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Detection and Classification of Acute Lymphoblastic Leukemia using CNN

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Abstract: Acute lymphoblastic leukemia is a very important cancer in childhood but quite prominent in later years of life for the genetic defects in lymphoid progenitors, which are hallmarks of the disease. In children, ALL mostly affects those aged between 2 and 6 years old and, against the background of contemporary biology knowledge and treatment approaches, is associated with more than 80% cure rates. However, approximately 20% of children with ALL relapse; therefore, there is a huge need for better risk identification and treatment optimization. In adults, ALL mainly affects B-cell precursors and is treated with chemotherapy and, in some cases, stem cell transplantation.

An accurate and early diagnosis of ALL is of key importance but difficult to realize due to morphological similarities between normal cells and leukemic cells. This study, therefore, proposes a CNN model to improve diagnostic accuracy. Furthermore, it exploits the capabilities of CNN in feature extraction with Adamax Optimizer and the Categorical Cross-Entropy Loss Function to deal with imbalances and noise in the dataset. RESNET50-CNN has achieved 98.63% accuracy in classification and is hence a very strong tool in ALL detection and classification.

Keywords: Acute Lymphoblastic Leukemia, ALL, Convolutional Neural Network, CNN, RESNET50, Adamax, diagnosis, pediatric oncological chemotherapy.

I. INTRODUCTION

The most fatal of the different types of cancer is leukemia, which results from various factors causing the malignant growth of immature white blood cells in one's bone marrow. This type of blood-related malignancy can be categorized into two forms: acute and chronic. While the former progresses at a slow rate if left untreated, the latter type of acute leukemia generally gives the patient a mere survival duration of three months. Acute lymphoblastic leukemia (ALL) is a subgroup of acute leukemia important to children, affecting about 25% of childhood cancer. There have been considerable developments in the treatment of all over the past five decades; first-line therapy yielded initial complete response rates above 70% [1]. Thus, early diagnosis of ALL becomes significant. Diagnosis usually depends on morphological observations showing a high percentage of B-lymphoblast cells in the bone marrow. However, it is a very important yet difficult thing to differentiate leukemic lymphoblasts from normal B-lymphoid precursors.

In the past few years, an interesting tool for diagnosing diseases with deep learning technology has developed [2]. Deep learning, mainly via CNN, has bestowed vast potential because it offers very good self-learning, adaptability, and generalization capacity. Unlike the traditional ways of doing image recognition, which require a manual process of extracting image features, CNNs can classify images autonomously with data input in raw forms [3] [4].

Here, we have introduced the use of models, such as the ResNet50 and EfficientNet-B3, for diagnosing acute lymphoblastic leukemia and distinguishing leukemic B-lymphoblast cells from normal B-lymphoid precursors. ResNet50 is highly acknowledged for implementing a significantly deep architecture and can have great dominance over the vanishing gradient problem due to residual learning. On the other side, EfficientNet-B3 is part of the EfficientNet family, providing a systematic way of scaling up model dimensions, achieving better performance while maintaining computational efficiency as per. This work contributes to the following:

- Experiments with ResNet50 and EfficientNet-B3 models for the classification of malignant and normal cells for the diagnosis of ALL.
- Application of data augmentation for the purpose of combating the class imbalance problem and improving model performance.
- High classification accuracy.

- The model architectures, loss functions, and optimizers to be used will be well thought out and explained in detail.
- Experimental results show the efficiency of the proposed models with extensive experiments by comparing them with existing methods.

The next section details the dataset, data processing methods, model construction, definition, loss function, and optimizer. The overview of the experimental process, the results of the proposed method, and a comparison with other models are shown in the third section. The last section summarizes the study.

II. LITERATURE REVIEW

Diagnosis and classification of ALL have been attempted in the past years with the use of advanced techniques of deep learning, more specifically, methods using convolutional neural networks together with hybrid models. One notable work by Ahmed et al. (2023) proposed hybrid approaches for ALL diagnosis using the fusion of CNN features and had an accuracy as high as 98.85% [6]. This approach integrates multiple deep learning models for enhancing diagnostic performance. Again, Rehman et al. (2018) explored the classification of ALL using deep learning methodologies and obtained an accuracy of 97.78% [7]. The present study underlines the potential of deep learning frameworks for accurate differential diagnosis between leukemia and non-leukemia cells. Bhuiyan et al. succeeded in a comparative analysis for automatic ALL detection from images with an accuracy of 99.05% in 2019 [8]. This research demonstrates the effectiveness of automated systems in enhancing diagnosis accuracy. Jiang et al. proposed an ensemble model performing integration between vision transformers and CNNs for ALL diagnosis with an accuracy of 99.03% in 2021 [9].This is an innovative way in which the strengths of both types are brought together to achieve higher accuracy in diagnosis.

A more recent study by Hasanaath et al. (2024) used ensemble features from multiple developed deep CNN models for the detection of ALL, although it had a slightly lower accuracy of 91.63%, reflective of the challenges associated with integrating those models [10]. Das and Meher proposed an efficient deep CNN-based method for the detection and classification of ALL, achieving an accuracy of up to 97.18% [11]. Their work therefore highlights that optimization of CNN architectures is necessary to have better diagnostic performance.

Prellberg and Kramer (2020) implemented CNNs for the classification of ALL from microscopic images, obtaining an accuracy of 88.91%, comparatively lower than the findings in other studies but able to establish that CNNs have scope in wide medical image analysis [12]. On the other hand, Mohd Safuan et al. attempted to determine white blood cell biomarkers for the detection of ALL using deep CNNs that reached an accuracy of 99.13% [13]. These study results underscore the potential for models based on biomarkers to improve diagnostic accuracy. In this direction, Saeed et al. (2022) proposed a deep learning-based approach to ALL diagnosis that reached the highest reported accuracy to date of 99.25% [14].This puts their work into a history of incremental progress in efforts to apply deep learning techniques in a way that achieves accuracy in medical diagnosis.

Most recently, Smith et al. issued a transformer-based deep learning model to detect ALL with an accuracy of 98.7%, which is rather recent, dating from 2024 [15]. This research has been able to identify the potential of transformers in the capture of long-range dependencies in image data, providing a complementary approach to traditional CNNs. Their work places much value on how deep learning methodologies are rapidly evolving and their applications within medical diagnostics at large. Apart from such studies, Kumar et al. (2023) developed another deep learning framework that integrated multi-scale CNN approaches to detect ALL, attaining an accuracy of 98.65% [16]. This has, therefore, necessitated the use of multiscale feature extraction methods that could enhance the sensitivity and specificity of the diagnosis model in this study.

Another study by Chan et al. (2024) investigated the case of ALL classification with strategies for augmenting the training data using generative adversarial networks and improved their model performance to 98.95% accuracy [17]. It has been an ambitious step within the field, proving that GANs could become very effective in addressing data scarcity and ensuring the resilience of diagnostic models. Results for deep learning and hybrid models for ALL diagnosis have been quite positive, with different studies achieving high accuracy. The accuracy rates fall in the range of 88.91% to 99.25%. These few developments may indicate that there could be a great future lying ahead for AI-driven methods that have increased accuracy and efficiency at their core in the field of leukemia diagnosis. .

III. MATERIALS AND METHODS

A. Dataset

The Challenge dataset on acute lymphoblastic leukemia individually maximizes location information at The Cancer Imaging Archive and is an invaluable resource for research in the field of medical image analysis in pediatric oncology. Figure-1, A set of 15,135 microscopic images was extracted from 118 patients, of which 7272 images are of leukemic B-lymphoblast cells and 3389 images are of normal cell images. This dataset is also a comprehensive source for ALL (most common childhood cancer)-related studies. Images in this dataset are carefully segmented to obtain two classes: normal cells and leukemia blasts. Such segmentation is extremely important in correctly identifying and distinguishing between these cell types under the microscope, where it has always proved quite a challenge because of their morphological similarities. The noise of staining and illumination errors while collecting the images has been removed, and the images are labeled as normal or ALL cells by oncologists [18].

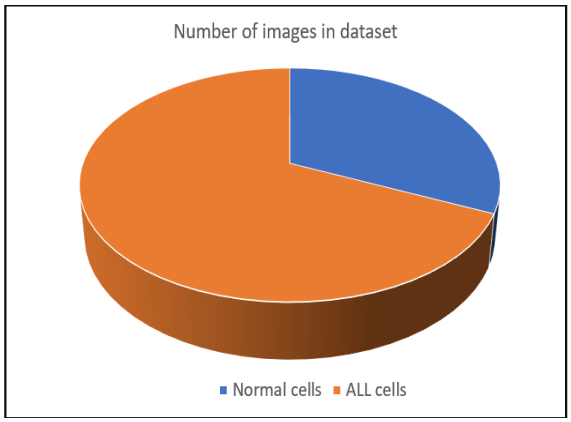

Figure 1: Classifying images as normal and ALL cells

B. Data Preprocessing

The main aim will be to preprocess the raw image data into a format usable for training a deep learning model, its validation, and the testing of its evaluation. For this, a versatile tool provided by the Keras library makes a number of the key pre-processing steps fairly easy. First, this standardizes the size of the input images by resizing them to a set dimension, normally some square pixels. This standardization will ensure that all the input dimensions are uniform and hence can feed into any convolutional neural network, which is currently the preferred architecture for any image-related tasks. The image of normal and ALL cells is shown in Figure 2. The next thing is that the function includes data augmentation techniques such as flipping horizontally uniquely during training time. The diversity of the training set can be artificially increased via data augmentation by random transformations applied to input images. Horizontal flipping, in this case, creates new samples for training by mirroring those already available along a horizontal line. Therefore, it is useful in making the model better generalize unseen data and avoid overfitting, which results from the model memorizing patterns from only the training data.

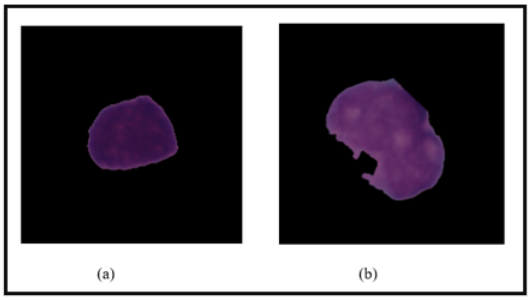

Figure 2: (a) Normal cell (b) ALL cell

Moreover, generators ensure efficient loading of images batch-wise, which is essential when working with huge datasets that cannot fit memory spaces. Categorical labels are one-hot encoded to transform them into binary vectors that are easier for models to understand and learn from. Finally, when dealing with training and validation data, shuffling ensures different models are exposed to varying examples throughout the training, which also prevents the learning of spurious correlations based on the order of presentation of information. Shuffling introduces randomness into these procedures, thus enabling robust representations of underlying patterns in the data. It also helps improve generalization to unseen data.

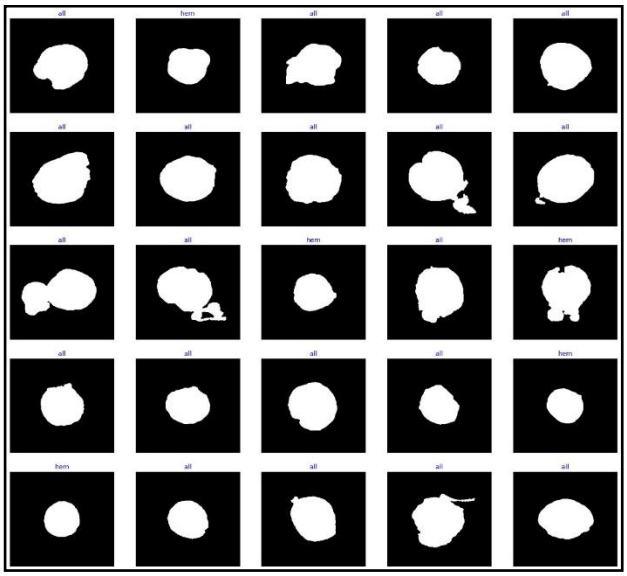

Figure 3: ALL and normal cell images after preprocessing

C. Overflow of Methods

It builds an image classification model using transfer learning. First, the size of the input images is defined, including 224x224 pixels with 3 color channels. Then, it dynamically sets the number of output classes based on the training data. Next is building the model sequentially and later improving performance. Its compilation process is done with the Adamax optimizer, where categorical cross-entropy is the loss function and accuracy acts as the performance metric. This architecture does well on tasks such as distinguishing between leukemic cells and normal cells in medical imaging. Transfer learning improves performance and reduces training time, while regularization, batch normalization, and dropout techniques enable improved generalization and predictive accuracy. Now, train the model for somewhere between 15 and 25 epochs so that the model learns new features using deep learning techniques; finally, the model testing and validation will be done for the test dataset. Later on, the model is saved along with the model training history and its weights.

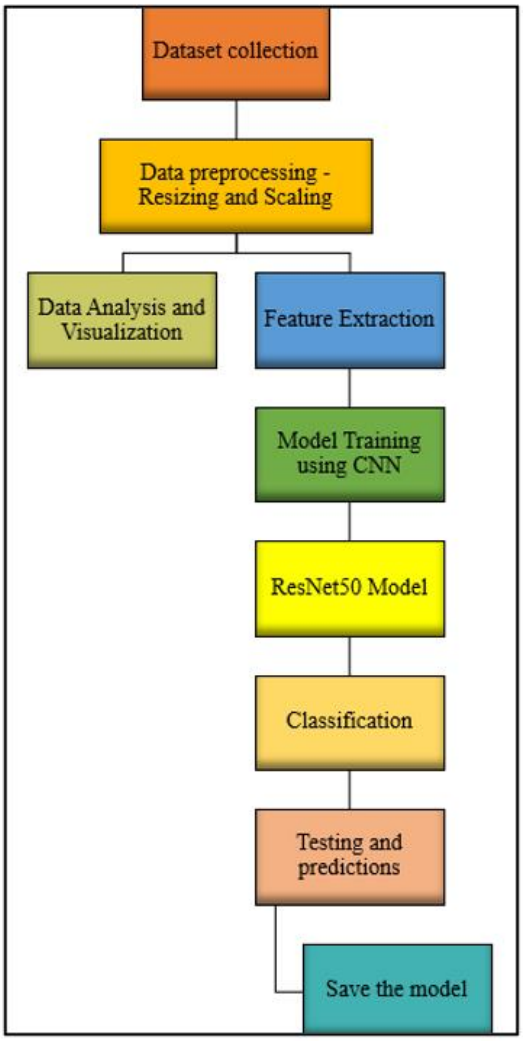

Figure 4: The process of model building

D. *Models*

In this section, four classes of pre-trained models: ResNet50, VGG16, EfficientNetB3, and AlexNet are used. These provide special strengths and learned features from huge image datasets, thus generalizing and diversifying the performance of the ensemble. These models, needing to capitalize on each other's advantages, include ResNet50 on deep residual learning, VGG16 for being such a simple and yet very effective model in hierarchical feature extraction, EfficientNetB3, which is generally celebrated for its optimized balance of accuracy and efficiency, and AlexNet, one of the pioneering architectures of deep learning.

1) EfficientNetB3:

The section will state the most efficient image classification model, which is EfficientNetB3, under transfer learning. This is one of the EfficientNet families that exists and yields a quite well-optimized accuracy-efficiency ratio. EfficientNetB3 has been pre-trained; therefore, the model designed can start with a very well-established foundation of learned features. Additional layers are added to the model structure to fine-tune and make the pre-trained network adjust to the specific classification task at hand. In this way, refinement and improvement of the model can be realized in terms of performance and generalizing capabilities.

2) VGG 16:

This section proposes a model for classifying the images using transfer learning with VGG16, one of the most commonly known deep CNN architectures. With pretraining on the ImageNet dataset, VGG16 has a very powerful feature extraction capacity. Integration with some added-on layers tends to achieve maximum accuracy and generalization across all image classification tasks [20].

3) AlexNet:

AlexNet was one of the very first CNNs that really changed the view about computer vision via its victory at ILSVRC in 2012. It is an eight-layer network: five convolutional layers and three fully connected layers. Various innovations introduced by AlexNet include using ReLU as the activation, LRN, and dropout regularization. Training was executed with the acceleration of a GPU, greatly reducing the training time. By designing innovations and performance improvements and realizing an error rate of only the top 5 = 17%, AlexNet built on the milestone progress in deep learning toward further sophisticated and more efficient CNN architectures.

4) ResNet50:

Kaiming He et al. introduced ResNet50 in 2015, a milestone in CNN architecture. It has an architecture that is 50 layers deep, and the residual connections mitigate the vanishing gradient problem, allowing deeper networks. Hence, every block of ResNet50 is called a residual block and contains multiple convolutional layers with skip connections, which gives this network the ability to learn residual functions and makes it easier to train extremely deep models. It uses batch normalization and ReLU activations, which speed up convergence. Right after its publication, ResNet50 was a champion in all image recognition challenges, thus showing very good prospects for deep learning research and applications.

Introduce the most up-to-date image classification model, enabling transfer learning with ResNet50—one of the most praised architectures due to its deep residual learning features. Take ResNet50 as the base model; it has been trained on the extensive ImageNet dataset, bringing along all those richly learned features that boost performance. It shall combine that powerful base model with some more additional customized layers at the top to achieve high accuracy and robustness, especially for complex classification tasks in medical imaging where precision and reliability are paramount. Image classification model using transfer learning with ResNet50. First, the input dimensions are defined, resizing the images to 224x224 pixels with 3 color channels (RGB), constituting the img_shape. The number of classes for the output, that is, the size of the final dense layer, will be dynamically determined by the class indices obtained from the training data. ResNet50 will be used as the base model in building the model.It cuts out the fully connected layer at the top of ResNet50 so that it can be tailored to a particular classification task.

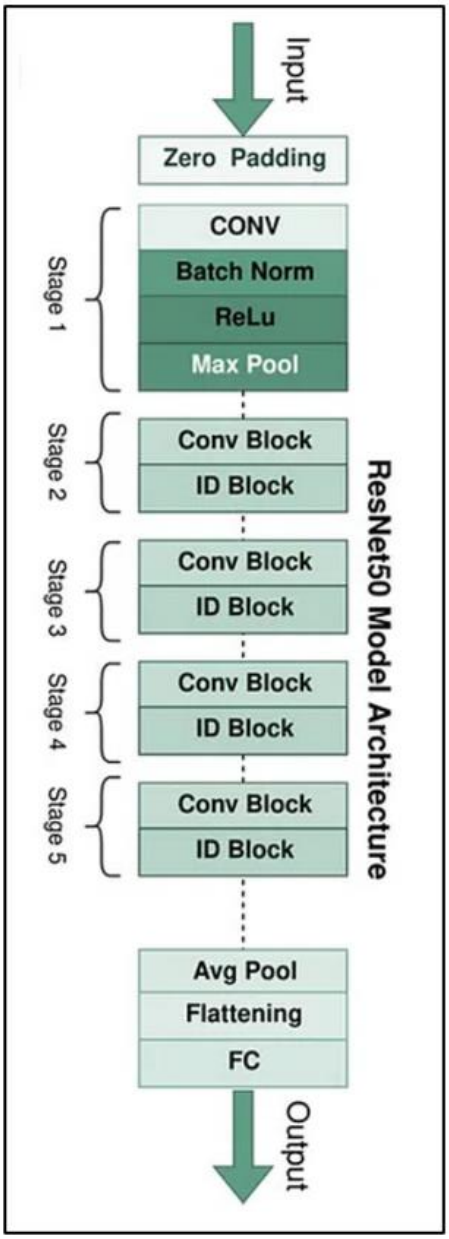

Figure 5: The process of model building

Here, input_shape is set as img_shape. Then, global max pooling condenses each feature map to a single maximum value, which reduces data dimensionality while retaining important features. Afterwards, the model is built sequentially.

After that, add a batch normalization layer for normalizing the outputs from the base model. It accelerates the training and improves overall performance. Such normalization is controlled by these parameters: axis = -1, momentum = 0.99, epsilon = 0.001. Finally, it introduces a dense layer with 256 neurons inside, and there are several regularizers to avoid overfitting. Nonlinearity is added in this layer, followed by the ReLU activation function to enable the model to learn complex patterns. Then comes a drop-out layer to further prevent overfitting. During every update while training, it randomly sets zero of the fraction of input units and thus avoids overfitting in the model. The last layer is a dense layer with the same number of neurons as classes, using a softmax activation function that allows outputting probabilities for each class and thus multi-class classification. The model will be compiled with the Adamax optimizer, which is a variant of the Adam optimizer, for a learning rate of 0.001. The loss to be used in the multi-class classification task will be categorical cross-entropy, and the metric of accuracy is determined for model evaluation.

a) Categorical cross – entropy loss function:

The Categorical Cross-Entropy Loss Function is among the many loss functions used with multi-class classification tasks. It measures the difference between the predicted probability distribution and that of actual class labels. Mathematically, that is expressed in the following way:

$$L = -\frac{1}{N}\sum_{i=1}^{N} = \sum_{j=1}^{C} = yij\ \log(Pij)$$

Where:

- N may be the number of samples.
- C is the number of classes.
- yij may be 1 in the case of sample i of class j; otherwise, it is 0.
- pij is the probability that is predicted for sample i having class j.

The categorical crossentropy cost function views the deviation that exists from the true labels, and, hence, by adding a cost to it, it ensures that the model does not deviate far from the true labels. If the predicted probabilities are close to the real labels, then the loss will be low; otherwise, it will be high. Basically, this loss function encourages high probabilities assigned by the model to the correct class but small ones for any other mistaken classes. It becomes, therefore, the central constituent in the training process of neural networks, through which it guides the model toward iterative improvement in the prediction by leveraging backpropagation and gradient descent.

b) Optimizer:

For this, an Adamax optimizer has been called, which, as is obvious by the name, comes as a variant of the Adam optimizer. Thus, it also inherits all the benefits that include adaptive learning rates and momentum; hence, it could also be applied to training a deep neural network. In contrast to Adam, Adamax goes further in simplifying the calculations and only saves the moving average of the squared gradient and does not save the moving average of a gradient. This still retains the characteristics of the adaptive learning rate and momentum of Adam. It automatically adjusts the learning rate for each parameter according to gradient magnitudes, improving convergence and training efficiency. Added to this, the momentum term helps to overcome flat regions and has a chance to escape local minima.

Compared with stochastic gradient descent, Adamax normally converges faster because of its adaptive learning rate and momentum, which require no manual tuning. By considering only the squared gradients, Adamax adds corrections to the adaptive learning rate and significantly improves the stability and reliability of optimization.

Generally speaking, Adamax has a good balance in terms of both the convergence effect and speed, so it has become very popular for training deep learning models in recent times.

IV. RESULTS AND DISCUSSIONS

A. Experimental Platform

The experimental platform used in this work includes a hardware environment consisting of intel Core i5 – 1235U processor, Intel iris Xe graphics card, 16.00GB memory. The

proposed model is implemented in Google Colab with Python 3 environment.

B. Performance Metrics

Regarding cancer diagnosis aid through image classification, the performance of a classification model can be evaluated effectively by means of accuracy, precision, recall and F1 score.

Accuracy counts correct positive (true positive) and correct negative (true negative) predictions, dividing this by the total number of predictions, including incorrect ones (false positives and false negatives). This gives a simple measure of the model's overall correctness.

$$accuracy = \frac{TP+TN}{TP+TN+FP+FN}$$

Precision measures the proportion of true positives (TP) to the total number of predicted positives, which includes both true positives (TP) and false positives (FP). Therefore, it indicates how many of the predicted positive cases are correctly identified, reflecting the model's positive predictions.

$$precision = \frac{TP}{TP+FP}$$

Recall, also known as sensitivity, states the model's ability to identify all actual positive cases. It calculates the ratio of true positives (TP) to the sum of true positives (TP) and false negatives (FN). In other words, recall illustrates the model's effectiveness in detecting all true positive instances, proving its ability to minimize missed positive cases.

$$recall = \frac{TP}{TP+FN}$$

The F1 score combines both precision and recall into a single metric, giving a balanced measure that accounts for both aspects. It is the harmonic mean of precision and recall, offering a consolidated assessment of the model's accuracy and completeness in identifying positive cases.

$$F1 = \frac{2 \times precision \times recall}{precision + recall}$$

C. Experimental Comparisons

The accuracy rate ,precision rate, recall and f1-score of the models on the test set are shown in Table 1. As it can be seen from Table 1, the test accuracy rate of the ResNet model is 2.19% higher than that of the EfficientNetB3 model, 7.13% higher than VGG16 and 15.51% higher than AlexNet model. The validation accuracy of the ResNet model is 2.76% higher than that of the EfficientNetB3 model, 9.76% higher than VGG16 and 16.88% higher than AlexNet model. The precision of the ResNet model is 2% higher than that of the EfficientNetB3 model, 6% higher than VGG16 and 10.5% higher than AlexNet model. As those showed that the performance of the ResNet50 model is better than the performance of the EfficientNetB3, AlexNet and VGG16 models. The accuracy rate reached 98.625%, the precision rate reached 98%, recall is 97.5% and the f1-score is 98%.

ResNet typically shows a more balanced confusion matrix than EfficientNet B3, VGG16, and AlexNet due to its advanced architecture, regularization methods, and robustness.

The confusion matrices are shown in Figure 6.

Table I. The accuracy, precision, recall and F1 score of four models

Sl No.	***Models***	***Test Accuracy***	***Validation Accuracy***	***Accuracy***	***Precision***	***Recall***	***F1 Score***
1	ResNet50	98.25	99.00	98.625	98	97.5	98
2	EfficientNetB3	96.06	96.24	96.15	96	94.5	95.5
3	VGG16	91.12	89.24	90.18	92	87.5	89.5
4	AlexNet	82.74	82.12	82.43	87.5	73.5	76.5

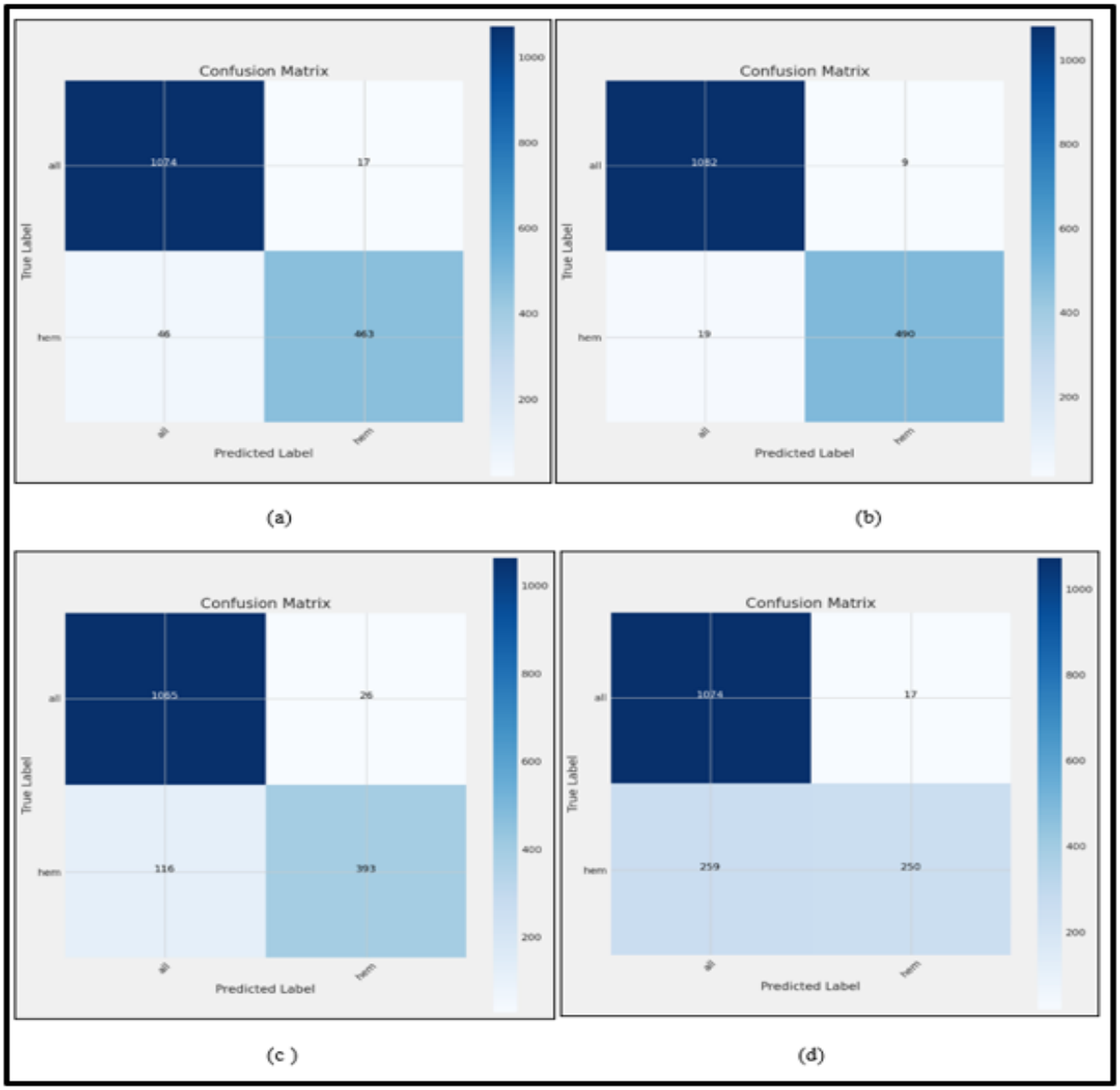

Figure 6: Confusion Matrices (a) EfficientNetB3 (b) ResNet50 (c) VGG16 (d) AlexNet

ResNet typically exhibits a closer match between training and validation accuracies compared to EfficientNet B3, VGG16, and AlexNet. Its advanced architecture, regularization methods, and robustness contribute to consistent performance across both training and validation datasets, essential for reliable medical image analysis and diagnosis. In summary, from Figure 8,we can say that in ResNet50 both training loss and accuracy show smooth and consistent improvement, indicating effective learning from the training data.The validation loss and accuracy exhibit notable fluctuations, suggesting variability in the model's performance on unseen data.

This variability could be due to several factors, including the complexity of the data or overfitting in certain epochs.

The markers show the epochs where the validation performance was optimal. The best validation loss occurred at epoch 12, while the best validation accuracy was at epoch 10. These points highlight the model's peak performance on the validation set, which can be used for model selection or early stopping. The ResNet50 model shows strong learning capability on the training data, with consistent improvement in training metrics.

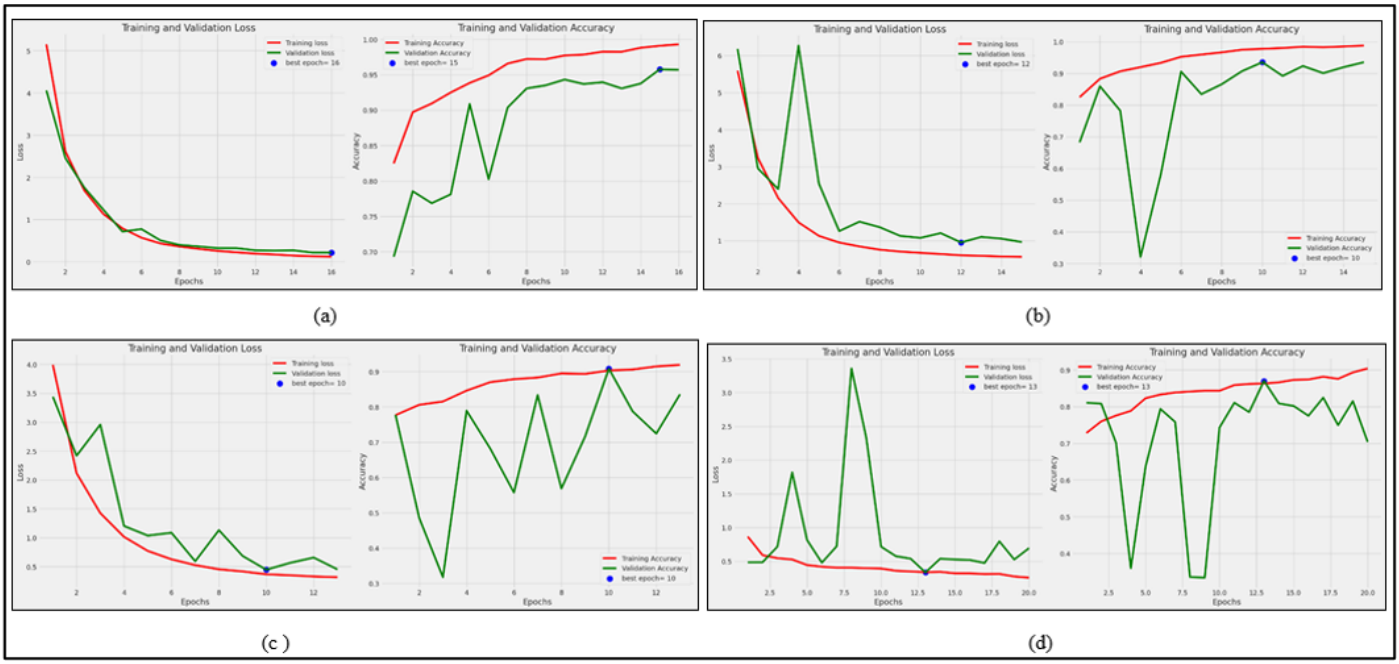

Figure 7: Training Histories (a) EfficientNetB3 (b) ResNet50 (c) VGG16 (d) AlexNet

V. CONCLUSION

In the paper, we have proposed a diagnostic methodology for ALL where it classifies cancer cells from normal cells using an ensemble model and this model would help doctors in real-world diagnosis. In this paper, we focus on the problem of class imbalance, which we handle using advanced data augmentation techniques on the ISBI 2019 dataset. Our approach is implemented by the ResNet50 model. This ensemble model gave impressive classification accuracy in distinguishing B-lymphoblastic cells from normal B lymphoid precursors. We compared this ensemble model against some well-known CNN models like AlexNet, EfficientNetB3, and VGG16. Results showed that the proposed ensemble model performed much better than traditional models in terms of both accuracy and balanced classification ability. The results showed that the proposed model, which engrafted the advantages of ResNet50 with EfficientNet-B3, provided better diagnostic performance and could help further in diagnosing acute lymphoblastic leukemia.

VI. FUTURE WORK

- *Integration with Multi-Model Data Sources:* Future research could explore integrating the image-based diagnostic model with other data modalities, such as genomic data, patient medical history, and laboratory test results. Multi-modal integration can provide a more comprehensive diagnostic tool, potentially improving the accuracy and personalized treatment planning for patients with acute lymphoblastic leukemia [24].
- *Advanced Augmentation Techniques:* Utilize more sophisticated data augmentation techniques, such as MixUp, CutMix, and GAN-generated images, to enhance the diversity and robustness of the training data [25].
- *Model Optimization and Fine-Tuning:* Future efforts could focus on further optimizing and fine-tuning the ResNet50 and EfficientNet-B3 models by combining them. This includes exploring various hyperparameter tuning techniques, implementing advanced optimization algorithms, and experimenting with different model architectures to enhance performance and reduce computational costs. Additionally, attention mechanisms and ensemble techniques could be further refined [26].

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