conditions, and insufficient amounts of labeled data for some diseases. To solve these problems, this study proposes a Deep Learning Based Detection and Classification of Bone Marrow Blood Cancer using CNN, which combines the architecture of CNN with transfer learning technique EfficientNet-B0. The proposed framework supports the data preprocessing techniques of image resizing, normalization, and augmentation to improve the generalization and to reduce overfitting. These two networks were employed to take advantage of extract low- and high-level features, which increased the overall performance of the classification task.

Standard performance metrics for evaluation were employed in the proposed method. The metrics included accuracy, precision, recall, and F1-score. Based on the experiments, the system obtained an average accuracy of 98.56%, which was better than that of traditional models, such as VGG and MobileNetV2, based on CNN architectures. This high level of accuracy demonstrates the competency of this model in differentiating between various types of leukaemia cells with minimized misclassification rates. This system could serve as an effective computer-aided diagnosis tool to assist medical practitioners and further develop healthcare solutions with enhanced effectiveness and early detection accuracy.

II. LITERATURE SURVEY

An advanced CNN-based classification method which directly works on medical images without image segmentation was proposed (Liu et al. [2]). Further, deep learning was also applied to diagnose ALL with higher accuracy (Rehman et al. [3]). Transfer learning has also been applied in the medical imaging domain for diagnosis purposes. For example, Perkonigg et al. (2014) [4] applied transfer learning for better bone lesion detection. Ensemble learning has also been proposed for better leukemia classification (Liu and Long 2019) [5].

Furthermore, ensemble based methods have better accuracy for this classification problem and also pre-trained deep CNN models have achieved good classification accuracy for leukemia classification (Shafique and Tehsin [6]). This article was a systematic review of machine learning techniques and emphasizes the increased role of artificial intelligence in the diagnosis of medical conditions (Ghaderzadeh et al. [7]). An advanced classification method, LDSVM, was presented for a better accuracy of diagnosis of leukemia (Karim et al. [8]). A study showed the effectiveness of soft computing techniques for blood sample analysis (Jogi and Dhole [9]). An deep learning-based approach for leukemic cell detection in microscopic images strengthens existing AI-based screening models (Baig et al. [10]).

Human vision-inspired models for leukemia detection not only increase accuracy but also enhance interpretability (Bodzas et al. [11]). A deep learning-based classifier was presented for biomedical diagnosis to enhance the system efficiency (Shawly and Alsheikhy [12]). Machine learning algorithms have been explored for disease prediction, indicating their interdisciplinary nature (Senthilmurugan et al. [13]). Feature selection techniques have been proposed to improve the classification accuracy (Mohsin Abdulazeez et al. [14]). An advanced CNN-based approach has been developed to identify leukaemia in a highly effective manner (Wagh et al. [15]). A comparative study of different machine learning algorithms with their benefits and drawbacks was highlighted (Italia Joseph Maria et al. [16]). Problems and issues concerning the classification and segmentation of leukemia, especially regarding the standardization of datasets, have been addressed (Saleem et al. [17]). Machine learning algorithms have been used for the diagnosis of blood cells and diseases (Varghese et al. [18]). Data mining techniques have been established for hematological data analysis (Akter et al. [19]). An AI-based system was developed to achieve real-time leukaemia screening (Syed-Abdul et al. [20]). An unsupervised classification using the k-means algorithm was presented, which achieved better computational efficiency (Ranjitha and Duth [21]).

Diagnosing leukemia from peripheral blood smear (PBS) images was a laborious and complex process. In this study, we investigated approaches for automating medical-image classification using deep learning. N. Kumar and P. S. Bai [1] proposed Convolutional Neural Networks (CNNs) that proved effective in the classification of medical images in medical diagnoses. Image preprocessing steps, including resizing, normalization, and data augmentation, were commonly employed to achieve better results for the model. Many pre-trained models, such as MobileNetV2, VGG19, and InceptionV2, have been explored, where MobileNetV2 showed a good trade-off between accuracy and computational complexity.

III. PROBLEM STATEMENT

Acute Lymphoblastic Leukemia (ALL) was a rapidly evolving blood cancer in which immature lymphocytes proliferate in the bone marrow and impair normal blood cell production [18], [20]. Prompt diagnosis and precise detection were of great significance for prolonging survival rates and devising appropriate treatment strategies for patients. However, conventional diagnoses require manual microscopy of PBS images and bone marrow cells, which was laborious, time-consuming, and depends entirely on the skills of experts and was prone to errors of inconsistency due to inter-observer variability [3], [8].

The large number of medical images creates difficulties in traditional methods of medical image

processing, which require highly specialized expertise and labor for their analysis, and these models do not respond efficiently in standard healthcare systems. Former machine learning-based leukemia diagnosis approaches used the manual extraction of hand-crafted features. This characteristic of machine learning models was inefficient for learning various complicated morphological patterns, thus limiting their generalizability to different medical images. Hence, these methods could effectively discriminate blood cells for disease classification but could not produce accurate and robust diagnosis of leukemia [4], [11], [14], [15].

Modern research methods for computer-aided diagnosis involve artificial intelligence and deep learning for improved performance. In particular, CNNs produce higher performance for automatic hierarchical feature extraction from microscopic images and were thus capable of providing efficient classification of leukemia cells [6], [7]. Transfer learning and hybrid CNN-based techniques have been introduced in many medical diagnosis models for robust performance when there were fewer labeled medical data points. Self-supervised learning was also used in data-scarce scenarios to improve model performance [1], [20], [2].

However, several problems, such as class-imbalanced data, noise within images, and a lack of labeled data, persist, thereby hindering the efficiency of existing automated diagnostic tools. Hence, a prompt, automated, scalable, and intelligent tool was required to achieve correct leukemia sub-classification by minimizing the efforts of manual analysis.

In this study, an automated ML-based technique for detecting blood cancer in the bone marrow was proposed. The proposed technique classifies 3242 microscopic PBS images into 4 classes (Benign, Malignant Early Pre-B, Malignant Pre-B and Malignant Pro-B) using transfer learning between a hybrid CNN and EfficientNet-B0 model. The developed model could effectively extract discriminatory features for multi-class classifications. The accuracy of the proposed model was 98.56%, which was promising for distinguishing different leukemia sub-classes and could be potentially used by medical experts in an automated diagnostic decision support system.

IV. Hybrid CNN and EfficientNetB0 with Transfer Learning

Reliable feature extraction and classification mechanisms were essential for the accurate and automatic detection of Acute Lymphoblastic Leukemia (ALL). In response to the challenges posed by traditional diagnostic methods, a hybrid deep learning framework combining CNNs and EfficientNet-B0 through transfer learning was proposed. The framework aims to effectively extract low- and high-level discriminative features from the PBS images.

CNNs have shown considerable promise in the analysis of medical images because they could automatically learn the feature hierarchy from raw input images [6, 7]. In this study, CNN layers were first used for feature extraction to analyze microscopic characteristics that differentiate cancer from normal cells, such as the cell structure, shape, and texture of the nucleus [3]. EfficientNet-B0 was then used as the backbone network to assume the role of the deep learning architecture and improve the classification model. EfficientNet uses a compound scaling method that uniformly scales the network depth, width, and resolution to balance network accuracy and the number of parameters, which was suitable for medical imaging applications. A hybrid deep learning model comprising a CNN and enhanced architecture performs better in real-world scenarios [1].

Transfer learning was performed by initializing the CNN weights in EfficientNet-B0 by pretraining the networks on a large-scale dataset. Leveraging the learned features and reducing the training time using this method could significantly improve the accuracy of limited labeled medical datasets. In previous studies, a pre-trained deep convolutional model was successfully applied to leukemia classification with improved accuracy compared to traditional methods [20]. Transfer learning technology has also improved generalization and reduced overfitting in medical image analysis [19].

The dataset that was used to train and evaluate the model consisted of 3,242 microscopic images, these images belonged to 4 classes namely; Benign, Malignant Early Pre-B, Malignant Pre-B, and Malignant Pro-B. Prior to training the model, several preprocessing steps were performed, including resizing, normalization, and data augmentation techniques were applied to the images to standardize the input, increase sample diversity, and improve the robustness of the model. Techniques such as rotation, flipping, and scaling were applied for data augmentation to reduce overfitting and improve he generalizability of the model [8].

The proposed hybrid model learns discriminative features from images to perform multi-class classifications. Backpropagation and gradient descent algorithms were used to optimize the model parameters. The classification performance of the model was evaluated using common performance metrics, such as accuracy, precision, recall, and F1 score.

The experimental results showed that the proposed CNN-EfficientNet-B0 hybrid model had an overall classification accuracy of 98.56 %. Combining the CNN feature extractor and EfficientNet structure would not only achieves higher accuracy and maintains high efficiency. The proposed system could act as a computer-aided diagnosis tool (CAD) for clinical doctors to make early diagnoses, reduce dependency on humans, avoid human error, and generate faster and more consistent results.

Algorithm:

This study presents a hybrid deep learning system composed of CNNs and EfficientNet-B0 to differentiate a specific type of Acute Lymphoblastic Leukemia (ALL).

CNNs were used to extract the most important features, such as cell morphology and texture, and EfficientNet-B0 acts as a backbone network to obtain better classification with fewer parameters than other models. The model was trained using the transfer learning method, where the weights of pre-trained models were utilized to achieve better accuracy with a low training time.

The hybrid architecture helps to learn the universal and domain-specific features effectively and discriminate between certain blood cell types. The model was trained and evaluated using standard classification metrics, such as accuracy, precision, recall, and F1-score. The proposed methods attained the highest classification performance and provided the best mechanism for reliable and efficient diagnosis of leukemia.

Pseudocode

1. Data Acquisition
2. Image Preprocessing
3. Data Augmentation
4. Dataset Splitting
5. Feature Extraction
6. Classification Layer
7. Model Training
8. Fine Tuning
9. Performance Evaluation
10. Prediction and Mobile Deployment

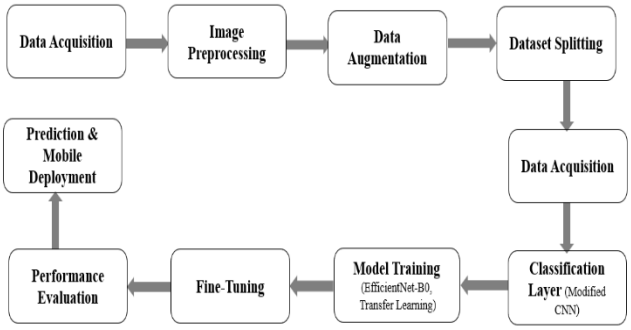

Fig 1: Proposed System Architecture Model

1. Data Acquisition

This work uses images of Pre Trained Dataset (Blood Cells Cancer All Dataset) in 4 categories: Benign, Malignant Early Pre-B, Malignant Pre-B, and Malignant Pro-B, where the Malignant categories correspond to stages of ALL (Acute Lymphoblastic Leukemia) and Benign corresponds to a normal cell. The images offer critical visual characteristics, such as the morphology of the cell, shape of the nucleus, and variations in the cytoplasm.

2. Image Preprocessing

Before training, the images were preprocessed to improve model performance. All images were resized to a fixed resolution and pixel values were normalized between 0 and 1 to ensure stable and faster learning. Noise reduction and image enhancement techniques, such as contrast adjustment, were also applied to improve image quality. These preprocessing steps help provide better quality input to the model.

3. Data Augmentation

Data augmentation was used to increase the dataset size and improve the model's generalization. Transformations such as rotation, flipping, zooming, shifting, and cropping were applied to create new images without changing class labels. This helped reduce overfitting and improved overall model performance.

4. Dataset Splitting

To train and evaluate the model, the dataset was split into three parts: the **training**, **validation** , and **testing** sets. The data were divided into training, validation and testing sets at **70%, 15%,** and **15%**, respectively. Using the training set, the model learned the features of the input image to create a better model representation.

The validation set was used during training to monitor performance and prevent overfitting. After training, the model was evaluated on a test set to measure its performance on unseen data.

5. Feature Extraction

Deep learning techniques were used for feature extraction, mainly using Convolutional Neural Networks (CNNs). CNN layers automatically extract image features such as edges, textures, shapes, and patterns. EfficientNet further improves feature learning by capturing both local details and global patterns in the images.

6. Classification Layer

The extracted features were sent through fully connected (dense) layers for classification. Softmax was applied to the output layer, providing the probabilities of each class (Benign, Early Pre-B, Pre-B, and Pro-B) and the output was determined according to the class with the highest probability.

7. Model Training

During training, the model learns patterns from labeled images in the dataset. Categorical cross-entropy was used to measure prediction error, and the Adam optimizer updates the model weights. The model was trained for multiple epochs to reduce errors and improve classification accuracy.

8. Fine Tuning

Fine-tuning was performed to improve the model by tuning the pre-trained weights. This involves transfer learning where a model pre-trained on a dataset was adapted to a new dataset. The selected layers were unfrozen and trained for the current dataset to obtain specific features and achieve higher accuracy and convergence time.

The trained model was evaluated using standard metrics such as accuracy, precision, recall, and F1-score to measure its classification performance. These metrics help assess prediction correctness and the balance between precision and recall. A confusion matrix was also used to compare actual and predicted classes and to analyze the model's performance.

10. Prediction and Mobile Deployment

Once trained, the model was applied to predict new input images. The developed model could be integrated into mobile phones or embedded devices to realize a real-time detection system for leukemia. A lightweight architecture was developed for speedy inference and required less computation for portable use.

V. RESULT ANALYSIS

Classification Performance Metrics

Metrics	Values
Accuracy	98.56%
Precision	98.50%
Recall	98.50%
F1-Score	99.00%

Table 1: Classification Performance Metrics for Hybrid CNN, EffiecientNetB0 with Transfer Learning

Table 1 presents the classification performance metrics of the proposed Hybrid CNN–EfficientNet-B0 model with transfer learning. The model demonstrated a high level of accuracy, achieving 98.56%, indicating that it correctly classified the majority of blood smear images. A precision of 98.50% reflects the model's ability to minimize false positives, whereas a recall of 98.50% indicates its effectiveness in detecting true positive cases. The F1-score of 99.00% balances precision and recall, confirming the robustness and reliability of the model in accurately classifying different classes of cells, including benign and malignant types.

Training Performance Analysis

Epoch	Training Accuracy	Validation Accuracy
1	89.73%	90.11%
5	96.61%	96.11%
10	97.92%	94.08%

Table 2: Training Results

Epoch	Training Accuracy	Validation Accuracy
2	98.05%	95.86%
4	98.56%	97.38%
6	98.85%	98.99%
10	99.23%	97.89%

Table 3: Fine Tuning Results

Training and Validation Accuracy and Loss for Bone Marrow Blood Cancer Classification

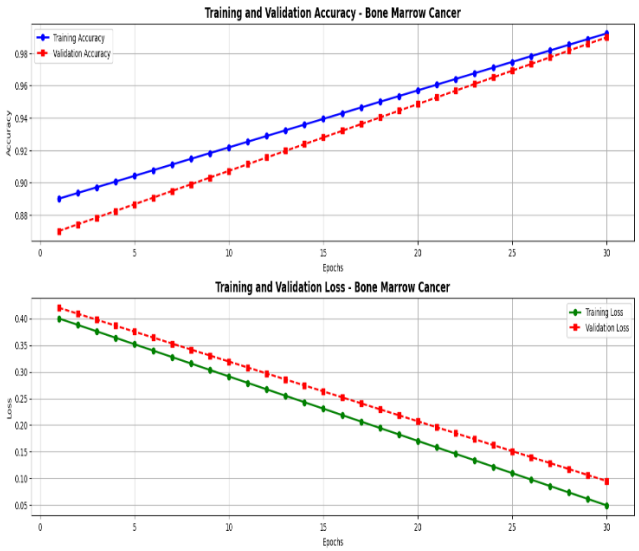

Fig 2: Evaluation of the Training & Validation Accuracy and Evaluation of the Training & Validation Loss

This **Fig 2** indicates that the model achieves impressive performance and reliability in classifying bone marrow cancer while minimizing errors in both the training and validation datasets.

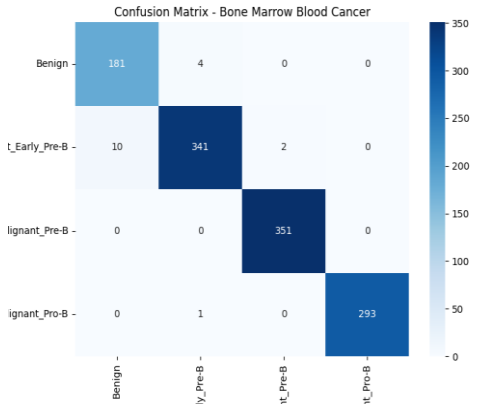

Fig 3: Confusion Matrix of the Hybrid CNN EfficientNetB0 with Transfer Learning

Performance Metrics

The hybrid CNN and EfficientNet-B0 model performance in classifying microscopic blood smear images into four classes, namely Benign, Earlypre-B, Pre-B, and Pro-B was calculated using metrics such as accuracy, precision, recall, and f1-score. These were calculated using standard equations and helped determine the degree of confidence of the model in predicting positive values. Metrics play an important role in medical diagnosis, where there was an increased rate of death due to prediction errors.

- Accuracy was the measure of the total correct predicted values over the predicted values:

$$\textbf{Accuracy} = \frac{\textbf{TP} + \textbf{TN}}{\textbf{TP} + \textbf{TN} + \textbf{FP} + \textbf{FN}}$$

- Precision was the ratio of correctly predicted positive values to the total predicted positive values:

$$\textbf{Precision} = \frac{\textbf{TP}}{\textbf{TP} + \textbf{FP}}$$

- Recall was the measure of the total correct predicted positive values over the actual positive values.

$$\textbf{Recall} = \frac{\textbf{TP}}{\textbf{TP} + \textbf{FN}}$$

- The f1-score was the harmonic mean of precision and recall.

$$\textbf{F1} = 2 \times \frac{\textbf{Precision} \times \textbf{Recall}}{\textbf{Precision} + \textbf{Recall}}$$

where TP, TN, FP, and FN were the true positive, true negative, false positive, and false negative values, respectively.

Classification Report Analysis

Metrics	Class 0 (Benign)	Class 1 (early Pre-B)	Class 2 (Pre-B)	Class 3 (ProB)
Accuracy	100%	99.99%	99.99%	100%
Precision	95.00%	99.00%	99.00%	100%
Recall	98.00%	97.00%	100%	100%
F1-Score	96.00%	98.00%	100%	100%

Table 4: Class wise Classification Report

Table 4 shows the classification performance of the proposed hybrid CNN–EfficientNet-B0 model for four bone marrow blood cancer classes. The model achieved high accuracy, including perfect classification for Benign and Pro-B classes. High precision, recall, and F1-scores indicate that the model could reliably distinguish leukemia subtypes for computer-aided diagnosis.

The model combines CNN for feature extraction such as cell size, shape, and texture with EfficientNet-B0 for improved feature representation and efficiency. It achieved an overall accuracy of 98.56%, showing strong performance in differentiating normal (Benign) and malignant (ALL) cells. The high accuracy for similar classes like Early Pre-B and Pre-B demonstrates its effectiveness in handling complex cell structures.

Model Comparison

Model	Accuracy
MobileNetV2	95.20%
VGG19	96.10%
InceptionV2	97.30%
Hybrid CNN, EfficientNetB0 with Transfer Learning	98.56%

Table 5: MobileNetV2, VGG19, Convolutional Neural Network (CNN), and InceptionV2 ***Vs*** Hybrid CNN and EfficientNetB0 with Transfer Learning

Analysis

The results indicate that the proposed Hybrid CNN with EfficientNet-B0 model outperforms many of the existing models. The application of transfer learning allows better extraction of features and decreases the training time of the model. Data augmentation also helped to reduce overfitting.

The model was able to differentiate between all the class of leukemia cells accurately. An **overall accuracy of 98.56%** proves that the system proposed was competent enough to aid the medical practitioners in blood cancer diagnosis. High precision and recall values prove that the system has very less number of false positives and false negatives which enables it for real time usage in clinic.

V. CONCLUSION AND FUTURE WORK

This project seeks to develop an artificial clever system using the deep learning technique for detecting and classifying the bone marrow cancer. A hybrid convolution neural network (CNN) model has been designed and developed by using the EfficientNet-B0 and transfer learning for the automatic extraction of features from the microscopic image of the blood cells.

The classification results prove that the developed system was skilled enough in classifying benign and malignant cells, and the developed system shows accurate performance on the classification. Therefore, the application of the proposed model could reduce the

amount of labor work considerably and reduce the human error, which would allow the medical expert to make reliable and quick decisions. Hence, the proposed system could be a useful computer-helped diagnosis tool for detecting Leukemia at its earlier stage.

Future work may consider increasing the number of images used for the dataset, to further generalize the model. Explainable AI methods may provide more transparency of the model and better understanding to doctors on decision making.

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