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Harnessing CNN and Smartphone Microscopy: A Mobile Application for Automated Leukemia Detection and Classification

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Abstract
This paper presents a novel approach to leukemia detection and classification by integrating Convolutional Neural Networks (CNNs) with a custom-built smartphone microscope and a mobile application. Leveraging the portability of smartphones and the power of deep learning, we developed a cost-effective diagnostic tool designed to capture high-resolution blood smear images using a dual-magnification smartphone microscope and process them in real-time through a CNN, built with Keras, for the automated detection and classification of leukemia. The system is capable of classifying four primary types of leukemia: Acute Lymphoblastic Leukemia (ALL), Acute Myeloid Leukemia (AML), Chronic Lymphocytic Leukemia (CLL), and Chronic Myeloid Leukemia (CML) directly on the smartphone without the need for cloud-based services. This enables on-site diagnostics, particularly in resource-limited or remote settings. The proposed solution addresses the limitations of conventional laboratory microscopy and cloud-dependent systems, offering a portable, scalable, and accurate tool for medical professionals. Extensive testing with a novel blood smear dataset has demonstrated the efficiency of our approach, achieving high accuracy in both detection and classification tasks. By eliminating reliance on external infrastructure and focusing on mobile-based computation, this system brings affordable and accessible healthcare to the forefront, with potential applications in both clinical settings and field diagnostics. This work highlights the potential of combining smartphone microscopy and deep learning for early and accurate disease detection, representing a significant advancement in portable medical diagnostics.

Keywords: *mobile application, CNN, deep learning, Keras, leukemia*.

1. Introduction

Leukemia, a life-threatening blood cancer, requires early and precise diagnosis for effective treatment and improved patient outcomes [1]. The detection and classification of leukemia have traditionally relied on laboratory-based methods, particularly the microscopic examination of blood smears by trained pathologists [2, 3]. However, these methods are resource-intensive, require specialized equipment, and are not always accessible in low-resource or remote areas [4]. In recent years, advances in smartphone technology, artificial intelligence (AI), and mobile applications have introduced innovative solutions to overcome these challenges, enabling the automation of leukemia detection and classification [5]. Among these, Convolutional Neural Networks (CNNs) have proven highly effective in image classification tasks. CNNs, a type of deep learning model, are particularly well-suited for processing medical images such as blood smears due to their ability to automatically extract relevant features from the images [6, 7]. Researchers have demonstrated that CNNs can achieve high accuracy in detecting abnormal cells and classifying various subtypes of leukemia, outperforming traditional machine-learning methods in some cases [8].
Recent advancements in smartphone-based microscopy have further enhanced the potential of mobile applications for leukemia detection [9]. Smartphones, when equipped with external optical lenses or customized 3D-printed components, can function as portable microscopes capable of capturing high-resolution images of

blood smears. These images can then be analyzed by embedded deep-learning models, including CNNs, to detect and classify leukemia in real time [10].

While some mobile applications rely on cloud-based systems to process images and classify leukemia, this approach introduces concerns about data privacy, network dependency, and latency [11]. Cloud-based systems require a stable internet connection, which may not be available in remote areas. Additionally, transmitting sensitive medical data to the cloud raises concerns about patient privacy. In contrast, applications that perform image processing locally on the smartphone, without cloud dependency, offer a more secure, real-time, and self-contained solution [12].

Despite the advancements in leukemia detection via mobile applications, challenges remain. Many of the existing systems are designed to classify only one type of leukemia, limiting their clinical applicability. There is also a need for more comprehensive testing and validation of these applications in real-world healthcare settings. Moreover, most studies have focused on developing CNN models using small or standard datasets. Still, there is a growing need for systems trained on large, diverse datasets to improve model robustness and generalizability.

This paper presents a novel solution that integrates CNNs with a custom-designed smartphone microscope to create a mobile application for the automated detection and classification of leukemia. The application utilizes blood smear images captured with the smartphone microscope, performing real-time analysis and classification of leukemia types directly on the mobile device. By enabling rapid, on-site diagnosis without the need for laboratory equipment or internet connectivity, this solution is particularly suited for use in remote or resource-limited areas.

2. Method

To the best of our knowledge, no mobile application is currently available for detecting and classifying leukemia using a proposed smartphone microscope for capturing blood images and a CNN model. Therefore, the application developed in this study can bridge the gap in the existing literature and act as a valuable resource for clinicians and researchers in laboratory settings. The primary aim of this research was to create a CNN algorithm-based application for portable devices that could be utilized to analyze blood microscopic images for diagnosing leukemia and categorizing its types (AML, ALL, CLL, and CML). The experimental methodology is illustrated in the Figure (1).

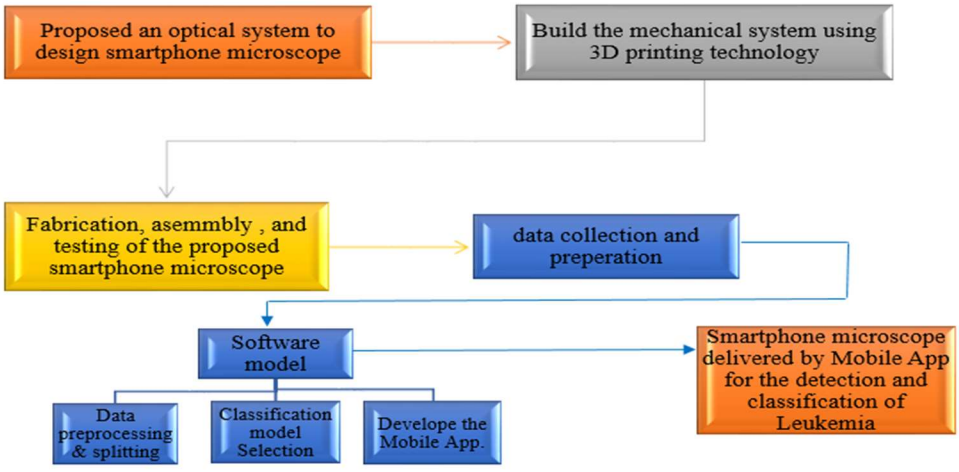

Figure 1: Overview of the proposed method.

2.1. Proposed smartphone microscope design

The design of a smartphone microscope for capturing leukemia blood smears integrates optical components with mobile technology to create an accessible diagnostic tool. This low-cost alternative to traditional microscopes is especially beneficial in resource-limited areas where standard microscopy equipment is often unavailable.

The smartphone microscope's fundamental aspect is its optical design, which needs to deliver adequate magnification and resolution to examine the intricate structures within a blood smear. Detecting abnormalities in white blood cells is vital for leukemia diagnosis. The smartphone microscope accomplishes this by utilizing lenses that can provide magnification levels of up to 1000x.

2.1.1. System Configuration

Figure (2) exemplifies the configuration of the proposed smartphone microscope's optical system. It represents the block diagrams that illustrate the optical system consisting of a light source that provides illumination for the sample (white LED), a diffuser (white filter), a sample (i.e., the object being observed), and an objective lens (40x) positioned closest to the sample, followed by the tube lens and eyepiece. The lenses are aligned sequentially, and light rays pass through each lens to focus on the smartphone's camera sensor.

The smartphone microscope typically incorporates 3D-printed components to support the optical system, which holds the lenses and smartphone in place. Figure (3) illustrates the assembly of the final model.

This customizable design ensures precise alignment between the lens and camera sensor, enhancing image quality and consistency. It also allows for easy assembly and disassembly, making it convenient for use in fieldwork or clinical environments.

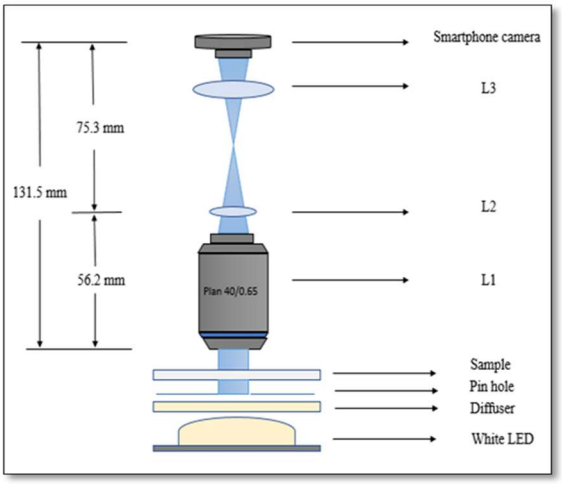

Figure 2: Block diagram that represents the optical configuration of the proposed smartphone microscope.

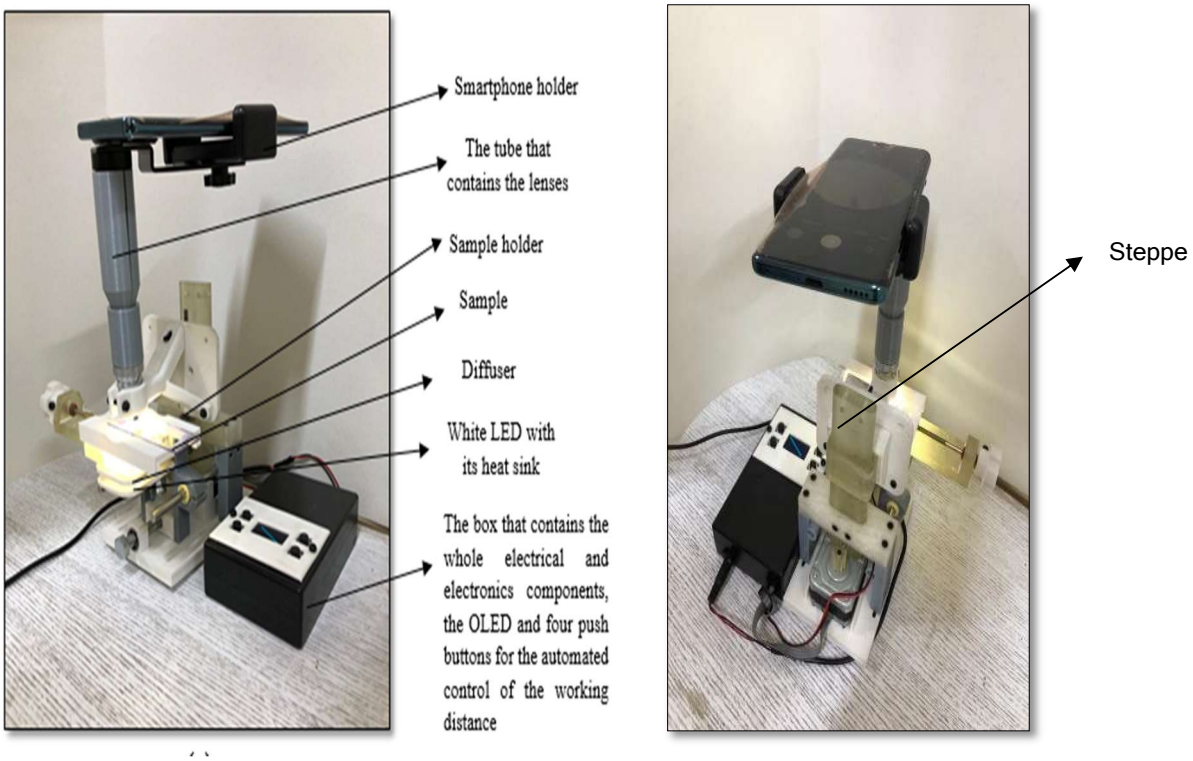

Figure 3: Assembly of the final model.

2.2. Data collection and preparation

The novel dataset consists of microscopic blood smear images of four types of Leukemia (ALL, AML, CML, CLL) and normal cases. Cancerous samples were taken from the Medical City Hospital in Baghdad, Iraq, while healthy samples were taken from a private medical laboratory in Baghdad, Iraq. Expert doctors diagnosed and labeled these blood samples before using them in this study.

There were two volumes in the dataset, the first for training and the second for testing. The training folder contains (5000) microscopic images of blood smears collected from 500 subjects for benign (normal) and malignant (Leukemia) types, while the test folder contains (500) images of benign and malignant. The number of images for each category and other details are illustrated in Table (1). Images were obtained from September 2022 to March 2023.

Furthermore, the blood smear slides were prepared by following the standard method. The blood sample (2 ml) is collected in ethylene diamine tetraacetic acid (EDTA) vacutainer. The smear was produced by putting a drop of blood on a neat, clean slide and spreading it using the wedge technique. The smear was then allowed to dry. The dried smear is stained with Leishman stain (3 min) followed by Giemsa stain (1: 10 dilution; 15 min). The slide was washed in running tap water and allowed to dry. Finally, the prepared slides were observed under high power magnification (1000×) of the proposed smartphone microscope to get high-quality and magnified images of blood cells, especially WBC. Figure (4) shows the samples of the dataset, while Table (2) compares the proposed dataset with another current public dataset.

Table 1: The number of images and patients corresponding to benign and malignant cases all taken under a high magnification power of (1000x).

Type of dataset	Type of preferable blood smear	No. images	No. patients
Train	Normal	1000	100
	Leukemia (ALL)	1000	100
	Leukemia (AML)	1000	100
	Leukemia (CLL)	1000	100
	Leukemia (CML)	1000	100
Test	Normal	100	50
	Leukemia (ALL)	100	50
	Leukemia (AML)	100	50
	Leukemia (CLL)	100	50
	Leukemia (CML)	100	50

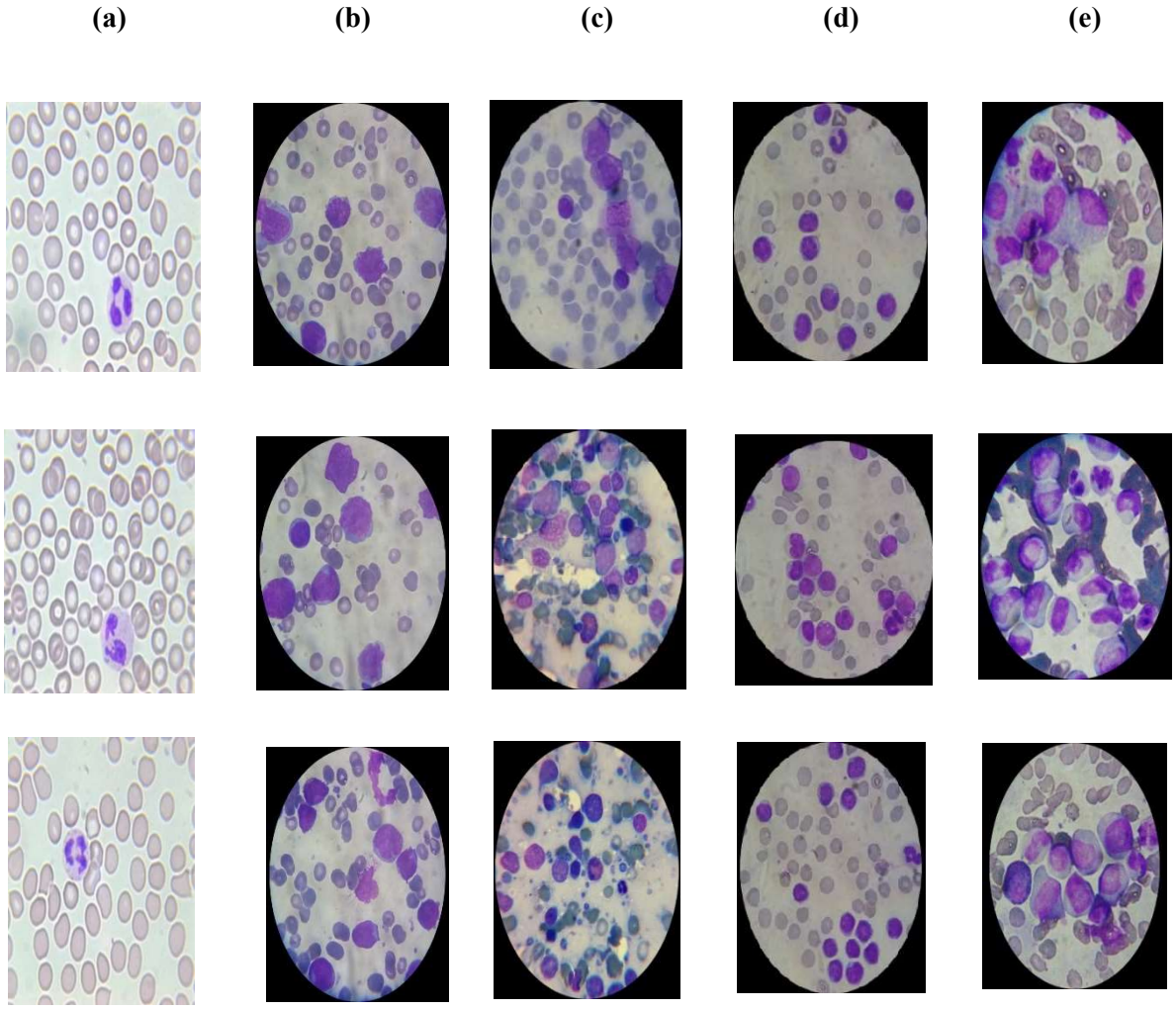

Figure 4: Samples of the dataset captured by the proposed smartphone microscope under 1000x magnification for (a) Normal, (b) ALL, (c) AML, (d) CLL, and (e) CML cases.

Table 2: Comparison of the current public databases with the proposed dataset for leukemia detection.

Authors	Leukemia type	No. of images
S. Agaian et al. [13]	AML & normal	80
R. D. Labati et al. [14]	ALL & normal	108
D. Kumar et al.[15]	B-ALL & MM	190
A. Abhishek [16]	ALL, AML & normal	500
Proposed dataset	ALL, AML, CLL, CML & normal	5000

2.3. The software model

The software model aims to provide an accessible and efficient solution for detecting and classifying leukemia from blood smear images. Figure (5) illustrates the proposed framework for the software model.

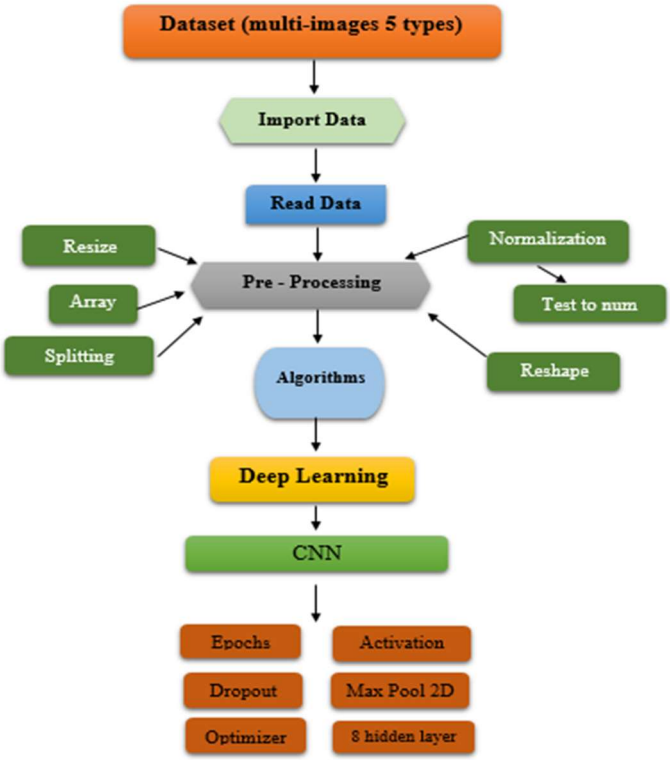

Figure 5: The proposed framework for the software model.

2.3.1. Data Preprocessing

Data preprocessing is a vital initial step in preparing raw data for an AI model, involving tasks such as cleaning, transforming, and organizing the data into a usable format. These preprocessing steps are crucial to enable the

classification model to effectively learn from the data and accurately detect and classify leukemia in blood smear images. The data preprocessing steps were as follows:

1. Image Resizing

Resizing images is one of the most essential steps in this context. Standardizing image sizes helps to increase the efficiency of algorithms. All images were resized to 200 x 200 pixels.

2. Normalization: Pixel values were normalized to ensure that all pixels were within a specific range, typically (0, 1), for faster convergence during training.

3. Label encoding: ML and DL algorithms cannot directly process categorical (text-based) data and require it to be in numeric form for mathematical computations. Therefore, labels for categorical were converted to numerical values.

```
"normal": 0,
"Leukemia(ALL)": 1,
"Leukemia(AML)": 2,
"Leukemia(CML)": 3,
"Leukemia(CLL)": 4
```

4. Data Augmentation: To increase the diversity of the training data and reduce overfitting, the training set was augmented using techniques such as rotation, flipping, and zooming.

5. Convert to Array: images were converted into numerical arrays (pixel values) since AI models cannot directly handle images in their original file formats. Therefore, each pixel in an image is represented by a numerical value. 6. Train/Test Split: The dataset was split into training and test sets. This approach ensures the model is trained on one portion of the data and ultimately tested on an unseen set, as shown in Figure (6). Figure (7) depicts the percentage of each dataset category.

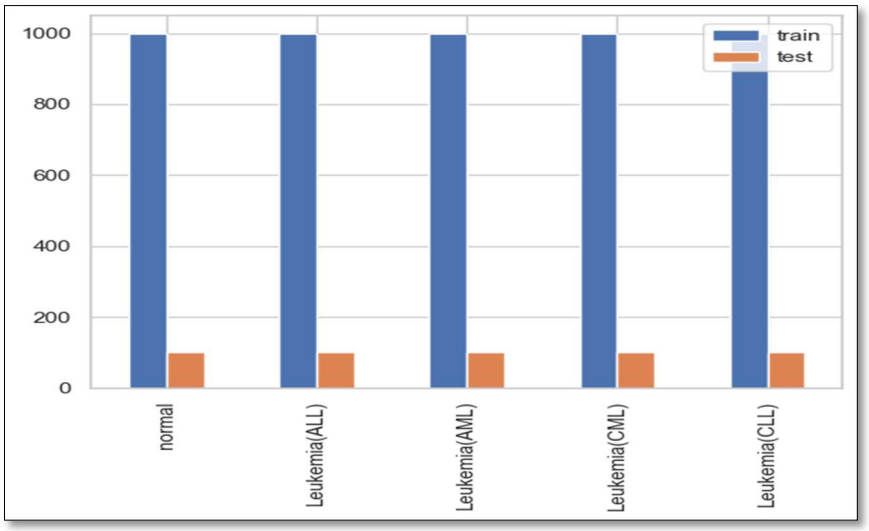

Figure 6: The count for each label.

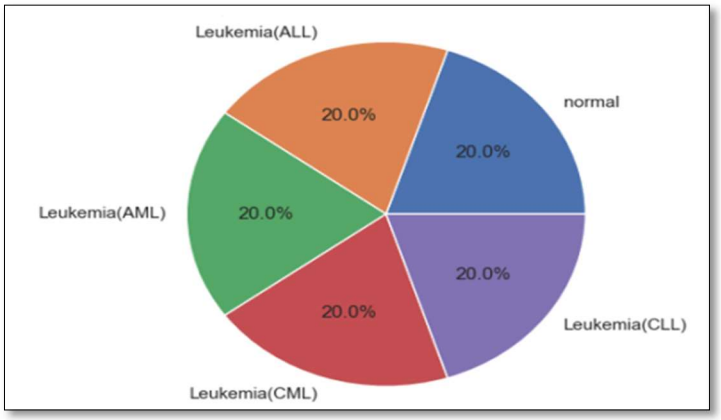

Figure 7: The percentage of each dataset category.

2.3.2. CNN classification model

The CNN was built using the Keras framework. The architecture consisted of several layers designed to extract and learn complex features from the blood smear images:

- Input Layer: RGB images. In this step, the Keras sequential model was initialized, and layers were added one after the other in a linear stack.
- Convolutional Layers: (Conv2D Layers) convolutional layers that apply a series of convolution filters to the input images to extract features (edges, textures, and shapes). These layers have (200, 150, 120, 80, and 50) convolution filters (kernels) with a size of 3x3 pixels. The ReLU (Rectified Linear Unit) activation function introduced non-linearity, allowing the model to learn more complex patterns. It replaces negative values with zero and keeps positive values unchanged.
- Pooling Layers: Max pooling layers followed the convolutional layers to reduce the spatial dimensions and retain essential features.
- Flatten Layer: to convert the feature maps into a 1D vector for dense layers.
- Fully Connected Layers: Four dense layers were added, as well as a Dropout Layer, which is not a hidden layer but is used for regularization.
- Output Layer: The output layer has as many neurons as the number of classes (leukemia subtypes and healthy cells). Therefore, it has 5 neurons (one for each class), using softmax activation for multi-class classification.

A sequential neural model (Keras Sequential API, n.d.) uses activation functions as the core mathematical logic of each neural layer. This CNN model consists of eight hidden layers, five convolutional layers that extract features from the input, and three dense layers that assist in classifying the input before reaching the final output layer, as revealed in Figure (8).

The model was compiled and trained using the Adam optimizer, with categorical cross-entropy as the loss function. 8 epochs of training were used with 64 batch sizes. Early stopping was used to monitor the validation loss and stop training if no improvement was seen for 5 consecutive epochs.

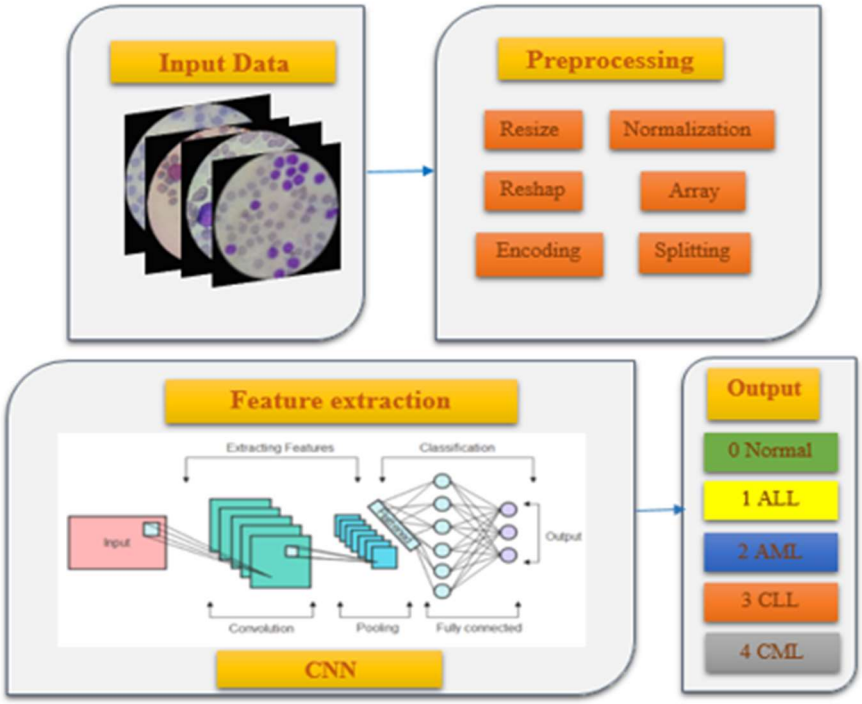

Figure 8: CNN model's schematic diagram.

2.3.3. Performance evaluation of CNN model

The performance of a CNN is best evaluated through a combination of metrics, each providing insights into different aspects of the model's effectiveness. Combining these metrics ensures that the CNN is accurate, efficient, and reliable for real-world leukemia detection. These metrics are:

1- Accuracy: the ratio of correctly predicted instances (both positive and negative) to the total instances. It is essential to measure how often the CNN correctly classifies the blood smear images [24].

$$\boldsymbol{Accuracy} = \frac{\boldsymbol{TP+TN}}{\boldsymbol{TP+Tn+FP+FN}} \qquad \textbf{(1)}$$

Where:
TP (True Positive): Correctly predicted leukemia cases.
TN (True Negative): Correctly predicted healthy cases.
FP (False Positive): Incorrectly predicted leukemia cases.
FN (False Negative): Missed leukemia cases.

2- Precision: measures the proportion of true positive results out of all positive predictions made by the model. It focuses on the accuracy of positive predictions.

$$\boldsymbol{precision} = \frac{\boldsymbol{TP}}{\boldsymbol{TP+FP}} \qquad \textbf{(2)}$$

3- Recall (Sensitivity): measures the proportion of true positives out of all actual positive cases. It focuses on the model's ability to detect leukemia when it is present.

$$\boldsymbol{Recall} = \frac{\boldsymbol{TP}}{\boldsymbol{TP+FN}} \quad \textbf{(3)}$$

4- F1-Score: the harmonic mean of precision and recall. It balances the two, making it useful when the dataset is imbalanced (e.g., when there are more healthy samples than leukemia samples).

$$\boldsymbol{F1-score} = \mathbf{2} \times \frac{\boldsymbol{Precision \times Recall}}{\boldsymbol{Precision+Recall}} \quad \textbf{(4)}$$

5- Specificity measures the proportion of true negatives out of all actual negative cases. It focuses on the model's ability to identify healthy individuals correctly.

$$\boldsymbol{Specificity} = \frac{\boldsymbol{TN}}{\boldsymbol{TN+FP}} \quad \textbf{(5)}$$

These metrics can estimate the standard performance evaluations for all AI algorithms [25].

2.3.4. Mobile Application Development

The trained CNN model was compressed and optimized for mobile platform deployment, facilitating real-time offline leukemia classification. The TensorFlow Lite framework was employed to convert the model into a mobile-compatible format.

The Mobile app was developed using the cross-platform tool Flutter (Dart). To align with the research objectives, the mobile application prioritizes maximum usability for its users and can retrieve images from both the camera and the device's memory. Figure (9) illustrates the mobile application interface. The application receives the original images from the mobile phone, extracts their features, and classifies them to determine whether the image of the preferable blood smear is leukemia or not and its class.

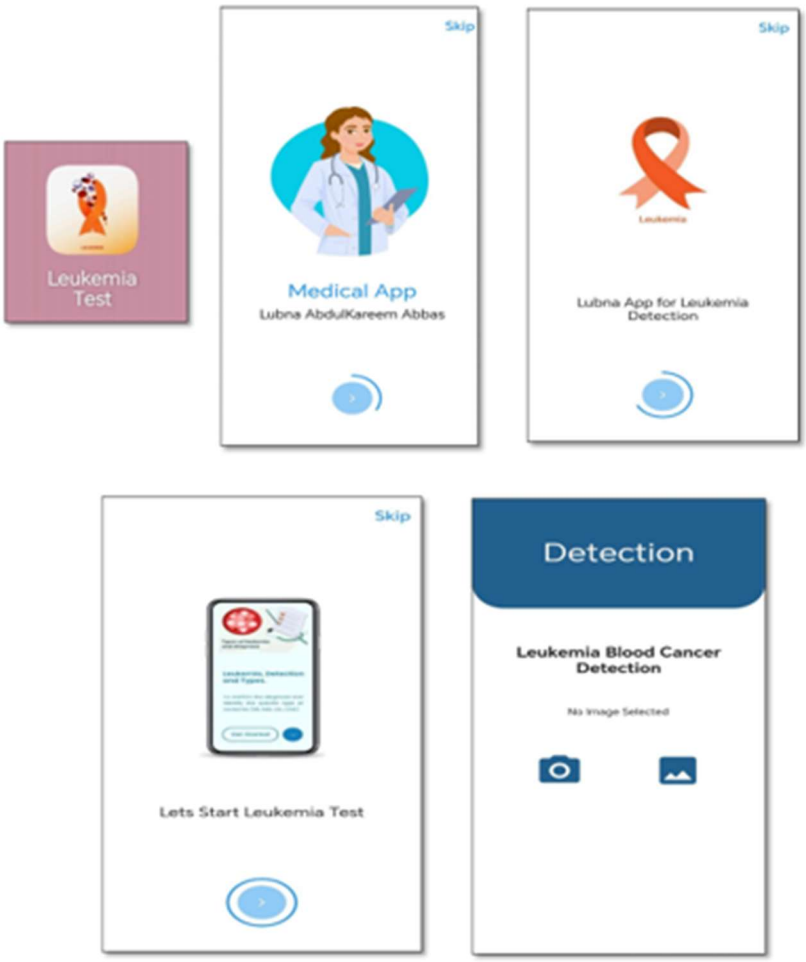

Figure 9: Mobile app user interface.

3. Results and discussion

3.1. Performance Evaluation of CNN

Python code was utilized to implement the proposed method to assess their performance in terms of precision, recall, accuracy, and specificity.

1- Accuracy: The model achieved an overall accuracy of 98%, meaning it correctly classified 98% of all the samples in the test dataset, both for leukemia-positive and negative cases. While this is a strong indicator of the model's overall performance, accuracy alone can sometimes be misleading, particularly in datasets with imbalanced classes (e.g., significantly more non-leukemia cases than leukemia cases). Therefore, additional metrics provide a more nuanced understanding of the model's effectiveness.

2- Precision: The precision score of 97% indicates that out of all the cases that CNN predicted as leukemia, 97% were correct. This reflects the model's ability to avoid false positives misclassifying healthy individuals with leukemia. High precision is critical in clinical settings as it reduces the likelihood of unnecessary anxiety or invasive follow-up procedures for patients misdiagnosed with leukemia.

3- Recall (Sensitivity): The model's recall (or sensitivity) was also 97%, correctly identifying 97% of the actual leukemia cases in the test set. A high recall ensures that most true leukemia cases are detected, which is vital in medical diagnostics to minimize false negatives (i.e., cases where leukemia is present but undetected). In the context of leukemia detection, where missing a diagnosis can have serious consequences, a high recall demonstrates the model's robustness.

4- Specificity: The specificity of 98% signifies the model's ability to correctly classify non-leukemia cases, effectively identifying 98% of healthy individuals. High specificity is crucial in ensuring that individuals without leukemia are not mistakenly diagnosed as having the disease, thereby reducing the burden of unnecessary further testing or treatments.

5- F1-Score: The F1-score of 96% provides a balance between precision and recall. The harmonic mean of the two metrics offers a comprehensive measure of the model's overall performance. The high F1 score reflects that the model is well-balanced in identifying true leukemia cases while minimizing false positives. This is particularly valuable in scenarios where false positives and negatives have significant implications.

Consequently, CNN demonstrated strong performance in detecting and classifying leukemia, with high accuracy, precision, recall, and specificity scores. The model's high accuracy and F1 score confirm its effectiveness in correctly identifying leukemia cases while maintaining low error rates in classifying healthy individuals. These results suggest that the model can serve as a reliable tool for early detection and diagnosis of leukemia, potentially improving patient outcomes through timely and accurate diagnosis.

Figure (10) conveys training accuracy and loss; in this figure, there are 6 epochs, and an epoch refers to one complete pass of the training dataset through CNN during the training process. This means the model has been trained on the entire dataset six times. As the number of epochs increases, the model has more opportunities to learn from the data, which should generally result in improved accuracy and reduced loss. However, too many epochs can lead to overfitting, where the model becomes too specialized to the training data and performs poorly on new, unseen data.

For accuracy (left plot), the training accuracy (dashed line) increases rapidly from around 60% in the first epoch to over 90% by the third epoch, and it plateaus around 98% in subsequent epochs. This indicates that the model is learning quickly in the initial epochs and converges to a high level of accuracy.

The right plot represents the training loss, which measures the model's prediction error, which means how far the model's predictions are from the actual labels. A lower loss value indicates better model performance. Training Loss (dashed line) starts high (close to 1.0) but rapidly decreases as the epochs progress. By epoch 6, the loss has dropped significantly and is close to zero (0.2), suggesting that the model has become very good at minimizing errors in the training data. This sharp decline in training loss indicates that CNN quickly learns from the data, reducing its error rate significantly as training progresses.

The error rate in this context is the inverse of accuracy, and it measures the proportion of incorrect predictions. Since the accuracy in this figure is relatively high (above 90%), the error rate is relatively low. The error rate is 2%, meaning the model only makes incorrect predictions for 2% of the training examples.

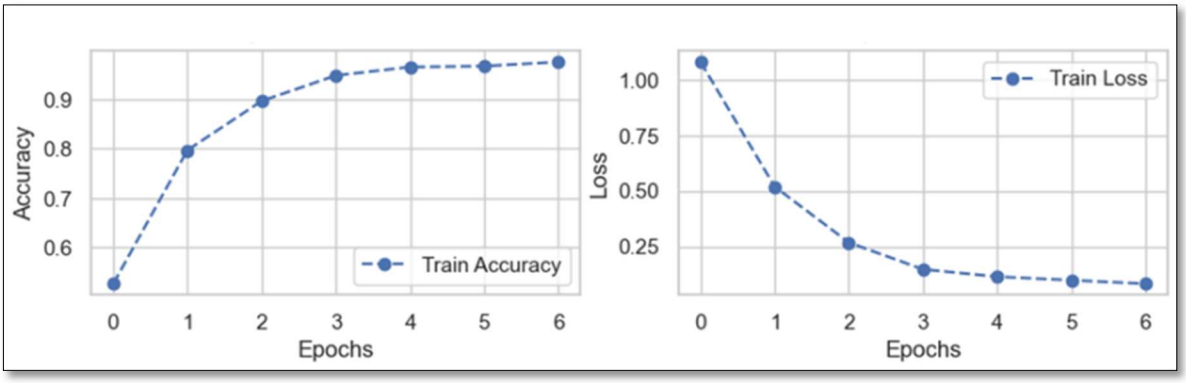

Figure 10: Training Accuracy and Loss.

In summary, CNN shows strong performance in terms of both training accuracy and training loss. The training accuracy improves quickly in the first few epochs and reaches a high value, suggesting that the model is learning effectively. The training loss also decreases rapidly, indicating that the model reduces errors as it learns. Moreover, the model seems to converge after about 3-4 epochs, as both accuracy and loss stabilize. This suggests that additional training may not yield significant performance improvements and could lead to overfitting if continued for too many more epochs.

Table (3) compares the proposed model for leukemia classification with other related works.

Table 3: Comparison with related works.

Authors	Leukemia type	Classification model	Accuracy
A. Rehman et al. [17]	ALL	CNN	97.78%
S. Anwar et al. [18]	ALL	CNN	99.5%
M. Claro et al. [19]	ALL, AML	CNN	97.18%
S. Rezayi et al. [20]	ALL	ResNet-50, VGG-16, and CNN	81.63%, 84.62%, and 82.10%
M. Zhou et al. [21]	ALL	CNN	89%
A. Hosseini et al. [22]	B-ALL	CNN	98.6%
P. M. Shafi et al. [23]	ALL	CNN	85%
Proposed work	4 types (AML, ALL, CML, CLL)	CNN	98%

3.2. Mobile Application Results

The proposed mobile application for leukemia detection provides a rapid, accessible, and cost-effective method for identifying leukemia in blood smear images. Figure (11) elucidates the detection screen of this app. By using

a Convolutional Neural Network (CNN) model trained on a dataset of labeled images, the app can classify blood samples in real-time as either leukemia-positive (specifying the type: ALL, AML, CLL, or CML) or leukemia-negative. The app features a user-friendly interface that enables healthcare providers to easily upload images, which are processed and classified by the integrated DL model. Performance tests show that the app is highly reliable and has high classification accuracy, making it a valuable tool for early detection. This current version highlights the potential of mobile technology to enhance clinical diagnostic workflows.

The test dataset was utilized to evaluate the model and determine the efficiency of the proposed application. The model accurately classified items by testing all the images in the test dataset. After this evaluation, the mobile app demonstrated outstanding results. The model was tested with a series of images, and the study data was correctly identified. The efficiency assessment findings were based on 300 random samples to analyze the model's potential weaknesses; real-time testing shows that this app's accuracy is 97%.

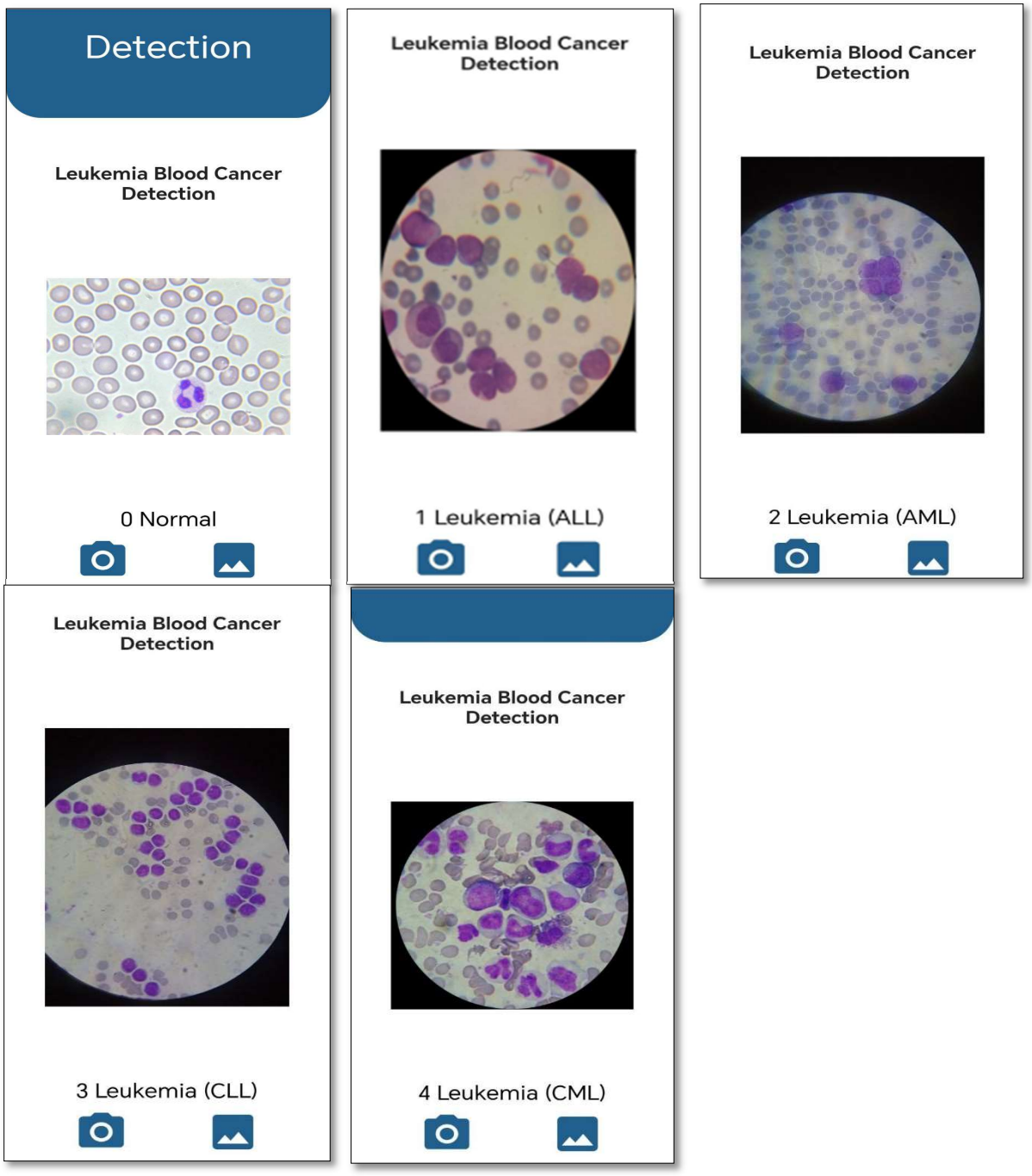

Figure 11: The detection screen of the developed mobile app.

4. Conclusions

This paper demonstrates the transformative potential of combining smartphone-based microscopy with deep learning techniques for automated leukemia diagnosis. By leveraging Convolutional Neural Networks (CNNs) built with Keras, the mobile application provides a portable, low-cost, and efficient diagnostic solution for resource-limited settings.

The proposed mobile application bridges the gap between high-performance diagnostic tools and accessibility, enabling real-time detection without the need for cloud-based services or traditional laboratory infrastructure. It significantly improves the feasibility of early leukemia detection in underserved regions, providing an alternative to the manual examination of blood smears.

This study paves the way for mobile health innovations, highlighting the importance of integrating AI-powered diagnostics with portable microscopy to revolutionize healthcare accessibility and efficiency, particularly in low-resource settings.

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