



e-ISSN: 2319-8753 | p-ISSN: 2347-6710

IJRSET

International Journal of Innovative Research in
SCIENCE | ENGINEERING | TECHNOLOGY



INTERNATIONAL JOURNAL OF INNOVATIVE RESEARCH

IN SCIENCE | ENGINEERING | TECHNOLOGY

Volume 13, Issue 3, March 2024

ISSN INTERNATIONAL
STANDARD
SERIAL
NUMBER
INDIA

Impact Factor: 8.423

Malaria Detection Using Deep Learning

CHemavathy¹, M Monika², S K Raahid³, S Razaulla⁴, D Narendra⁵, M Prem Kumar⁶

¹Assistant Professor, Department of CSE, AITS, Tirupati, India

^{2, 3, 4, 5, 6}Student, Department of CSE, Annamacharya Institute of Technology and Sciences, Tirupati, India

ABSTRACT: Malaria remains a global health challenge, necessitating advanced diagnostic tools for timely and accurate identification of infected individuals. This research investigates the application of the VGG-19 convolutional neural network (CNN) architecture for malaria detection through the analysis of blood smear images. VGG-19, known for its deep and intricate layers, offers a compelling solution for image classification tasks due to its capacity to capture complex features. The study employs transfer learning by fine-tuning the pre-trained VGG-19 model on a diverse dataset comprising malaria-infected and uninfected blood smear images. The dataset is meticulously curated, encompassing a range of malaria parasite species and stages. Images are labelled as infected or uninfected, forming the foundation for supervised model training and evaluation. The dataset is partitioned into training, validation, and testing sets to ensure robust model development and unbiased performance assessment. During training, the VGG-19 CNN adapts its internal parameters through backpropagation, learning to distinguish between malaria-infected and uninfected blood cells. Regular monitoring using the validation set helps prevent overfitting, ensuring the model's generalization capability to new and unseen data. Results indicate the VGG-19-based malaria detection system's effectiveness, demonstrating high accuracy and robust performance.

I. INTRODUCTION

Malaria, sometimes called the "King of Diseases", is caused by protozoan parasites of the genus Plasmodium. The gold standard test for malaria is the hundred-year-old method of preparing a blood smear on a glass slide, staining it, and examining it under a microscope to look for the parasite genus plasmodium. While several rapid diagnostic tests are also currently available, they still have shortcomings compared to microscopical analysis [2]. Early diagnosis and prompt effective treatment are required to avoid anemia, organ failure, and malaria-associated deaths. Microscopic examination of stained blood smears remains the gold standard technique of detecting malaria both in the laboratory and field [3]. Given the limitations in these settings, this update focuses on testing options that are widely available in middle- to high-income settings and provides guidance on how these different methods may be employed for routine patient care [4]. In 2016, approximately 3.2 billion people, which is nearly half of the population of the world, were at risk of contracting malaria. According to the latest World Health Organization (WHO) estimates, there were 216 million cases of malaria in 2016 and 445 000 deaths. Sub-Saharan Africa continues to carry a disproportionately high share of the global malaria burden, with 90% of malaria cases and 90% of malaria deaths, mostly in young children. The WHO recommends diagnostic confirmation of Plasmodium falciparum in all individuals with suspected malaria before treatment with antimalarial drugs. This parasitological confirmation can be done by microscopy or malaria rapid diagnostic tests (RDTs). The sale of 221 million malaria RDTs across the globe in 2016 is a proof of their utility [5]. The conventional approach for the diagnosis of malaria is microscopy that requires interpretation of the results by a skilled technician. Using this approach, a sample of blood is drawn from a patient and smeared on a glass slide stained with Giemsa. This blood sample can be either thin or thick. A thick smear is more efficient for parasite detection with an 11 times higher sensitivity rate [6].

II. RECENT WORKS

Malaria is a worldwide life-threatening disease. According to the 2018 World Health Organization (WHO) malaria report [1], about 219 million malaria cases were detected worldwide in 2017, causing approximately 435,000 deaths. Microscopy examination of stained thick and thin blood smears is the gold standard for malaria diagnosis [2], [3]. Microscopy examination is low-cost and is widely available, but is time-consuming. Moreover, the effectiveness of microscopy diagnosis depends on the parasitologists' expertise [4]. It is very common for parasitologists to work in resource-limited environments, with no rigorous system in place that can ensure the maintenance of their skills or/and diagnostic quality. This leads to incorrect diagnostic results and thus inappropriate treatment [4]. For example, false positive diagnostic results lead to unnecessary use of anti-malaria drugs and suffering from their side effects such as abdominal pain, nausea, etc., whereas false negative diagnosis leads to unnecessary use of antibiotics, second

consultation, and potential progression of more severe malaria [5]. In recent years, several approaches have been proposed for image processing and analysis on both thin and thick blood smears, aiming at automated detection of parasites. Reviews of the published literature may be found in [7]. In the following paragraph, we provide a brief overview of the approaches for malaria detection in thick blood smears. Feature-based approaches involve feature extraction and classification based on machine learning techniques. Elter et al. [8] extract 174 features from pre-detected plasmodia candidates and apply a Support Vector Machine (SVM) classifier to the feature set for parasite identification. The authors report a sensitivity of 97% for 256 images on patch level. Purnama et al. [9] extract features from histograms of RGB channel, H channel from HSV space, and H channel from HIS space, and then use Genetic Programming to identify parasite type and stage.

III.MALARIA DETECTION IMAGES DATASET

The dataset containing infected and uninfected images of malaria is a collection of digital images of blood smears captured under a microscope. Each image in the dataset represents a microscopic view of red blood cells, and the dataset is meticulously labeled to indicate whether the blood cells are infected with malaria parasites (infected) or free from the parasites (uninfected).

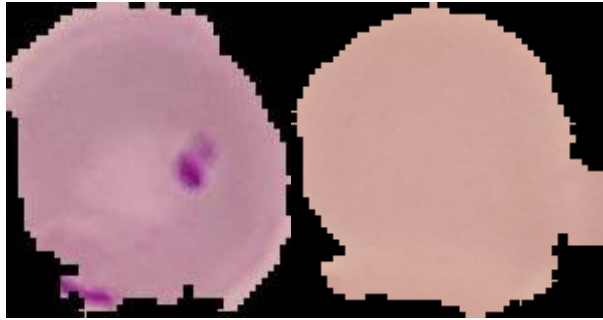


FIGURE 1. Malaria Infected and Uninfected image

3.1.1VGG19 Model

In the context of malaria detection, the VGG19 model serves as a powerful convolutional neural network (CNN) architecture to automate the identification of malaria-infected cells in blood smear images. Leveraging its 19-layer structure with small 3x3 convolutional filters, VGG19 can effectively capture intricate spatial features associated with malaria parasites. The model is trained on a dataset consisting of both infected and uninfected blood smear images, learning to discern subtle patterns indicative of infection. The deep architecture allows the network to generalize well to diverse cases and enhances its ability to differentiate between healthy and malaria-infected cells. The final softmax layer provides probability scores for each class, facilitating accurate classification. $A^{[L]} = \text{Softmax}$

3.1.2 ResNet50 (Residual Networks):

ResNet introduces residual learning, which helps in training deeper neural networks more effectively. The skip connections enable the model to learn residual functions, making it easier to optimize and train.

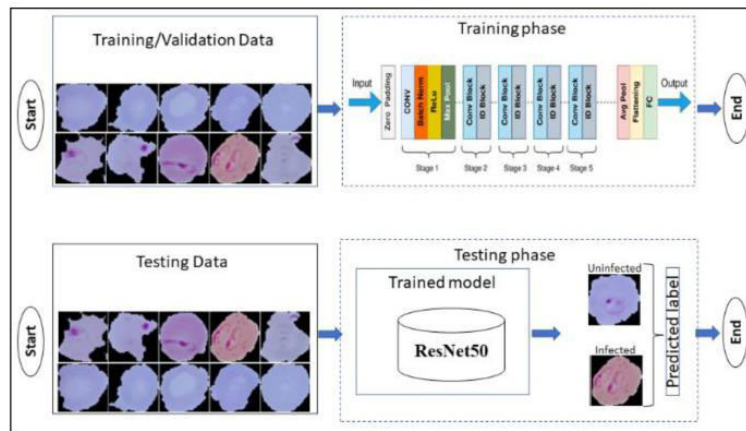


FIGURE 2. Block diagram of MobileNetV2 model.

3.1.3 MobileNetV2:

MobileNet is designed for mobile and embedded vision applications. It uses depthwise separable convolutions to reduce computational complexity while maintaining performance. This makes it suitable for resource-constrained environments.

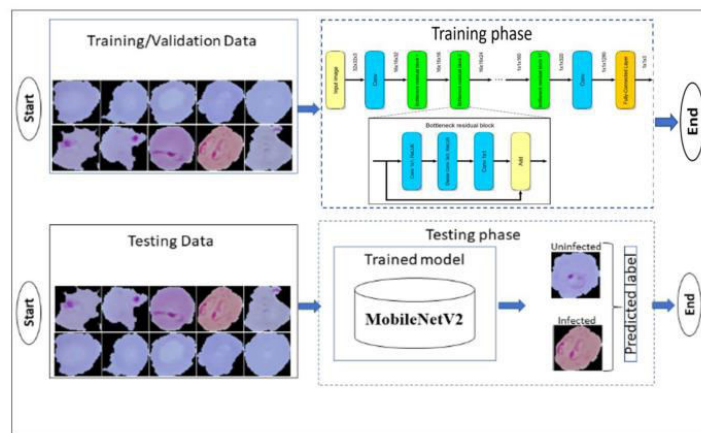


FIGURE 3. Block diagram of MobileNetV2 model.

3.2 Proposed Methodology Architecture

The proposed approach presented in Figure 2. This flow diagram depicts the comprehensive process of malaria detection utilizing a VGG19 model. It commences with the user providing a blood smear image as input, which undergoes meticulous image preprocessing to ensure compatibility with the subsequent convolutional neural network (CNN) model. The VGG19 model, renowned for its capacity to capture intricate features in images, is then employed for classification, discerning whether the blood smear indicates the presence of malaria parasites. The model's output, a probability distribution across potential classes, is subjected to a malaria detection logic component, which interprets the results based on predefined thresholds or criteria. The final classification, indicative of the presence or absence of malaria infection, is communicated back to the user as the detection result. This seamless and automated process underscores the potential of deep learning in enhancing the efficiency and accuracy of malaria diagnosis through sophisticated image analysis.

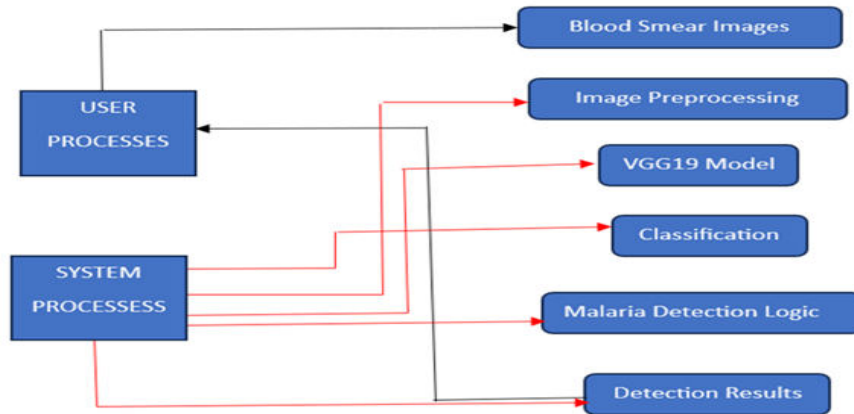


FIGURE4: Proposed approach based on Vgg19 model

3.3 Evaluation Parameter

The evaluation of a malaria detection model employing the VGG19 architecture involves assessing key metrics such as accuracy and loss for both the training and testing datasets. Training accuracy signifies the proportion of correctly classified instances within the training set, demonstrating the model's ability to learn from the provided data. Conversely, testing accuracy evaluates the model's generalization to new, unseen data, emphasizing the importance of avoiding overfitting. Training and testing loss metrics provide a quantitative measure of the model's learning performance, with lower values indicating better alignment between predicted and actual outcomes. Monitoring these metrics throughout the training process ensures that the VGG19-based malaria detection model achieves a balance between accuracy and generalization, thereby enhancing its reliability and efficacy in identifying malaria-infected blood smear images.

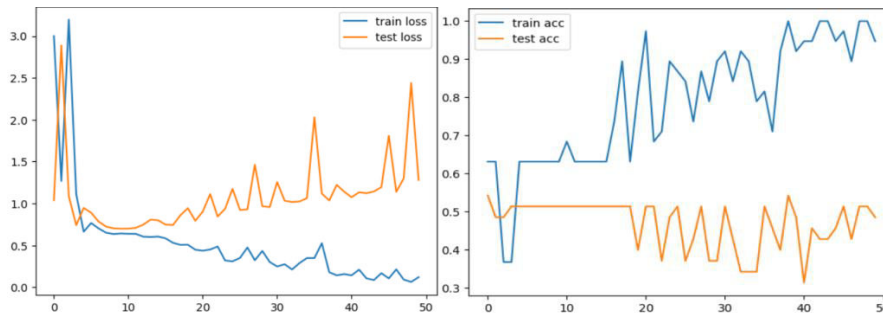


FIGURE5: Experimental results of the VGG19 model

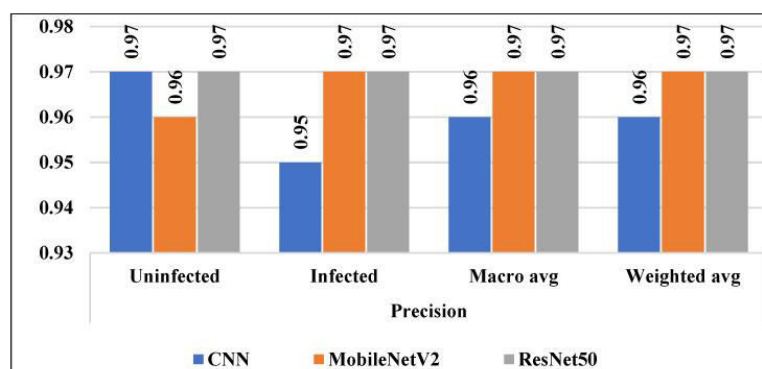


FIGURE6: Precision of all considered models.

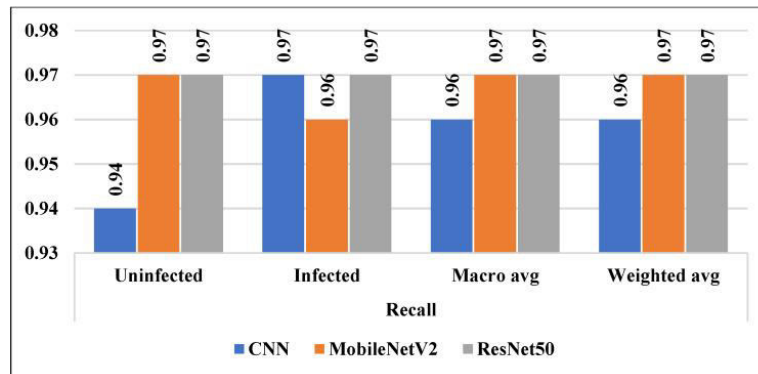


FIGURE7:Recall of all considered models.

IV.CONCLUSIONS

In this paper, we compare three deep learning techniques like CNN, MobileNetV2, and ResNet50 in terms of detecting malaria disease. The developed models were compared, and conclusions were reached based on which was superior. It can be concluded that environmental elements are crucial in facilitating malaria's presence and transmission. Among all of the models, VGG19 outperformed and provided better results for the detection of malaria disease. Statistical measurements such as Accuracy, loss, precision, recall, etc. were calculated to validate the results. It can be concluded that this research work presents the state of art results when compared to the existing research. The work can be extended to explore the other deep learning techniques with different preprocessing techniques for image processing for better results.

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