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Detection of Acute Lymphoblastic Leukemia Through Blood Cell Imaging Using Deep Learning

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Abstract: Acute lymphoblastic leukaemia (ALL) is notoriously difficult to diagnose since patients are typically subjected to intrusive, expensive, and potentially harmful tests. Unfortunately, in many parts of the world, people do not have easy access to these diagnostic instruments, which compounds the problem. The primary method for screening and diagnosing ALL in the past has been blood microscopic analysis. Laboratory workers and haematologists can only do so much when working manually. This work set out to address this issue by investigating the feasibility of using AI methods to analyse blood microscope 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. This program reliably distinguished ALL patients from other groups with high sensitivity and specificity in actual laboratory settings, making it a valuable screening tool. In final analysis, this innovative approach illustrates the need of applying technology to enhance healthcare outcomes while also showcasing the advantages of AI in medical diagnostics.

Keywords: Acute lymphoblastic leukemia, MobileNetV2, CNN, Microscopic images.

I. INTRODUCTION

Leukaemia of all kind (ALL) affects people of all ages. The precise diagnosis of this illness calls for a battery of diagnostic tests. Analysis of bone marrow samples using either bone marrow aspiration (BMA) or bone marrow biopsy (BMB) is the gold standard for diagnosis, however these invasive lab procedures necessitate specialised equipment [1]. The majority of children with ALL have difficulties related to these invasive procedures, which can lengthen the diagnosis process by several days and causes major obstacles. Moreover, healthcare systems bear an excessive proportion of the investment related to surgical treatments [2].These limitations highlight the critical role of laboratory personnel doing early microscopical investigation of blood samples in the diagnosis of leukaemia. Nevertheless, laboratories face a major challenge with the large volume of blood samples, which increases the possibility of diagnostic errors. The possibility for mistakes in detecting ALL is further exacerbated by the difficult

procedure of microscopic analysis, the knowledge necessary of laboratory staff, and regular lack of energy [3]. 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 [4]. 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 [5]. 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

A leukaemia diagnosis using microscopic blood samples is an enormous undertaking in the field of medical image analysis. in [6], Data capture, data augmentation, a complex convolutional neural network (CNN) architecture, squeeze learning, and excitation learning are all part of the novel method presented in this article. In order to overcome the problem of insufficient data, the process starts by obtaining photographs of tiny blood samples. Data augmentation strengthens the model by artificially expanding the dataset used for training [7]. The technique relies on a deep convolutional neural network (CNN) architecture that uses squeezing and excitation learning to isolate abnormal cells from healthy ones. The methodology is validated by many trials that include data augmentation, full-scale photos, and cropped cells [8]. The model is trained efficiently on a 12GB NVIDIA Tesla K80 GPU using Python and Keras on Google Colab. Crucially, their suggested system has a remarkable 94% accuracy rate [9], In this study, we explore advanced image processing techniques, with a focus on CNNs, which are used for picture classification. Noise reduction via median filtering and greyscale picture conversion are both part of the pre-processing phase. Image binarization, adaptive thresholding, and greyscale segmentation are some of the methods used. The use of training datasets for supervised learning is central to this work, and the report highlights the benefits of employing a large amount of training data for CNNs, making it an asset in image and signal processing [10]. In order to enhance the image quality, this study presents a strategy that incorporates preprocessing approaches such as colour conversion, filtering, and histogram equalisation. For data segmentation, the K-means algorithm is used, and for thresholding, the Zack method is implemented [11]. The need of improving the identification, thresholding, and segmentation steps for accurate detection is emphasised throughout the paper. In addition, the study highlights how shape feature extraction might improve white blood cell counts and segmentation accuracy in general. The outcomes show that the proposed approach attains accuracy rates between 72.2% and 97.8% on a variety of characteristics, such as K-means, share-based features, histogram equalisation, and linear contrast stretching.[12]. In this research, we investigate the possibility of merging machine learning and image processing. With a special emphasis on Linear Discriminant Analysis's (LDA) efficacy in picture enhancement, it covers preprocessing techniques like thresholding and noise removal filters [13]. This study also emphasises how CNN and other ML algorithms may be used for picture categorisation. The effectiveness of linear classifiers, K-NN, and SVM classifiers is researched extensively [14]. According to previous studies, accuracy rates utilising various methods can range from 88% to 93%. Anyone working or studying in the sector will find this study to be a valuable resource.

III. Methodology

A lightweight Convolutional Neural Network (CNN) model is not yet available in any smartphone or web app that can detect and classify Acute Lymphoblastic Leukaemia (ALL). The end goal of this study is to develop a web and mobile app that can aid medical practitioners and laboratory researchers. The primary goal is to create a convolutional neural network (CNN) algorithm that can analyse microscopic images of blood and detect ALL and its subtypes (Early, Pre ALL, and Pro ALL) using cellphones and PDAs.

A. Dataset

The research relied on a regional database compiled from various Tehran, Iran, hospitals. A total of 89 patients suspected of having ALL had their microscopic blood images included in the set. Experts in the lab painstakingly cleaned and dyed these pictures. There were benign and malignant groupings in the database. The former included hematogones, which look similar to ALL but aren't cancerous and usually go away without treatment. Among the malignant lymphoblasts, there were three subtypes linked to ALL. A Zeiss camera linked to an optical microscope captured the images, which were then saved in JPG format. The subclasses of the cell type were determined using flow cytometry.

B. Data preparation

The research data, which was originally given in PNG or JPG format, was transformed into numerical arrays that represent the image pixel values (this is called decoding). Resizing input images in convolutional neural networks (CNNs) is a frequent approach to reduce computational overhead and keep the network design flexible. The researchers in this study used a pre-trained network that had specified dimensions that the input photos needed to exceed. 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

Segmenting ROIs was the main goal of this phase. This involved identifying critical parts of the model that were essential to both clinical professionals and the ML model. The goal of the segmentation procedure was to highlight clinically relevant regions while removing background noise and other extraneous features. For more precise and trustworthy targeting of lymphoblast cells, a novel segmentation method was used. 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:

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- 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.

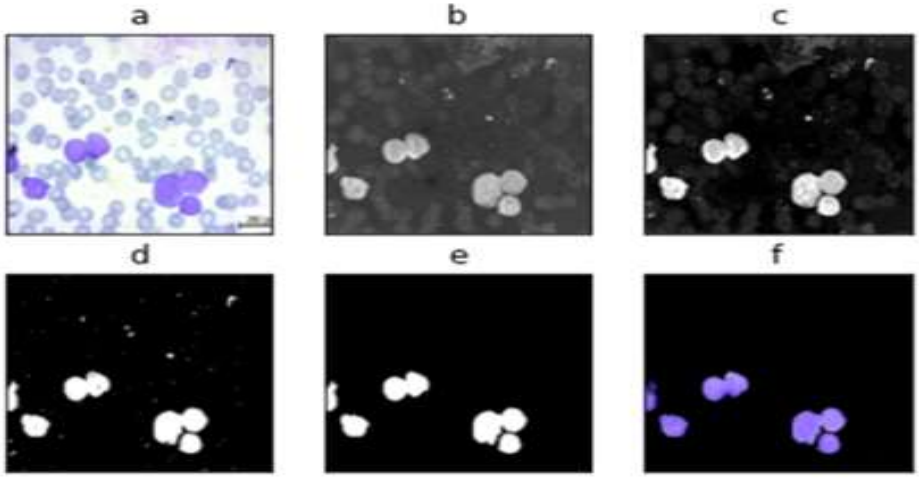


Fig. 1. showcases the segmentation process: a) RGB color space, b) LAB color space, c) K-means clustering, d) Binary thresholding, e) Methods for mask generation and cleaning, f) Applying the mask generated on the original RGB image.

1. The use of a mask to remove image backgrounds allowed for the isolation of blast features and the elimination of extraneous information. After this process, the pictures would be free of any extraneous cells or components of the blood. After that, the ROI areas were extracted for further analysis by mapping the segmented outputs back to the source images.

E. Data rescaling, augmentation, and categorization

It was essential to set the pixel values to a common interval so that the image presentation would be consistent and uniform. The process of pixel intensity normalisation was used to do this, as it transferred the pixel values to the interval [0, 1]. By standardising the input data, we were able to facilitate comparison and analysis of photographs. For machine learning models to function at their best, data augmentation is crucial. Improving the diversity of training samples without changing their semantic or intrinsic details is what data augmentation is all about. Data augmentation helps make the model more elastic and resilient by simulating noise and other real-world data perturbations. To make the training samples louder, this study used two common transformations: horizontal flip and vertical flip. Classifying the data was a prerequisite to training the pre-trained networks and the proposed model. We prepared the research data for training by classifying it after we segmented, resized, and enhanced it. Grouping the data according to important attributes or classes was part of this categorisation process, which made sure the model got correctly labelled data for effective learning. Segmentation, normalisation, augmentation, and classification were all steps in getting the data ready for splitting. For the purpose of training, evaluating, and validating the model, it was necessary to partition the data into distinct subsets, usually called training, validation, and testing sets. In this manner, the data might be partitioned such that the model could be trained on one part, validated on another, and then tested on a third, hidden component, enabling a thorough evaluation of its performance.

F. Convolutional neural network structure

The primary goal was to prioritise lightweight models so that a highly effective model may be deployed on less powerful equipment. We achieved this by carefully selecting three compact and efficient lightweight versions. Evaluation of their efficiency and selection of the best model for use in feature extraction were the main objectives. 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.

Efficient Net

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 × 224 x 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.

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.

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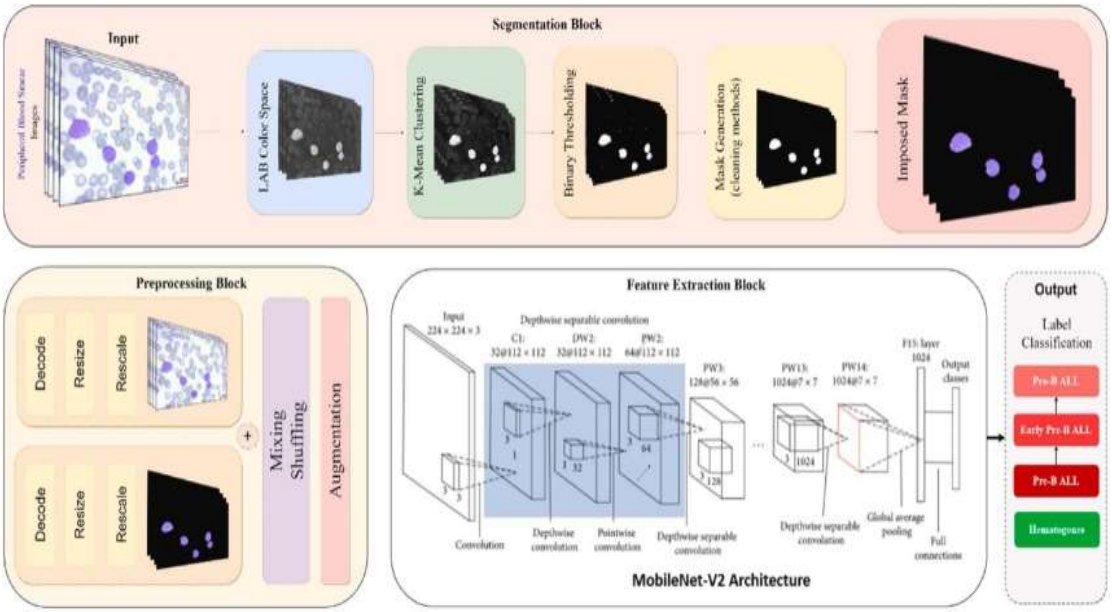


Fig. 2. The suggested model's schematic.

Table. 1.1. Performance of chosen networks in distinct circumstances

Feature Extractor	Epoch	Training Accuracy	Batch Size	Size (MB)	Depth	Parameter	Test Accuracy
EfficientNetB0	40	99.1	35	28	132	5.3 million	100
MobileNetV2	40	99.62	35	15	90	3,538,999	100
NASNet Mobile	40	86.3	35	25	760	4,326,702	93.4

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.

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.

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.

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.

The selected Model’s performance in detection and classification

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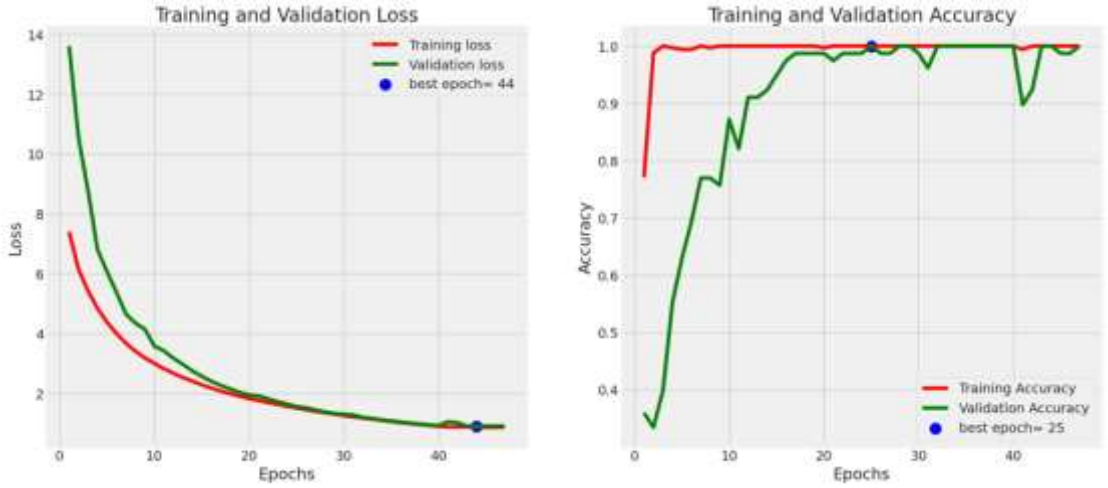


Fig. 3. The proposed model reached convergence after 25 epochs, achieving a training accuracy of 100% and a loss of 0.0035.

In Figure 3, we can see the selected model's learning curve during the training phase. It demonstrates how the model's accuracy and robustness are enhanced with each training period, leading to gradually decreasing error rates. With the capacity to adapt to new validation data, the model demonstrates potential in correctly detecting new occurrences of blood microscopic pictures. Use of both original and segmented pictures as inputs allows the proposed model to exhibit good feature coverage and extraction capabilities. Consequently, it perfectly categorises every item in the test dataset. This model effectively gains classification-relevant characteristics by utilising the MobileNetV2 pre-trained network. To put this model's capabilities to use on devices in the lab, web and mobile apps were created afterwards. With this effort, we hope to make the model more usable in real-world settings, which will improve medical diagnostics' accessibility and efficiency.

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.

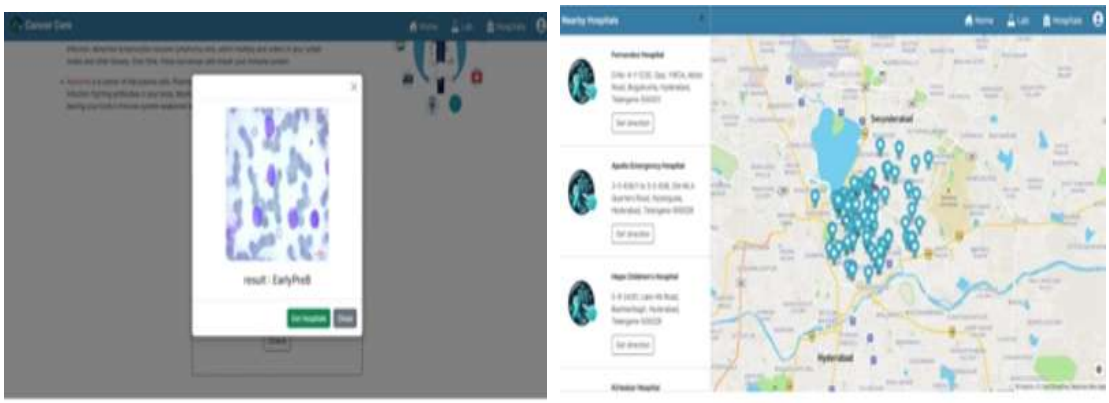


Fig. 4. Cancer Detection and Nearby Hospitals Web Screens

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Fig. 5. Cancer Detection and Nearby Hospitals Mobile Screens

Figures 4 and 5 show the user interfaces of the web and mobile apps, respectively. Applications detect the ALL class by extracting picture features and classifying original photographs received from mobile phone inputs. Displaying the final picture after categorising picture features into data classes is a visual representation of the applications' performance. Users can see which data class is most likely to have the model's output by calculating the probability of each class using the SoftMax function. 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

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 conclusion, to introduced a novel AI-driven approach to the diagnosis and classification of acute lymphoblastic leukaemia. The proposed model outperformed its predecessors in regards to efficiency and accuracy due to the use of convolutional neural networks (CNNs) and transfer learning. 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 apps streamline ALL screening, which means less time and resources spent on diagnostics and less invasive procedures needed. The findings of this study show that AI-based models have the ability to change the face of medical diagnostics, especially when it comes to detecting leukaemia. These results highlight the revolutionary influence of AI technologies in improving healthcare outcomes and minimising diagnostic costs, while additional validated study is necessary.

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