

<https://doi.org/10.48047/AFJBS.6.14.2024.6657-6668>**African Journal of Biological Sciences**Journal homepage: <http://www.afjbs.com>

Research Paper

Open Access

Acute Lymphoblastic Leukemia Detection from Blood Cell Imaging Using Deep Learning

Gnana Prakash Thuraka¹, Chinthala Lokesh Kumar², Mangilipelly Sai Kumar³,
Mohammed Faizan⁴, Poorna Chander Thumu⁵

¹ Assistant Professor, Dept. of Computer Science and Engineering, VNR Vignana Jyothi Institute of Engineering and Technology, Hyderabad, India - 500090

^{2, 3, 4, 5} Students, Dept. of Computer Science and Engineering, VNR Vignana Jyothi Institute of Engineering and Technology, Hyderabad, India - 500090

Article History

Volume 6, Issue 14, Aug 2024

Received: 03 July 2023

Accepted : 31 July 2023

Published : 22 Aug 2024

doi:10.48047/AFJBS.6.14.2024.6657-6668

Abstract: Diagnosing acute lymphoblastic leukemia (ALL) presents a considerable obstacle, often requiring invasive and costly examinations that may have adverse effects on patients. Regrettably, the problem is worsened by the fact that access to these diagnostic tools is restricted in numerous regions. Traditionally, blood microscopic examination has been the main method for screening and diagnosing ALL. However, manual performance by laboratory staff and haematologists has its limitations. To tackle this challenge, the present study explored the use of artificial intelligence (AI) techniques in analyzing blood microscopy images. The study focused on employing deep Convolutional neural networks (CNNs) to identify ALL cases, differentiate them from hematogones, and further classify the ALL subtype. The study aimed to develop a well-optimized model specifically for mobile and web applications to enhance accessibility. The modelling process included several crucial steps. Initially, a segmentation method was used, applying color thresholding in the LAB color space. This method combined K-means clustering and a mask to separate important elements and reduce image noise. Next, three lightweight CNN architectures (MobileNetV2, EfficientNetB0, and NASNet Mobile) were evaluated. After a thorough comparison, the best model was selected and fine-tuned. It is important to note that this model achieved outstanding accuracy in classification, showcasing its strength and effectiveness. Consequently, mobile and web applications based on this cutting-edge model were developed. Additionally, the implementation of a feature for locating nearby hospitals and providing directions enhances the utility of the application. This feature enables users to swiftly access further assistance from medical professionals, ensuring timely intervention and care. In practical laboratory environments, this software functioned as a reliable screening tool, effectively differentiating ALL cases from other groups with high sensitivity and specificity. Ultimately, this groundbreaking method not only showcases the capabilities of AI in medical diagnostics but also emphasizes the significance of utilizing technology to improve healthcare results.

Keywords: Acute lymphoblastic leukemia, Deep Learning, MobileNetV2, Convolutional Neural Network (CNN), Microscopic images.

I. INTRODUCTION

ALL is a highly common type of leukemia that impacts individuals across different age ranges. Pinpointing this condition accurately necessitates a suite of diagnostic tools and techniques. The most reliable method for diagnosis includes the analysis of bone marrow samples using either bone marrow aspiration (BMA) or bone marrow biopsy (BMB), both of which are invasive laboratory procedures that require specialized equipment. However, for the majority of ALL patients who are children, these invasive methods pose significant challenges and complications, often prolonging the diagnostic process by several days. Additionally, the associated surgical interventions incur substantial costs for healthcare systems.

Given these constraints, the early analysis of blood samples under a microscope by laboratory staff assumes paramount importance in diagnosing leukemia. However, the vast number of blood samples poses a significant obstacle for laboratories, which in turn raises the chances of diagnostic mistakes. The laborious process of microscopic analysis, combined with the expertise demanded from laboratory staff and their daily exhaustion, further amplifies the potential for inaccuracies in detecting ALL.

Furthermore, distinguishing between ALL and certain autoimmune or infectious diseases can be particularly tricky, as conditions like hematogones or benign ALL share morphological similarities with cancerous B cells. This resemblance often leads to misdiagnoses and perplexes haematologists. Hematogones, although resembling cancer cells morphologically, do not necessitate complex treatments, adding another layer of complexity to the diagnostic process.

To overcome current obstacles, a new strategy using deep learning principles is recommended for diagnosing and categorizing ALL. Previous research focused on traditional Artificial Intelligence techniques, but lacked real-world application in laboratory settings. This study introduces an optimized Convolutional Neural Network (CNN) architecture designed for mobile and web platforms to improve diagnostic efficiency in laboratory testing.

II. Related Work

In the realm of medical image analysis, the task of leukemia diagnosis from microscopic blood samples is formidable. [1], This paper presents an innovative approach that integrates data acquisition, data augmentation, and a sophisticated CNN architecture with squeeze and excitation learning. The methodology begins by acquiring microscopic blood sample images, addressing the challenge of limited data through data augmentation. By artificially diversifying the training dataset, data augmentation enhances the model's resilience. At its core, the methodology employs a deep CNN architecture with squeeze and excitation learning, highlighting the distinctiveness of features between leukemic and normal cells. Thorough experiments, encompassing both cropped cells and full-scale images, in conjunction with data augmentation, validate the effectiveness of the methodology. The model is implemented using Python and Keras on Google Colab, utilizing a 12GB NVIDIA Tesla K80 GPU for efficient training. Importantly, their proposed framework attains an impressive accuracy rate of 94%.

[2], This paper delves into sophisticated image processing methods, primarily emphasizing Convolutional Neural Networks (CNNs) for the purpose of image classification. The pre-processing stage encompasses the elimination of noise through median filtering and the conversion of RGB images to grayscale. The segmentation techniques employed involve grayscale, image binarization, and adaptive thresholding. A crucial aspect of this study is the application of supervised learning using training datasets, and the paper emphasizes the advantages of utilizing a substantial amount of training data for CNNs, rendering it a valuable asset in the realm of image and signal processing.

[3], 1. The solution presented in this paper includes preprocessing methods like color conversion, filtering, and histogram equalization in order to improve the image quality. The K-means algorithm is utilized for data segmentation, while the Zack algorithm is employed for thresholding. The paper highlights the necessity of refining the identification, thresholding, and segmentation phases to ensure precise detection. Furthermore, the study emphasizes the significance of shape feature extraction in enhancing the counting of white blood cells and the overall accuracy of segmentation. The results demonstrate that the suggested method achieves accuracy rates ranging from 72.2% to 97.8% across various features, including K-means, linear contrast stretching, histogram equalization, and share-based features.

[4], This study delves into the exploration of integrating machine learning with image processing. It encompasses preprocessing methods like noise removal filters and thresholding, with a particular focus on the effectiveness of Linear Discriminant Analysis (LDA) in enhancing images. Additionally, the research highlights the application of CNN and various machine learning algorithms for image classification. The performance of linear classifiers, K-NN, and Support Vector Machine (SVM) classifiers is thoroughly examined. Previous research has reported accuracy rates ranging from 88% to 93% using different approaches. This study offers valuable insights for professionals and researchers in the field.

III. Methodology

Based on current knowledge, there is no mobile or web app that can identify and categorize Acute lymphoblastic leukemia (ALL) using a lightweight Convolutional Neural Network (CNN) model. This research aims to create a mobile and web app that can be useful for healthcare professionals and scientists in labs. The main objective is to develop a CNN algorithm for smartphones and PDAs that can diagnose ALL and categorize its subtypes (Early, Pre ALL, and Pro ALL) by analyzing blood microscopic images.

A. Dataset

The study made use of a regional database acquired from multiple medical facilities in Tehran, Iran. It included 3242 microscopic blood pictures gathered from 89 patients who were suspected of having ALL. Skilled laboratory personnel meticulously prepared and stained these images. The database contained both benign and malignant groups, with the benign group containing hematogones that bear a close resemblance to ALL but are non-cancerous and typically resolve on their own without requiring chemotherapy. The malignant category included three subtypes of malignant lymphoblasts associated with ALL. Images were taken using a Zeiss camera connected to an optical microscope and saved in JPG format. Flow cytometry was used to identify the cell type and its subclasses.

To ensure accuracy and consistency, all slides were initially stained in a controlled setting by multiple laboratory experts. Standardization procedures were put in place to reduce variations in staining and imaging methods. Each image was captured by the same designated hematology specialist using the same equipment, including the Zeiss camera and microscope. These strict protocols were implemented to maintain uniformity and reliability across the dataset.

Preprocessing is crucial in computer vision to improve machine learning performance. Techniques are used to prepare data, eliminate noise, enhance accuracy, emphasize image attributes, and expedite training. The methodology includes preparation, segmentation, augmentation, rescaling, and categorization. These steps optimize input data and enhance model efficacy.

B. Data preparation

The research data, initially provided in PNG or JPG formats, went through a process of transformation where they were

converted into numerical arrays that represent the pixel values of the images (decoding). To enhance computational efficiency and maintain flexibility in network design, it is a common practice to resize input images in convolutional neural networks (CNNs). For this particular research, a pre-trained network was selected, which required input images to conform to specific dimensions. Typically, many standard architectures mandate input images to be sized at 224×224 pixels, a dimension that has also been preferred in recent medical diagnosis studies. As a result, all images in this study were resized to meet the 224×224 pixel criteria.

C. Segmentation

During this phase, the primary objective was to segment Regions of Interest (ROIs) by highlighting crucial areas of the model that are relevant to clinical specialists and the machine learning (ML) model. The segmentation process aimed to isolate and display clinically significant areas while filtering out irrelevant parts that could introduce noise and disrupt the learning process. A unique segmentation technique was used to target lymphoblast cells for improved accuracy and reliability. This method effectively distinguished blast cells from other blood components like erythrocytes and plasma using color interval separation and thresholding. In blood microscopic images, the RGB color space includes red, green, and blue channels. Segmentation was achieved using a clustering algorithm in the L^*a^*b color space, recognized by the International Commission on Illumination for its ability to account for perceptual color differences and facilitate segmentation based on color variations.

The conversion of images from the RGB space to the LAB space required the application of equations to obtain components L^* , a^* , and b^* . These transformations were essential for extracting relevant information for segmentation purposes. Subsequently, blast cells were isolated by applying the transformed mask to the input images.

Here are the equations involved:

1. Transformation of L component: $L^* = 116 \left(\frac{Y}{Y_n} \right) - 16$
2. Transformation of a component: $a^* = 500 \left(f \left(\frac{X}{X_n} \right) - f \left(\frac{Y}{Y_n} \right) \right)$
3. Transformation of b component: $b^* = 200 \left(f \left(\frac{Y}{Y_n} \right) - f \left(\frac{Z}{Z_n} \right) \right)$

where:

- X, Y, Z are the RGB color space coordinates.
- X_n, Y_n, Z_n are the reference white points.
- L^*, a^*, b^* are the components in the LAB color space.

After converting the color space channels and extracting the "A" component extracted from the LAB color space, K-means clustering was applied to obtain image outputs. Subsequent binary thresholding helped blur or ignore unnecessary background components, resulting in images with diagnostically non-significant elements.

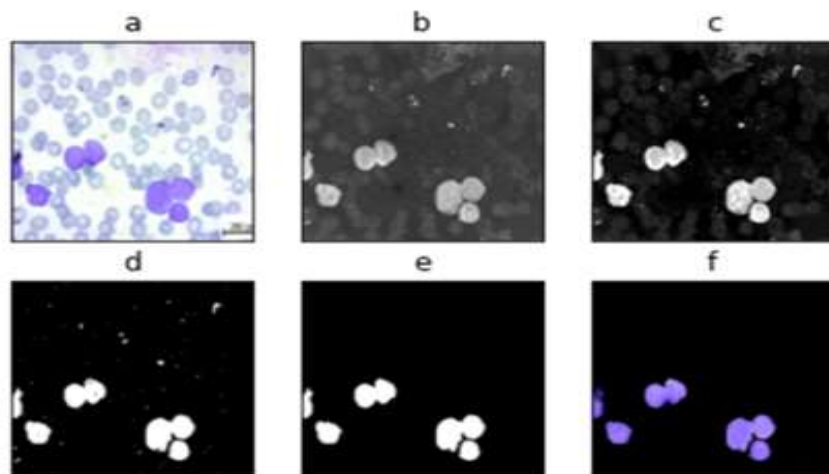


Fig. 1. showcases the segmentation process: a) RGB color space, b) LAB color space, c) K-means clustering, d) Binary thresholding, e) Methods for mask generation and cleaning, f) Applying the mask generated on the original RGB image.

1. In order to isolate blast features and eliminate unnecessary details, a mask was utilized to eliminate backgrounds from the images. This step ensured that the images were devoid of any irrelevant blood components or cells. Subsequently, the segmented outputs were mapped back to the original images to extract ROI areas for additional analysis.

E. Data rescaling, augmentation, and categorization

To maintain consistency and ensure uniformity in image presentation, it was necessary to standardize the pixel values within a common interval. This was achieved through pixel intensity normalization, which mapped the pixel values to the $[0, 1]$ interval. This normalization process homogenized the input data, making it easier to compare and analyze images. The importance of data augmentation in improving the performance of machine learning models cannot be overstated. Data augmentation is the process of applying modifications to images in order to enhance the variety of training samples while maintaining their semantic and intrinsic details. By replicating real-world data fluctuations like noise, data augmentation aids in making the model more resilient and flexible. This research employed two typical transformations, horizontal flip and vertical flip, to amplify the training samples. Prior to training the pre-trained networks and the suggested model, the data had to be classified. Following data segmentation, resizing, and augmentation, the research data was categorized to ready it for training. This categorization process involved grouping the data based on relevant attributes or classes, ensuring that the model received appropriately labelled data for effective learning. Once the data had been prepared through segmentation, normalization, augmentation, and categorization, it underwent a splitting process. This

involved dividing the data into separate subsets, typically training, validation, and testing sets, to facilitate model training, evaluation, and validation. By partitioning the data in this way, the model could be trained on one portion, validated on another, and finally tested on a separate, unseen portion, allowing for a comprehensive assessment of its performance.

F.Convolutional neural network structure

In order to deploy a highly effective model on less powerful equipment, the focus was primarily on prioritizing lightweight models. To accomplish this, three lightweight models were meticulously chosen, each selected for their efficiency and compactness. The aim was to assess their performance and identify the optimal model to be utilized as the feature extraction component. The models examined in this investigation encompassed MobileNetV2, EfficientNetB0, and NASNetMobile. These models were chosen based on their reputation for delivering robust performance while maintaining a lightweight architecture. Through a comprehensive assessment of their efficiency and compactness, the goal was to identify the optimal pre-trained network that could effectively extract features for subsequent processing.

1. EfficientNet

EfficientNetB0, known for its cost-effectiveness and resilience, has been selected as the model of choice for this research. The system functions by processing input images that have dimensions of $224 \times 224 \times 3$. It utilizes convolutional layers with a receptive filter size of 3×3 , and also incorporates the mobile inverted bottleneck Conv (MBConv) technique for extracting features. Its well-balanced scaling of depth, width, and resolution ensures both scalability and accuracy, surpassing other models trained on datasets such as ImageNet. With a range of scales available, from B0 to B7, EfficientNetB0 offers increased parameter size and accuracy. This versatility makes it an excellent option for deployment across various platforms and tasks, enhancing ubiquitous computing capabilities with the integration of deep learning functionality.

2. MobileNetV2

MobileNet is a model specifically designed to be efficient and run smoothly on embedded or mobile devices. Its architecture focuses on depthwise separable convolution, a technique that reduces the number of parameters while maintaining performance. This technique consists of two key layers: depthwise convolution and pointwise convolution. MobileNet achieves a reduction in the parameters of its convolutional layers without compromising classification accuracy by effectively utilizing separable convolution and depthwise convolution techniques. In MobileNetV2, additional improvements are introduced, such as residual bottleneck blocks that allow for the reuse of feature maps. This refinement enables MobileNetV2 to achieve comparable classification performance while significantly reducing training time. Our study utilizes both MobileNet and MobileNetV2, with MobileNetV2 standing out for its inverted residual blocks and reduced parameter count compared to the original MobileNet. MobileNets can process input sizes larger than 32×32 , with better performance achieved with larger image sizes. The key difference between the two versions lies in their convolution layers, as MobileNetV2 retains similarities with the original while incorporating inverted residual blocks for improved performance.

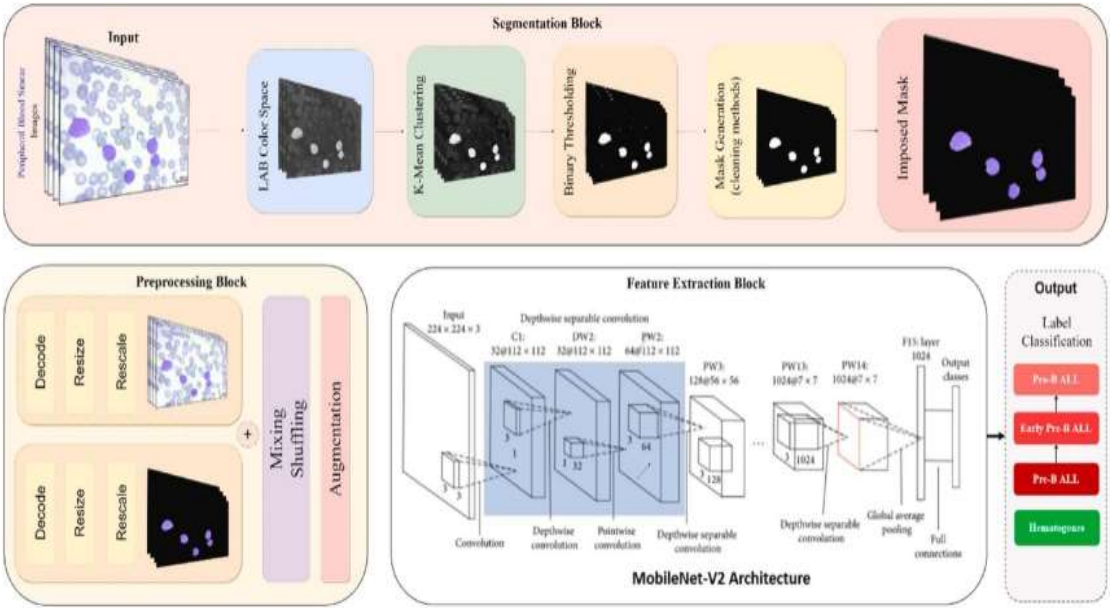


Fig. 2. The suggested model’s schematic.

Table. 1.1. Performance of chosen networks in distinct circumstances

Feature Extractor	Epoch	Training Accuracy	Batch Size	Size (MB)	Depth	Parameter	Test Accuracy
EfficientNetB0	30	99.1	32	29	132	5.3 million	100
MobileNetV2	30	99.62	32	14	88	3,538,984	100
NASNet Mobile	30	86.3	32	23	771	5,326,716	94.1

3. NASNet mobile

NASNet is a CNN architecture that stands out due to its scalability and construction through neural architecture search (NAS). This groundbreaking approach focuses on enhancing cells, the building blocks, by utilizing reinforcement learning techniques. These cells consist of a compact set of operations, such as separable convolutions and pooling, which are repeated multiple times to achieve the desired network capacity. NASNet introduces a mobile version called NASNet-Mobile, which stands out for its streamlined design. With 12 cells, it has 5.3 million parameters and 564 million multiple accumulates (MACs). NASNet-Mobile is specifically designed to prioritize lightweight and efficient performance, making it ideal for use on mobile devices or in resource-limited environments.

G. Selective structure, train and evaluation

After exploring different fitting methods and designs, our team made the decision to utilize segmented images in order to increase the sensitivity of the network to lymphoblast cells. This was done with the intention of improving the accuracy and reliability of our results. We conducted tests using selected pre-trained models after preprocessing and segmenting the dataset. However, the performance of these models did not meet our expectations. Through discussions and consultations with haematologist’s, we identified a potential weakness in the results - the incomplete extraction of image features. As a result, we developed a novel

approach that combines both segmented and original images. This approach incorporates a channel of segmented image and a channel of original image, allowing for the extraction of a maximum feature space. By simultaneously utilizing images from both channels, our aim was to capture nearly all the features present in the research images. This method offers the advantage of comprehensively capturing the diverse features inherent in the dataset. The accompanying figure 2 illustrates the general framework of our proposed technique, highlighting the process of integrating original and segmented images to enhance feature extraction and improve the performance of the model.

H. Metric evaluation

The performance of a detection and classification model for acute lymphoblastic leukemia (ALL) was assessed in the study using key statistical metrics: specificity, recall (sensitivity), and accuracy. These metrics, which are derived from parameters such as True Negative (TN), True Positive (TP), False Negative (FN), and False Positive (FP), provide valuable insights into the effectiveness of the model. Accuracy, which was initially used to select the most efficient model, Computes the percentage of correctly forecasted cases from the overall number of cases. The model's capacity to accurately identify positive cases is assessed by recall, whereas its ability to correctly detect negative cases is measured by specificity.

Mathematically, accuracy is represented as $\frac{TN+TP}{TP+TN+FP+FN}$, recall as $\frac{TP}{FN+TP}$, and specificity as $\frac{TN}{FP+TN}$.

In summary, these metrics and formulas thoroughly evaluate the model's ability to identify and categorize all cases, highlighting its potential to improve diagnostic precision in clinical settings.

IV. Results

During this stage, we initiate the process by assessing the performance of different pre-trained networks on both the training and test datasets to identify the most efficient one, which we refer to as the selected network. Following this, once we fine-tune the hyperparameters, we assess the effectiveness of the chosen network using the test dataset. Ultimately, utilizing the preferred model, we create and validate a mobile application using authentic data in a controlled laboratory setting.

A. Selection of Efficient Model

1. Following the completion of 30 training epochs on the training dataset and subsequent testing on the test dataset, we have gathered efficiency metrics for the pre-trained networks under identical conditions. The assessment outcomes for both datasets are detailed in Table 3 for the three pre-trained models. Our objective in scrutinizing these metrics was to identify the most appropriate network for our research data. Our aim was to opt for a model that is tailored for mobile devices, emphasizing efficiency in terms of size, depth, and learnable parameters. These criteria were meticulously selected to ensure the adoption of a lightweight network capable of effectively handling data on mobile devices. Among the models assessed, MobileNetV2 demonstrated the highest level of efficiency, boasting minimal parameters,

layer depth, and size. Consequently, it has been designated as the selected network for our proposed model.

B. The selected Model's performance in detection and classification

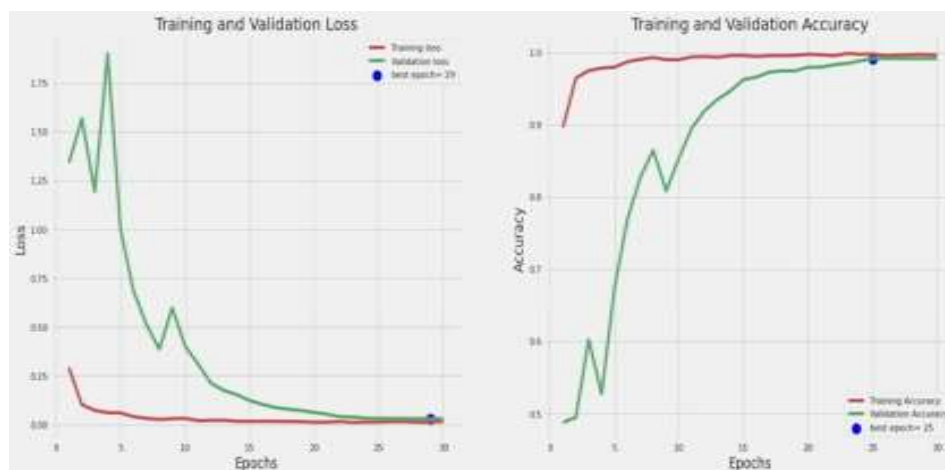


Fig. 3. The proposed model reached convergence after 25 epochs, achieving a training accuracy of 100% and a loss of 0.0035.

During the training phase, Figure 3 illustrates the learning curve of the chosen model. It showcases how the model's performance improves over time as it undergoes training, resulting in a decrease in error and an increase in accuracy with each epoch. The model shows promise in accurately identifying new instances of blood microscopic images through its ability to adjust to fresh validation data. By utilizing both segmented and original images as inputs, the proposed model demonstrates strong feature coverage and extraction capabilities. As a result, it accurately classifies all items within the test dataset. By leveraging the MobileNetV2 pre-trained network, this model efficiently captures relevant features for classification. Subsequently, web and mobile applications were developed to make use of this model's capabilities on laboratory devices. This initiative aims to enhance accessibility and efficiency in medical diagnostics by enabling the model to be utilized in real-world scenarios.

B. Applications for mobile and web platforms utilizing the suggested model for detecting and diagnosing ALL.

The mobile and web applications were developed in accordance with the research objectives, with the primary goal of improving user usability. These applications enable users to upload images from their device memory. Prior to analysis, these images undergo data preparation and segmentation.

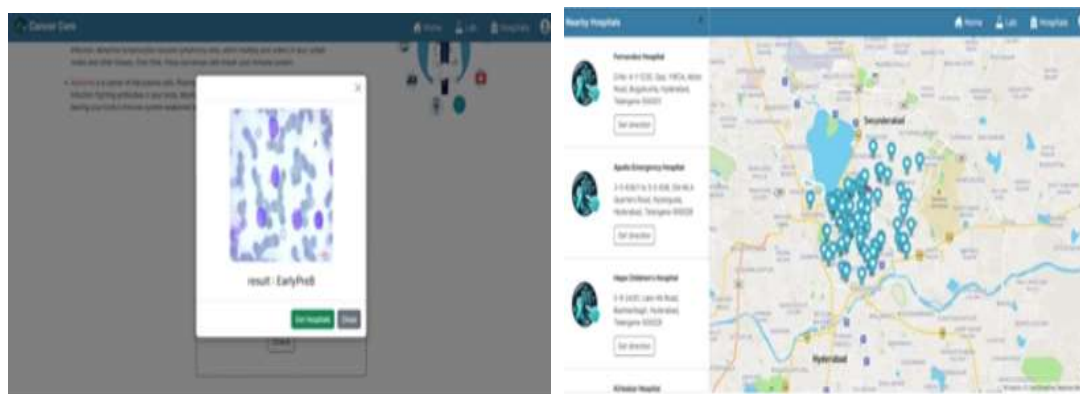


Fig. 4. Cancer Detection and Nearby Hospitals Web Screens

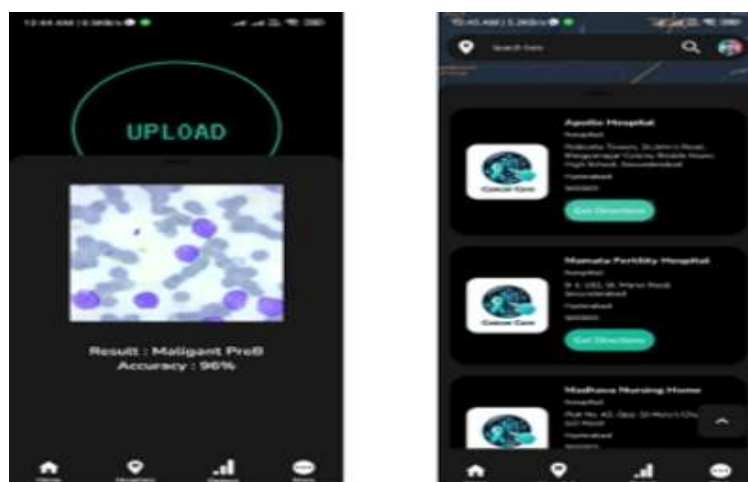


Fig. 5. Cancer Detection and Nearby Hospitals Mobile Screens

The interface of both the web and mobile applications is depicted in Fig. 4 & Fig. 5. Upon receiving original images from mobile phone inputs, the applications extract the image features and classify them to identify the ALL class. The performance of the applications is visually represented by showing the resulting image after organizing image features into data classes. By using the SoftMax function to determine the probability of the model's output in each class, users can observe the likelihood of the output belonging to the data class with the highest probability. The efficiency of the model was evaluated using the test dataset, where it accurately classified all items. Subsequently, the suggested model exhibited exceptional performance when tested with a series of photographs, accurately identifying the study data. To summarize, the designed applications prioritize user-friendly interfaces and efficient image processing, enabling accurate classification of ALL cases. The robust performance of the model highlights its potential usefulness in real-world medical diagnostics.

V. Discussion

1. The research presented a novel approach for identifying and categorizing ALL through the utilization of CNNs and transfer learning techniques. One of the key innovations was a unique image segmentation pipeline that combined segmented and original images to improve model accuracy. After evaluating different models, the research determined that the MobileNetV2 model was the most optimal structure for further development. Comparative analyses with previous models on various datasets showcased the superior efficiency of the proposed model. Factors contributing to its success included thorough feature extraction from two image channels and the careful selection of pre-trained

models for optimally extracting features and classifying. The transition of the model from theoretical development to practical application in clinical laboratory settings represented a significant advancement. Collaboration with oncology and hematology experts ensured the model's relevance and effectiveness in real-world scenarios. The resulting mobile and web applications simplified the process of ALL screening, allowing haematologists to analyze blood microscopic images efficiently and reducing the need for invasive procedures like bone marrow biopsy. While the model achieved high accuracy, it's important to note that the limited size of the test dataset could impact performance metrics. Strategies such as data augmentation and dropout were implemented to address overfitting and enhance model generalization.

VI. Conclusion

In summary, this study presented an innovative AI-driven method for identifying and categorizing acute lymphoblastic leukemia. By combining CNNs and transfer learning, the suggested model exhibited remarkable efficiency and accuracy compared to previous approaches. The successful implementation of cutting-edge techniques, such as image segmentation pipelines and meticulous model selection, greatly contributed to the effectiveness of this method. The validation of this approach in real-world clinical laboratory settings led to the creation of user-friendly mobile and web applications. These applications simplify the screening process for ALL, resulting in reduced diagnostic time and resource utilization, while also minimizing the need for invasive procedures. Overall, this research highlights the potential of AI-based models to revolutionize medical diagnostics, particularly in the realm of leukemia detection. Although further research and validation are necessary, these findings emphasize the transformative impact of AI technologies in enhancing healthcare outcomes and decreasing diagnostic expenses.

Acknowledgment

We wish to extend our sincere thanks to T. Gnana Prakash, our team mentor, for his unwavering technical support and guidance throughout the project, which has been instrumental in our progress thus far.

References

- [1]Maryam Bukhari, Sadaf Yasmin, Saima Sammad, and Ahmed A. Abd El-Latif, "A Deep Learning Framework for Leukemia Cancer Detection in Microscopic Blood Samples Using Squeeze and Excitation Learning", Hindawi, 2022, Article ID 2801227.
- [2]Vaibhav Rupapara, Furqan Rustam, Wajdi Aljedaani, Hina Fatima Shahzad, Ernesto Lee, ImranAshraf, "Blood cancer prediction using leukemia microarray gene data and hybrid logistic vector trees model, Scientific Reports, 2022.
- [3]Christo Ananth, P. Tamilselvi, S. Agnes Joshy, and T. Ananth Kumar, "Blood Cancer Detection with Microscopic Images Using Machine Learning, ResearchGate, 2022.
- [4]Supriya Mandal, Vani Daivajna, Rajagopalan V, "Machine Learning based System for Automatic Detection of Leukemia Cancer Cell", IEEE, 2019.
- [5]Patil Babaso S, S.K. Mishra, Aparna Junnarkar, "Leukemia Diagnosis Based on Machine Learning Algorithms", IEEE International Conference for Innovation in Technology (INOCN), 2020.
- [6]M.Saritha, Prakash.B.B, Sukesh.K, Shrinivas. B, "Detection of Blood Cancer in Microscopic Images of Human Blood Samples: A Review", International Conference on Electrical, Electronics, and Optimization Techniques (ICEEOT), 2016.
- [7]Preeti Jagadev, Dr. H.G. Virani, "Detection of Leukemia and its Types using Image Processing and Machine Learning", International Conference on Trends in Electronics and Informatics (ICTEI), 2017.
- [8]Deepika kumar, Aayush Khurana, Sweta Mittal, Suresh Chandra Satapathy (Senior Member, IEEE), Roman Senkerik (Member, IEEE), D.Jude Hemanth, "Automatic Detection of White Blood Cancer from Bone Marrow Microscopic Images Using Convolutional Neural Networks", IEEE Access.U

- [9]Mohammad Akter Hossain, Mubtasim Islam Sabik, Ikramuzzaman Muntasir, A.K.M. Muzahidul Islam, Salekul Islam, Ashir Ahmed, "Leukemia Detection Mechanism through Microscopic Image and ML Techniques", IEEE Region 10 Conference (TENCON), 2020.
- [10]Likhith N.G, Uzair Alam, Dr. Jagruthi H, "Leukemia Cancer Detection Using Deep Learning", International Research Journal of Modernization in Engineering Technology and Science, vol-5, 2023.
- [11]Tejal Nemade, Arjun Singh Parihar, "Leukemia Detection employing Machine Learning: a Review and Taxonomy", International Journal of Advances in Engineering and Management (IJAEM), vol-3, 2021.
- [12]Astha Ratley, Jasmine Minj, Pooja Patre, "Leukemia Disease Detection and Classification Using Machine Learning Approaches: A Review", First International Conference on Power, Control and Computing Technologies (ICPC2T), 2020.
- [13]Raghav Kandhari, Anupama Bhan, Parth Bhatnagar, Ayush Goyal, "Computer based diagnosis of Leukemia in blood smear images", Intelligent Communication Technologies and Virtual Mobile Networks (ICICV), 2021.
- [14]Christo Ananth, P. Thenmozhi, Stalin Jacob, Dr.A. Anitha, "Leukemia Blood Cancer Detection Using Matlab", ResearchGate, 2021.
- [15]M Sai Lasya, A Mahalakshmi, A B Suma, "Detection and Classification of Leukemia using Convolutional Neural Network and Updation in IoT", IRJET, vol-7, 2020.
- [16]K P Jayavikash, P Gopinath, U Nandheeswaran, R Sivabalan, T Divya Bharathi, "Detection of Leukemia Using Machine Learning Algorithms", IOP Publishing Ltd, 2021.
- [17]Mustafa Ghaderzadeh, Farkhondeh Asadi, Azamossadat Hosseini, Davood Bashash, Hassan Abolghasemi, Arash Roshanpour, "Review Article Machine Learning in Detection and Classification of Leukemia Using Smear Blood Images: A Systematic Review", Hindwai, 2021.
- [18]Sannihitha Peetala, DR B Leela Kumari, "Detection of Leukemia & its Staging Using Image Processing; Artificial Intelligence", International Journal of Signal Processing (IJSP), vol-7, 2022.