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**Multi-Class Classification Approach for Malaria
Detection in Blood Smear Images Using
EfficientNetB7**

Tahirah Mohi-ud-din, Sneha Haralayya, Prema T. Akkasaligar, Vivekanad Ramdurg, Vishwanath Ankalgi

Department of Computer Science and Engineering, KLE Tech, University's Dr.

MSSCET, Belgaum-590008, Karnataka, India.

premaakkasaligar.mss@kletech.ac.in



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Dr. M. S. Sheshgiri Campus, Belagavi

Abstract

Malaria remains a critical global health issue, with 263 million cases and 597,000 deaths reported in 2024, primarily in sub-Saharan Africa. Traditional diagnostic methods, such as Giemsa-stained blood smears, are labor-intensive, error-prone, and reliant on expert microscopists, making them unsuitable for high-burden regions. While machine learning models emerge as promising solutions, they mostly focus on binary classification, identifying infected versus healthy samples without addressing clinically relevant details. The proposed model introduces a multiclass classification framework using EfficientNetB7, a state-of-the-art CNN architecture that distinguishes healthy red blood cells (NEG), infected cells in the trophozoite stage (Trophozoite), and white blood cells (WBC). This model provides detailed diagnostic insights, enabling early detection of infection stages, reducing diagnostic ambiguities, and improving patient outcomes, especially in resource-constrained areas. Trained on the Lacuna Malaria Detection dataset with stratified sampling and data augmentation techniques such as rotation, zooming, and flipping, the model optimizes performance through categorical cross-entropy loss, the Adam optimizer, dropout regularization, learning rate scheduling, and early stopping. Achieving a validation accuracy of 76.1% and precision, recall, and F1-scores of approximately 75%, the framework demonstrates superior diagnostic capabilities compared to binary models by identifying infection stages and minimizing errors from morphological similarities. Scalable for mobile and cloud platforms, the model addresses diagnostic gaps in endemic regions. Future improvements include detecting additional parasite species and lifecycle stages, optimizing deployment on resource-limited hardware, and integrating explainability features for greater clinical adoption, establishing a transformative shift in malaria diagnostics from binary to multiclass classification.

Index Terms—Malaria detection, EfficientNetB7, multiclass classification, blood smear images, data augmentation, automated diagnosis.

I Introduction

Malaria remains a significant global health issue with the greatest burden in sub-Saharan Africa, which contributes to 94% of all malaria cases and 95% of malaria deaths. The World Health Organization (WHO) [1] reports malaria cases increased from 244 million in 2021 to 263 million in 2023 with more than 600,000 fatalities. Malaria disproportionately affects the vulnerable population of under-five children, accounting for 78% of malaria-related deaths in the region. Nigeria, the democratic republic of the Congo, Uganda, and Mozambique are some

of the countries whose statistics make it necessary to provide innovative and scalable diagnostic solutions for this disease.

Traditional methods of malaria detection include the manual examination of blood smear images under a microscope, which is labor-intensive, time-consuming, and prone to human error [2,3]. Such drawbacks delay the accurate diagnosis and prompt treatment, especially in resource-poor settings. With the massive amount of medical data, the need for automated, efficient, and accurate diagnostic systems has become critical. This is important because early and accurate diagnosis of malaria improve patient outcomes and reduce the disease burden, which makes this a research or innovation gap area [4].

Advances in machine learning (ML) and deep learning (DL) have shown promise in overcoming the limitations of traditional diagnostic methods. However, most existing automated solutions are limited to binary classification, distinguishing only between infected and non-infected samples. Although these models are effective to some extent, they lack the granularity required to identify specific cell categories, thus limiting their utility in real-world clinical scenarios [5].

The proposed model proposes a multiclass classification framework to address the limitations of existing binary classification models by categorizing blood smear images into three distinct classes. NEG (Negative) identifies healthy samples, minimizing false positives and avoiding unnecessary treatments. Trophozoite detects the active life cycle stage of the malaria parasite, facilitating early intervention and improving patient outcomes. (WBC) White Blood Cells separates white blood cells from malaria parasites, hence increasing the reliability of diagnosis, ensuring the quality of blood smears, and giving useful information about the immune response.

The framework utilizes a fine-tuned CNN based EfficientNetB7, a state-of-the-art model with superior scalability and feature extraction capabilities [6]. Compound scaling in EfficientNetB7 balances depth, width, and resolution, making it ideal for complex image classification tasks. The Lacuna malaria detection dataset is trained with class imbalance corrected by applying stratified sampling and data augmentation by rotation, zooming, and flipping. These measures increased the generalization of the model with an accuracy of 76.1%.

Although several of these techniques have been well developed, drawbacks such as overfitting and hardware dependency or limited generalizability across heterogeneous populations remain as significant challenges for further progress. The proposed regularized multiclass model is

hence a significant development in automated malaria diagnostics, particularly scalable and an effective solution that can be useful in resource constrained settings.

The paper is organized as follows. Section II provides a brief review of the literature survey on the recent works. Section III is the problem statement, background and provides the proposed methodology. Section IV discusses the implementation details along with results and discussions. Finally, the paper concludes in Section V.

II Literature Survey

The detection of malaria seen remarkable progress with the application of advanced imaging techniques and deep learning methodologies. In this literature survey, various approaches proposed by researchers for automated detection, classification, and diagnosis of malaria using computational methods are explored.

Alonso-Ramirez *et. al.*, [2] develops CNN-LSTM and CNN BiLSTM models for classifying parasitized (infected) and uninfected malaria-infected red blood cells that attain an accuracy of 99.89% without preprocessing. The CNN-biLSTM shows more accuracy than CNN-LSTM, but its processing time is slower because of the complexity of BiLSTM model. Precision without preprocessing, though high, is accompanied by the less desirable slow processing nature of the BiLSTM model. Alqudah *et. al.*, [3] proposed a deep learning method for identifying malaria parasites in blood smear images. Its efficiency is enhanced by a customized CNN architecture combined with transfer learning, reducing computing time; however, it has limited effectiveness due to variations in the preparation of blood smears besides being dependent on a curated dataset. Md. Khayrul Bashar *et. al.*, [4] developed a customized CNN to classify different stages of malaria parasites from thin blood smear images. Three layers of convolution with proportional weighting presented the improved classification accuracy of the model. The dataset used was imbalanced, the approach shows potential for real-world diagnostic applications.

Chakradeo *et. al.*, [5] presented a deep learning approach using a VGG-based model to detect malaria from thick blood smear images. The model with shallow architecture reduced the efficiency of computational resources and training time. However, distinguishing between infected and contaminated cells is challenging, indicating that improvement in making

suspicious region identification dawn. The model shows potential real world diagnostic applications.

Maria Delgado-Ortet *et. al.*, [6] developed a deep learning system for malaria detection in blood smear images by RBC segmentation, cropping, and classification using CNNs. The system helps to speed up diagnosis in clinical labs, but faces misclassification problems of platelets and white blood cells.

Anand Koirala *et.al.*, [7] also designed a deep learning framework named YOLO-mp specifically based on YOLO, targeting to detect the count of malaria pathogens in an image of a thick blood smear by providing mAP scores as high as 94.07% (@IoU=0.5). Standard YOLOv4 matches with that performance. The computation costs for YOLO-mp3l and YOLO-mp-4l are also reasonable in terms of 21.8 BFLOPs and 24.477 with model size below 25.4 MB. The models handle key concerns with real-time malaria detection in resource-constrained environments and clearly indicate the requirement for greater consistency and standardization in dataset labelling. The YOLO-mp models are a contribution to both accuracy and resources in terms of public application diagnostic systems in the hinterland.

Leila Malihi *et. al.*, [8] proposed a VGG-based deep learning architecture to detect malaria from thin blood smear images. The shallow architecture is efficient in terms of computational resources and training time, still faces challenges like distinguishing infected cells from contaminated cells. Overall, the model is quite efficient and well-balanced and suitable for real-world diagnostic applications.

Wan Azani Mustafa *et. al.*, [9] explored computational methods for detecting malaria, focusing on K-means clustering, neural networks and morphological techniques. They emphasized that automated methods are more efficient than traditional microscopy and discovered accuracy rates that go as high as 99.7% using neural networks, though it resolves problems of imbalanced datasets or differences in slide preparation to enhance the diagnostic systems.

Doni Setyawan *et. al.*, [10] reviewed CNN-based methods for malaria classification with a high accuracy. The study highlights the effectiveness of CNN techniques, the use of private datasets for direct comparisons between models cannot be made. Future researches focuses on public datasets and models that can differentiate among species as well as life stages.

Uzun Ozsahin *et. al.*, [11] proposed a deep learning framework using a custom CNN based method for automated malaria detection from both thin and thick blood smears. The model

performs better with thick smears, achieving accuracy of 96.97% compared to 96.03% for thin smears and results like precision and F1 score also support thick smears. Thick smear happened to be more effective to have accurate malaria detection, and thus it has underlined its importance in rapid diagnosis in malaria-endemic regions.

III Proposed Methodology

The proposed methodology focuses on deep learning techniques to automate and enhance malaria detection with greater accuracy. In this framework, a multiclass classification approach has been used. Blood smear images are classified into three different classes: NEG, Trophozoite, and WBC (White Blood Cells). The NEG class identifies healthy samples that minimize false positives and unnecessary treatments. The Trophozoite class detects the active life cycle stage of the malaria parasite, enabling timely intervention and improved patient outcomes. Lastly, the WBC class differentiates white blood cells from malaria parasites, improving diagnostic reliability and providing insights into blood smear quality and immune responses.

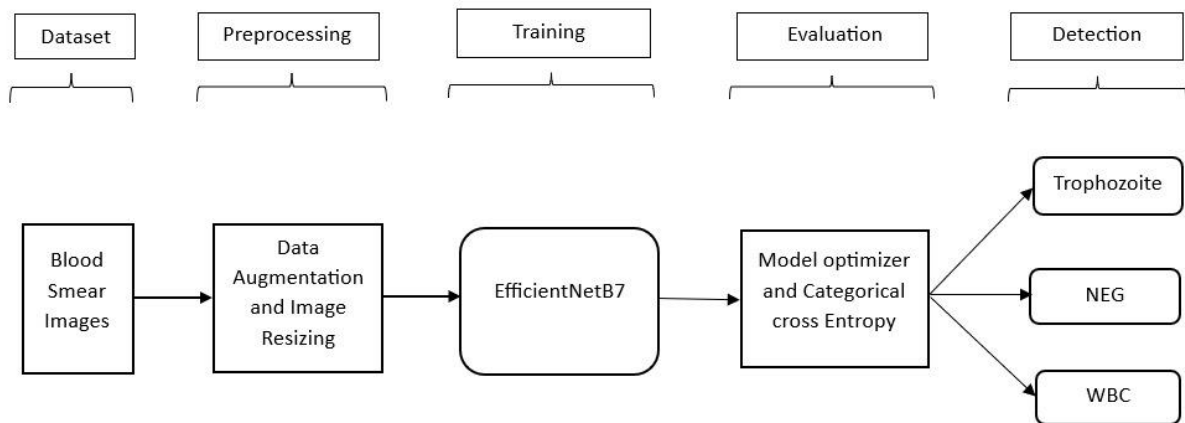


Fig.1 Proposed Methodology

To account for the intrinsic class imbalance within the Lacuna malaria detection dataset, a stratified sampling method is applied to maintain a balanced training set with a near equal ratio of each class. Other data augmentation methods such as rotation, zooming, flipping along the horizontal axis, and shifting along channels are applied, further increasing variability within the datasets to improve model generalization during the training phase.

The proposed system is primarily built on the top of an efficient fine-tuned CNN architecture based on EfficientNetB7. Known for its better scalability and feature extraction capabilities, the EfficientNetB7 architecture is used in the proposed system for handling complex classification tasks involving high-resolution images. The size of the input image is 600×600. Pixels to exploit the full potential of the architecture. Pre-trained ImageNet weights are used to initialize the model for transfer learning, and the output layer is modified to support three-class classification with a softmax activation function.

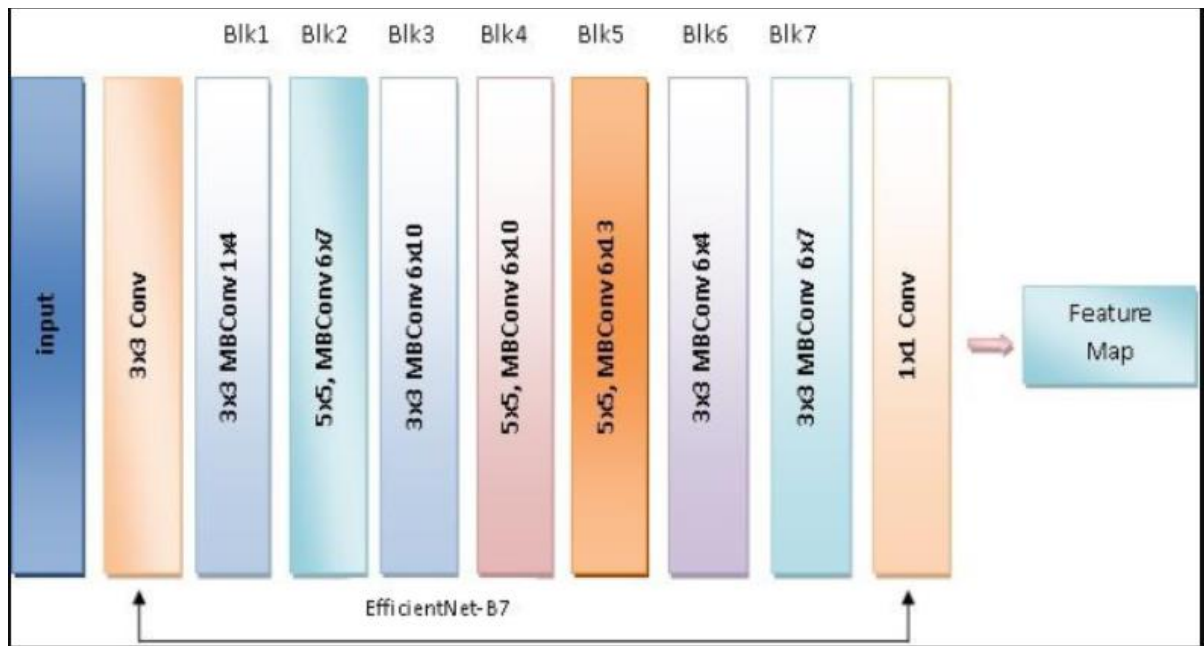


Fig.2 EfficientNetB7 Architecture for Malaria Classification. Source: ResearchGate, 2025

The training process is optimized using the Adam optimizer with a learning rate of 0.0001, balancing fast convergence with high accuracy. Categorical cross-entropy is selected as the loss function to handle the multiclass classification task effectively. To ensure the model's performance, validation accuracy and loss are monitored across epochs, with measures in place to prevent overfitting.

This framework shows several advantages over the traditional approaches. It provides granular and clinically actionable outputs, significantly enhances diagnostic accuracy, and addresses dataset limitations through robust preprocessing techniques. The methodology offers a promising solution for resource-constrained healthcare environments, facilitating timely and accurate diagnosis.

IV Results And Discussion

The experiments are carried out on a machine with the following specs: Processor: Intel(R) Core (TM) i3-7020U CPU @ 2.30GHz 2.30 GHz, RAM: 4 GB, Operating System: Windows 10 Pro. The model is implemented using the Python programming language. TensorFlow and Keras serve as the primary libraries for designing and the CNN model training. NumPy for numerical computations and Pandas are employed for data manipulation and analysis. Matplotlib/seaborn for visualizing the training progress and results.

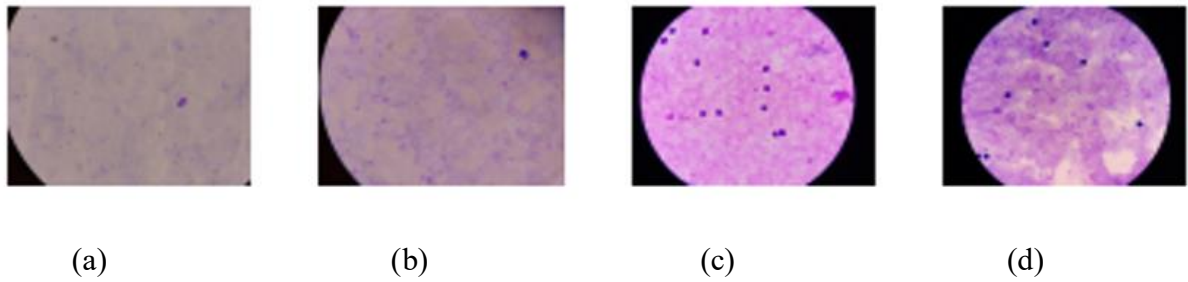


Fig.3 Representing the Dataset Images

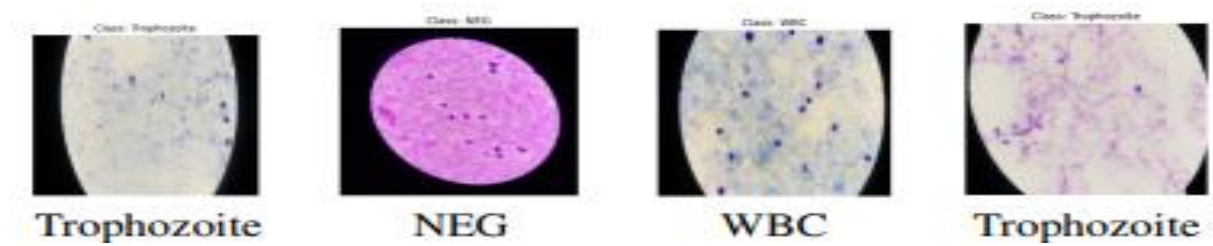


Fig.4 Representing the Images Classified by Model

The dataset contains 3,625 images, resized to 600×600 pixels to match with the input in EfficientNetB7. The sample images are shown in Fig.3. The proposed method utilizes an EfficientNetB7 architecture for automated classification of malaria blood smear images into three classes: Trophozoite, NEG, and WBC. EfficientNetB7 is a state-of-the-art convolutional neural network that uses compound scaling to optimize depth, width, and resolution to achieve better feature extraction with fewer parameters than traditional CNNs.

The model makes use of pre-trained weights for transfer learning with fine-tuning on the malaria dataset. ReLU activation is used along with dropout layers for preventing overfitting and softmax function for the multiclass classification problem. The model is trained with the Adam optimizer and categorical cross-entropy loss over 50 epochs with a batch size of 32 to

achieve a validation accuracy of 76.14%. Evaluation metrics further validate its performance, with a precision of 74.8%, recall of 75.2%, and an F1-score of 75.0%. These results underscore EfficientNetB7's efficacy in accurately classifying malaria-related blood smear images, demonstrating its potential for enhancing diagnostic reliability in clinical settings.

Model Performance Parameters

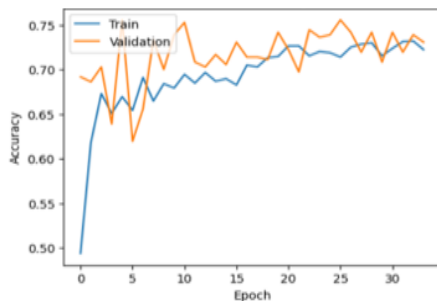


Fig.5 Model Accuracy

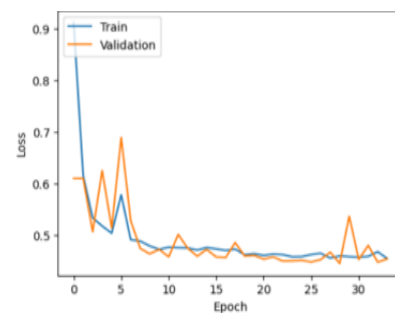


Fig.6 Model Loss

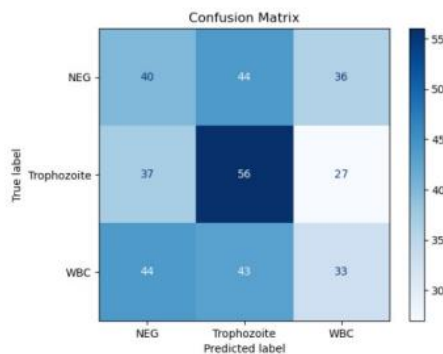


Fig.7 Confusion Matrix

Fig.5 shows the training accuracy of the model based on EfficientNetB7. From fig.5 it is seen that increasing the number of epochs leads to an increase in accuracy, thereby showing that the model learns progressively with time. The test accuracy of the model based on EfficientNetB7 is 76.14%. Fig.6 represents the categorical cross-entropy loss function. From the graph, it is observed that the loss decreases progressively with an increase in epochs, indicating effective optimization and minimal overfitting. The confusion matrix in Fig.7 sums up the model

performance on the three classes: NEG, Trophozoite, and WBC. Every cell reports the number of predictions made in terms of specific combinations of actual and the predicted labels. For instance, the model has correctly labelled 40 samples of Trophozoite, and 33 samples of WBC (diagonal values). Misclassification is also observed, like 44 samples classified as NEG when they are actually Trophozoite. This matrix highlights the model's strength in detecting Trophozoite but reveals room for improvement in distinguishing NEG and WBC due to significant misclassification.

V Conclusion

Diagnosis of malaria by visual examination of Giemsa-stained blood smear images is a laborious and error-prone process, especially when visually similar components, such as WBCs and parasitic RBCs, complicate identification. Most of the machine learning solutions developed so far focus on binary classification, that is, infected samples versus uninfected ones, which severely limits their utility in diagnosis. The paper presents a multiclass classification framework based on EfficientNetB7 that categorizes blood smear images into WBC, NEG (uninfected RBC), and Trophozoite (parasitic RBC). It applies advanced preprocessing techniques like stratified sampling and data augmentation to tackle class imbalance issues and enhance generalization. The proposed system is able to resolve diagnostic ambiguities and offers a more clinically relevant solution than binary classification methods. EfficientNetB7's architecture allows for efficient feature extraction and scalability, providing a robust foundation for automated malaria detection. Future work will focus on increasing dataset diversity, validating the model in real-world clinical environments, and optimizing it for mobile and resource-constrained deployments, enhancing its practical applicability and clinical trust.

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