

# Development of a Mobile-Based Convolution Neural Network Framework for Rapid Malaria Detection from Blood Smears

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## ORIGINAL RESEARCH

**Abstract-** Malaria, a vector-borne parasitic disease caused by Plasmodium parasites, continues to pose a substantial threat to global public health. Despite considerable progress in its control and treatment, malaria remains a significant cause of morbidity and mortality, particularly in resource-limited regions. The ability to diagnose malaria infections accurately and swiftly is paramount for effective disease management. Traditional methods of malaria diagnosis, relying on microscopic examination of blood smears, have proven to be accurate but are often hindered by limitations in infrastructure and expertise, particularly in remote and underserved areas. This research focuses on the development of a mobile-based Convolution Neural Network (CNN) framework for rapid malaria parasite detection from blood smear images using Android mobile phones. Blood smear images provide a reasonable and clinically relevant representation of malaria disease which makes it a preferred choice for malaria detection from mobile phones. By leveraging smartphone technology and state-of-the-art deep learning algorithms, this pioneering endeavour aims to normalize malaria diagnostics, providing healthcare workers with a powerful tool for early detection and treatment, irrespective of their location or access to advanced laboratory facilities. The dataset for infected and non-infected parasites was acquired online from Kaggle. The dataset was preprocessed and partitioned into training, testing, and validation sets. The developed model was converted to tflite and was used for the mobile application. A validation accuracy of 94.88% was obtained from the validation set while an accuracy of 95.81% was obtained from the testing set.

**Keywords-** Android smartphones, blood smear images, deep learning, malaria parasite detection, mobile-based framework.

## 1 INTRODUCTION

In the vast landscape of global health challenges, few adversaries have endured as resiliently as malaria. This formidable mosquito-borne parasitic disease continues to afflict millions of individuals each year, predominantly in tropical and subtropical countries in Asia and Africa (Sifat & Islam, 2020). Malaria, caused by Plasmodium parasites transmitted through the bite of infected female Anopheles mosquitoes, manifests in various forms, with Plasmodium falciparum and Plasmodium vivax being the most common culprits (Paul & Bania, 2021). Its symptoms, ranging from fever and fatigue to severe organ damage and death, have cemented its reputation as a formidable public health concern (Poosatchi et al., 2018). In 2021, approximately half of the global population faced a malaria risk, with an estimated 247 million malaria cases reported worldwide, resulting in around 619,000 malaria-related deaths during that year (WHO, 2023).

Early and accurate detection of malaria is a major challenge, as prompt treatment significantly improves outcomes and prevents its spread (Landier et al., 2016). The gold standard for malaria diagnosis has long been the microscopic examination of blood smears, allowing trained healthcare professionals to detect and identify the parasites' presence and species (Mbanefo & Kumar, 2020).

While highly accurate, this method is hampered by several critical limitations. Access to well-equipped laboratories and skilled personnel is often limited in remote and underserved regions, leading to delayed or inadequate diagnosis and treatment (Raj et al., 2021). Furthermore, the process is time-consuming and labour-intensive, rendering it ill-suited for large-scale, rapid screening required for effective disease control (Shah et al., 2020). The advent of mobile technology and deep learning algorithms has ushered in a new era of healthcare innovation. In recent years, smartphones have become nearly ubiquitous, even in resource-constrained areas, offering powerful tools for data collection, analysis, and communication. These devices are now poised to transform the landscape of disease diagnosis, bridging the gap between limited healthcare infrastructure and the pressing need for timely intervention.

The paper tends to harness the capabilities of Android mobile phones and deep learning algorithms to create a mobile-based framework for rapid and accurate detection of malaria parasite from blood smear images by empowering healthcare workers to access early detection and treatment capabilities regardless of their location or the availability of advanced laboratory resources.

## 2 RELATED WORKS

The landscape of malaria diagnosis has witnessed remarkable developments in recent years, with a multitude of related works contributing to the field's advancement. These endeavours span various technologies, methodologies, and strategies aimed at enhancing the accuracy, accessibility, and efficiency of malaria parasite detection. This section provides an overview of key related works, showcasing the diversity

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Section B- ELECTRICAL/COMPUTER ENGINEERING & RELATED SCIENCES

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of approaches, from deep learning-based automation to innovative mobile applications and cost-effective point-of-care solutions. Together, these studies and innovations collectively address the pressing need for more effective tools in the fight against malaria.

Olugboja & Wang (2017) developed an efficient and accurate system to detect malaria parasites in stained blood smear images. The research tends to overcome the limitations associated with conventional microscopy methods, such as their time-consuming nature and issues related to reproducibility. Additionally, the study seeks to address the challenge of limited accessibility to alternative diagnostic methods in developing countries. From the study, a dataset of  $300 \times 300$  images from the Centre for Disease Control (CDC) website was gathered and an algorithm was designed to handle the inherent variability within the dataset effectively. The authors adopted the watershed segmentation technique to distinguish between plasmodium-infected and non-infected erythrocytes, extracting pertinent features for further analysis. The research explored six distinct machine learning techniques for classification which are linear SVM, quadratic SVM, fine Gaussian SVM, Cosine KNN, Boosted tree and subspace KNN. Notably, the Fine Gaussian Support Vector Machine (SVM) stood out, achieving an impressive True Positive Rate of 99.8% in the accurate detection of plasmodium-infected erythrocytes, but produced a rather low accuracy of 82.0%.

In the study conducted by Sifat & Islam (2020), an entirely automated system is proposed to identify malaria parasites and their developmental stages in blood smear images. The research employed a U-Net model to accurately segment red blood cells (RBCs) within the images, achieving a commendable segmentation accuracy of 97.67% and a specificity of 92.05%. To identify infected RBCs, a convolutional neural network (CNN) model was employed, attained a detection accuracy of 100% along with a specificity of 95%. Furthermore, the Visual Geometry Group - 16 (VGG16) model is harnessed to recognize various malaria parasite types and stages, yielding an average accuracy of 95.55% and specificity of 94.75% for species classification, and 96.25% accuracy and 94.82% specificity for ring stage identification. However, the research only considered infected cells.

Yang et al. (2020) developed a smartphone application for automated parasite detection in thick blood smears using deep learning methods. An image set acquired from 150 patients, including 1819 thick smear images was used. The performance of the customized CNN model is evaluated using five-fold cross-evaluation, achieving a sensitivity of 93% and a specificity of 90%. However, a limited dataset of 150 patients was used which may not comprehend the real pattern.

Poojary and Sumithra (2022) researched the use of diverse deep-learning models to detect malaria infections. CNN, transfer learning, Convolution Neural Network – K-Nearest Neighbour (CNN-KNN), and vision transformer networks, are the methods used. To gauge the performance of these models, a set of evaluation metrics, such as accuracy, precision, recall, and F1 score, is employed. Furthermore, the study incorporates data

augmentation techniques, encompassing procedures such as standardization, brightness adjustment, rotation, flip, and shifts, to enhance the accuracy of the deep learning models. Significantly, the CNN model, particularly when combined with transfer learning using the pre-trained VGG-19 model, surpasses the CNN-KNN model, achieving an impressive accuracy rate of 96%. Notably, the performance of the CNN-KNN model is observed to decline when applied to large datasets, owing to the substantial memory and processing demands associated with the K-Nearest Neighbour (KNN) classifier.

Mahmood et al. (2023) introduced a deep CNN to identify malaria-infected cells. This model is based on a three-layered CNN architecture, supplemented by a two-layered dense neural network. The unique strength of this model lies in its capacity to capture both subtle and prominent features within the input data, harnessing the full spectrum of information available. The training process involved the model's exposure to the dataset for 20 epochs, where it learns to recognize distinct patterns associated with malaria cells. During evaluation, the binary cross-entropy loss function and the accuracy metric are employed to assess the model's performance. Remarkably, the proposed model demonstrated impressive results, achieving an accuracy of 96%. Notably, it consistently maintained a low loss value, staying below 0.2 for both the training and validation datasets.

Kundu & Anguraj (2023) focus on assessing the effectiveness of various machine-learning approaches to detect Plasmodium parasites in blood smear images acquired through conventional microscopy. This investigation delved into the realm of machine learning, comparing the performance of different algorithms in this critical diagnostic task. The study's findings revealed that among the array of machine learning algorithms examined, Random Forest emerged as the top performer with an accuracy of 96.6%, demonstrating superior accuracy in Plasmodium parasite detection. Following closely behind was the AdaBoost algorithm with an accuracy of 96.1%.

In Kuzhaloli et al. (2023), the discussion revolved around computer-assisted methods to detect malaria parasites in blood smear images. The research placed a strong emphasis on leveraging image analysis and machine learning techniques to enhance malaria diagnosis by quantifying parasitemia levels in blood slides. The approach outlined in the research involved several key steps, including data acquisition, image preprocessing, red blood cell segmentation, feature extraction and selection, and image classification. Notably, CNN models were employed for the recognition of Plasmodium parasites and erythrocytes within the images. The trained CNN and VGG-19 models showcased impressive detection capabilities, with VGG-19 achieving an impressive 96% accuracy and CNN attaining 94% accuracy. These high levels of accuracy underscore the potential of advanced machine learning techniques in significantly improving the accuracy and efficiency of malaria diagnosis.

Previous works in the field of malaria detection systems

have made notable strides through machine learning, deep learning, and automation-assisted microscopy or personal computer systems, achieving impressive accuracy rates. Few of the previous research that used mobile applications had limited datasets and showed impressive accuracy. However, this high accuracy might not necessarily reflect the model's ability to understand and recognize meaningful patterns. Instead, it could be a result of the model essentially memorizing specific examples from the small dataset without truly comprehending the broader patterns it should recognize. Different from existing works, this paper offers a self-contained mobile-based deep learning framework, eliminating the need for a microscope and personal computer systems for malaria parasite detection tools, thus increasing accuracy and accessibility for rapid malaria diagnosis.

### 3 MATERIALS AND METHODS

In this paper, a mobile application for the detection of malaria parasites in blood samples was developed. The developed application helps to differentiate between uninfected blood samples and those containing parasites. A dataset consisting of images of malaria-infected and normal images of blood cells was collected online and preprocessed. The preprocessed image was partitioned into training, testing and validation. The model was developed with Python 3.7 from Google Colab and the trained model was saved as tflite which was used for mobile development. The model was trained using the CNN algorithm and was tested on the developed mobile application. The mobile application was developed with Flutter using Dart programming language. A detailed block diagram of the proposed CNN model is shown in Fig. 1.

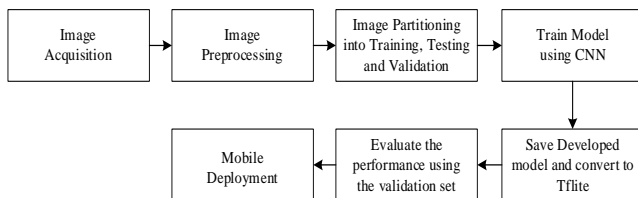
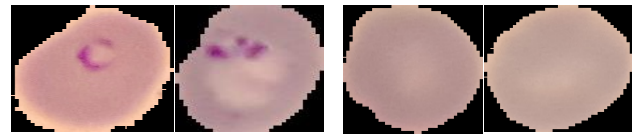


Fig. 1: Detailed visualization of the proposed mobile-based CNN model framework

#### 3.1 DATASET

The dataset used for the research is acquired from Kaggle from the official National Institutes of Health (NIH) Website: <https://ceb.nlm.nih.gov/repositories/malaria-datasets/>. The dataset consists of two folders, namely infected and uninfected with a total of 27,558 thin blood smear cell images with 13,779 infected and 13,779 uninfected cell images. The dataset consists of coloured images. A total of 8000 dataset is used while 70%, 20% and 10% of the dataset is deployed for training, testing and validation making a total of 5600, 1600 and 800 samples, respectively. The training set was used to train the model by identifying the patterns, the validation set was used to validate the model's accuracy and the testing set was used to test the model to evaluate the result before deploying on a mobile application. The sample of the dataset showing the infected and uninfected blood samples is shown in Fig. 2.



Infected sample Uninfected sample  
Fig. 2: Dataset samples showing infected and uninfected blood.

#### 3.2 IMAGE PREPROCESSING

Image preprocessing helps to prepare the blood smear images for accurate analysis by the deep learning model. In this work, the image analysis that was performed included image resizing, rescaling and augmentation. Image resizing ensures uniform dimensions, reduces computational complexity, and enhances the compatibility of deep learning models, making them suitable for efficient and consistent analysis. The images were resized into 150 × 150. Rescaling pixel values to the range of [0, 1] standardises the images, making them suitable for consistent analysis. Augmentation techniques performed are shear and zoom transformations and horizontal flips. This helps to introduce diversity into the dataset, helping the model generalise effectively and further augment dataset diversity.

#### 3.3 IMAGE PARTITIONING

The dataset was partitioned into training, testing and validation sets. As stated in Subsection 3.1, the training set consists of 70% of the dataset, the testing set is 20% and the validation set takes 10% giving a total of 5600 samples for training, 1600 for testing and 800 for validation. This partitioning served several crucial purposes, including training the model, evaluating its performance, fine-tuning hyperparameters, and assessing its robustness. It ensured that the model could effectively learn from the training data, provide accurate predictions on unseen testing data, and generalize well to real-world scenarios.

#### 3.4 MODEL TRAINING AND VALIDATION

CNN was used to train the model due to its exceptional ability to extract relevant features from images, their robustness to variations, and their capability to model complex relationships within the data. The training set was used and during each (epoch) training iteration, a batch of images is inputted to the network. The number of epochs specified was 50 and early stopping criteria were activated to prevent overfitting and reduce training time and as a result, the training stopped at epoch 11. Table 1 shows the training parameters exploited in this work.

Table 1. Training Parameters

Parameters	Value
Image size	150 × 150
Learning rate	0.001
Epochs	50
Batch size	32
Optimizer	Adam
Loss	Categorical_crossentropy
Metric	Accuracy
Trainable parameter	3,373,410
Training dataset size	5600
Validation dataset size	800

CNN consists of convolutional layers, pooling layers, and fully connected layers, which work collaboratively to automatically extract hierarchical features from the images. In this research, there is a combination of 2D Convolution layers, 2D Max Pooling layers, Dropout layer, followed by a single Flatten and some Dense layers. The pooling layer performs feature extraction. The training and validation accuracy during the training stage is shown in Fig. 3. It was observed from the graph that the training stopped at epoch 11.

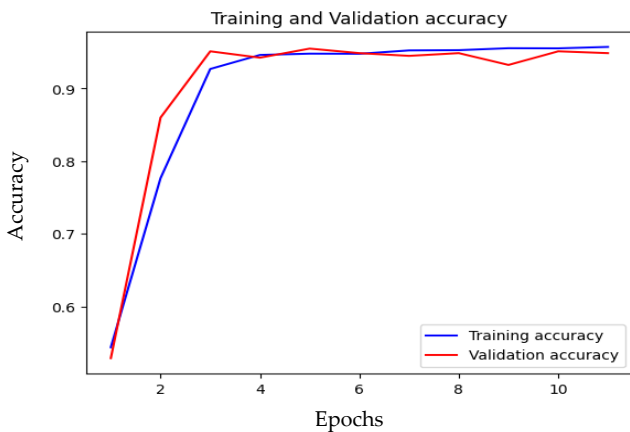


Fig. 3: Plot of the training and validation accuracy

The validation set is employed to monitor the model’s performance and prevent overfitting. If the model performs well on the validation set, it is expected to perform well on the mobile application using unseen data. Training the CNN involves iteratively fine-tuning its parameters to minimize prediction errors, ultimately enabling the model to accurately detect malaria parasites in blood smear images when deployed on a mobile device. The trained model was saved and converted to tflite which was later deployed to the mobile phone.

#### 4 RESULTS AND DISCUSSION

The results were tested using the testing set before deploying to a mobile application. A total of 1600 samples were used to test the performance of the developed application.

##### 4.1 EVALUATION RESULT

The developed system was validated on the testing images which consist of 1600 samples of infected and uninfected blood smears. The testing samples were used to test the performance of the developed model. From the results, a total of 1533 samples were correctly classified while sixty-seven (67) were incorrectly classified giving an accuracy of 95.81% which outperformed Olugboja & Wang (2017) with an accuracy of 82.0%.

Table 2 shows the precision, recall and F1-score from the testing set. It was observed that the infected sample has a precision, recall and F1-score of 0.95, 0.96 and 0.96, respectively. On the other hand, uninfected achieves a precision, recall and F1-score of 0.96, 0.95, and 0.96, respectively. This indicates that the model demonstrated strong and balanced performance in both detecting malaria-positive and malaria-negative cases, with high precision, recall, and F1-score values, making it a

promising tool for malaria diagnosis with reliable accuracy in both classes.

Table 2. Precision, recall and F1-support of the model.

Disease	Precision	Recall	F1-score
Infected	0.95	0.96	0.96
Uninfected	0.96	0.95	0.96

##### 4.2 CONFUSION MATRIX OF THE MODEL

The confusion matrix of the developed malaria disease detection system is shown in Fig. 4. It is observed that for the infected class, 771 samples are correctly classified while 29 samples are incorrectly classified as uninfected. For the uninfected class, 762 samples are correctly classified while 38 samples are incorrectly classified as infected. The results revealed that the model’s performance in classifying infected and uninfected cases for malaria detection is highly promising. It accurately classified 771 samples as infected out of the total infected cases, indicating its success in detecting malaria parasites. However, there were 29 instances where the model incorrectly classified infected samples as uninfected, representing missed detections (false negatives).

For the uninfected class, the model correctly identified 762 samples as uninfected out of the total uninfected cases, demonstrating its accuracy in identifying cases without malaria parasites. Nevertheless, there were 38 cases where the model incorrectly classified uninfected samples as infected, resulting in false positives.

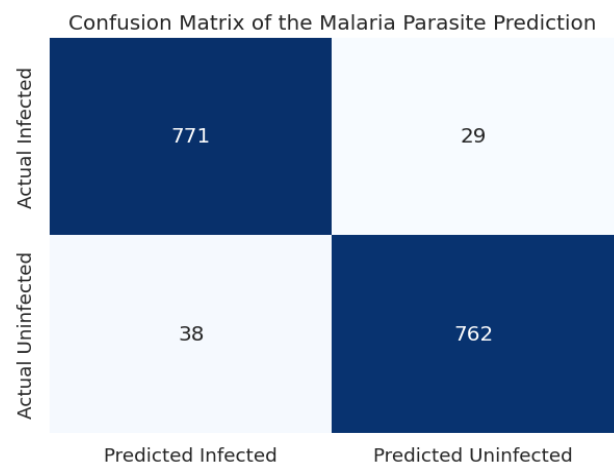


Fig. 4: Confusion matrix of the developed malaria disease detection system

##### 4.3 GUI OF THE MOBILE APPLICATION

The Graphical User Interface (GUI) of the developed mobile application is shown in Fig. 5. The mobile application was developed in Android Studio using Flutter and Dart programming. Flutter can be used for both Android and iOS applications. A sample image of the blood smear image was uploaded to the mobile app, compared with the saved model, and classified into infected or not infected.

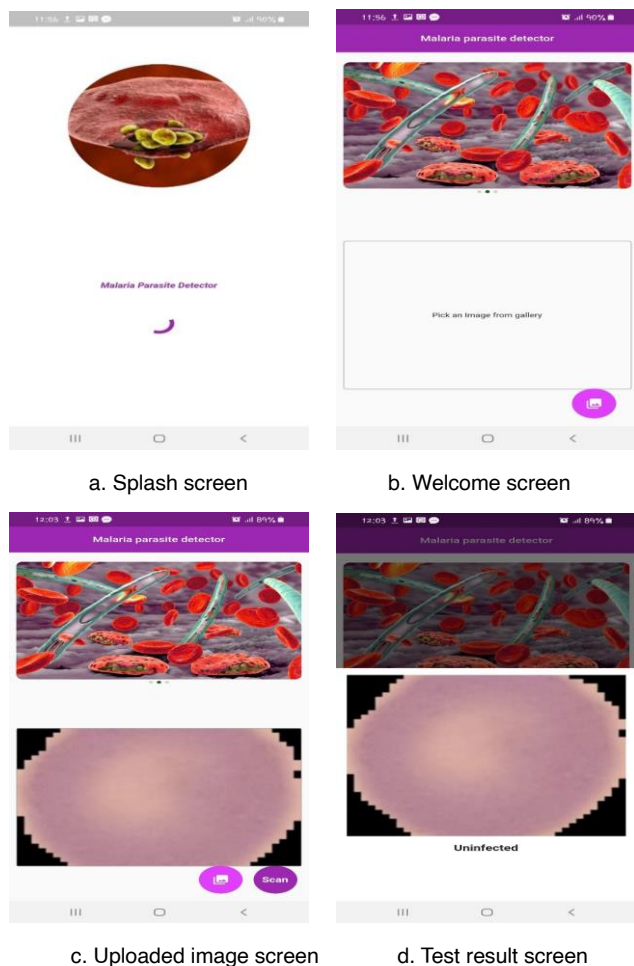


Fig. 5: Sample GUI of the mobile application

## 5 CONCLUSION

This study has demonstrated an automated malaria detection mobile application based on CNN to classify blood smears into either infected or uninfected. Sequential method was used to train the model and the trained model was later converted into tflite which was deployed in the developed mobile application. With the malaria parasite detection mobile application, this technology has the potential to greatly improve the speed and efficiency of malaria diagnosis, particularly in low-resource settings. With this mobile application in the hands of healthcare workers and patients, the outbreak and spread of malaria can be detected early and treated promptly, preventing the disease from becoming uncontrollable and threatening public health.

This technology has the potential to benefit millions of people living in malaria-endemic areas and ultimately contribute to the global efforts to control and eliminate the disease. This research could also explore ways to address the limitations of the technology, such as the quality of the mobile phone images and the ability of the models to detect low-level parasitemia. Future research in mobile-based malaria detection could focus on expanding and diversifying datasets, enhancing model architectures, optimising for low-resource settings, and enabling real-time diagnosis.

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