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Fusion of Inception Net and Efficient Net for Enhanced Malaria Parasite Detection

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Abstract

Accurately identifying malaria remains one of the most challenging medical endeavors globally. We present a hybrid neural network approach that integrates Inception V3 with EfficientNetB0 to address this challenge. Our hybrid architecture effectively distinguishes between parasitized and uninfected blood smear images, achieving a commendable accuracy of 94.27% through these two cutting-edge models' advanced feature extraction capabilities. This strategy yields a lightweight and highly accurate diagnostic tool by leveraging Inception's multi-scale feature extraction and EfficientNet's optimized performance. The innovative architecture of our model illustrates the potential for integrating complementary neural networks to enhance the accuracy of medical imaging diagnoses through the amalgamation of pooled data from both networks. This fusion-based technique may enhance malaria screening, which is particularly beneficial for healthcare practitioners in resource-limited regions requiring rapid and precise diagnoses.

Keywords: Multi-Model Ensemble; Healthcare AI; Convolutional Neural Network; Parasite Classification; Malaria Detection;

Introduction

Malaria, a life-threatening Plasmodium parasite disease, is a central communal health issue in stifling and subtropical locations where mosquitoes thrive. Spread by female mosquitoes, malaria is preventable and treatable. Effective diagnostic and management procedures are needed since it can cause severe complications and death if not treated immediately.

In 2015, the Plasmodium parasite was responsible for 405,000 fatalities, as reported by the World Health Organization (WHO) [1]. Malaria screening, which involves examining blood samples under a microscope to perceive sick red blood cells, may be tedious and time-consuming [2]. Studies indicate that the predominant incidence of malaria is found in Africa (85%), Eastern Mediterranean (71%), and South East Asia (71%). A large number of these cases need to be evaluated by pathologists. The high volume of cases may undermine the effectiveness of malaria screenings. The intricacy and density of blood smears, comprising numerous aggregated cells, render them only sometimes comprehensible. The alteration in cellular structure in a blood smear due to malaria contamination complicates the differentiation between healthy and infected samples. A swifter, more precise, and cost-effective diagnosis of infection can be attained by analyzing blood smear images from several perspectives. This has developed into a momentous social and financial health issue due to variable lighting conditions, an increased need for inspections, and a deficiency of pathologists. Digital cameras and high-resolution mobile phones have enabled the efficient creation of blood smear slides, thereby mitigating this issue and lessening the workload of pathologists [3].

Enhanced image quality and clarity generally yield more precise and reliable analysis. A comprehensive image data analysis can reveal various complex facets of biological activity. Portable cell phones are ubiquitous and transformative, serving as a cost-effective and efficient method for swiftly collecting image datasets. However, digital cameras often yield superior results to cell phones for capturing images of blood smear slides. Manual interpretation may be difficult due to low-resolution photos and the large patient volume, while disease detection utilizing conventional machine learning methods could provide challenges [4]. Accelerated preprocessing deep learning algorithms can autonomously assess essential characteristics for malaria diagnosis and grading. This will resolve these concerns [5].

The potential for developing automated malaria diagnosis systems through machine learning techniques has recently captivated the attention of scholars [6, 7]. Historically, researchers have utilized supervised learning techniques such as SVMs, NB classifiers, and NNs to detect infections with an accuracy ranging from 83.5% to 85% [6, 8]. However, constructing a discriminant feature vector with little redundancy is essential, as these algorithms are susceptible to the feature extraction methodology [9]. Researchers developed a malaria detection system using the CNN EfficientNet-B0 method based on red blood cell images from the National Institutes of Health (NIH) dataset. The model underwent preprocessing, class weighting, training, validation, and testing. In testing, the EfficientNet-B0 model demonstrated high accuracy, precision, specificity, sensitivity, and F-1 scores [10].

Complete diagnosis automation is unachievable because the process depends on human specialists for feature vector extraction, even though effective feature extraction can enhance detection accuracy. The ultimate goal of deep learning algorithms is an automated malaria cell detection tool without human feature extraction.

In a hierarchical data structure, advanced learning algorithms may extract representations that are less vulnerable to scaling and transformations at elevated levels. Although deep convolutional neural networks are employed for malaria diagnosis in thick blood smears, pathologists continue to struggle with differentiating infected from non-infected samples in thick films, as the distinction is less pronounced compared to thin films derived from images of individual red blood cells cropped from entire slides [11]. Machine learning models perform well in fundamental classification tasks but encounter difficulties achieving appropriate outcomes with increasingly complex issues. In contrast, deep learning excels at managing complex tasks.

The sections of the document are as follows: The "Literature Review" compiles the findings from studies on malaria detection. The study techniques are comprehensively detailed in the "Materials and Methods" section. The "Results and Discussion" section presents the experimental analysis and findings. The "Conclusion" section summarizes the findings.

Existing Literature

The Plasmodium parasite causes malaria, a deadly disease if untreated. Malaria testing requires skilled personnel and time reviewing samples under a microscope. Effective malaria treatment requires computerized diagnosis. This study uses an inception-based capsule network to identify infected and uninfected cells in microscopic pictures, improving malaria parasite detection and emphasizing the need for better diagnostics [12]. Many methods have been proposed for malaria diagnosis. Rajaraman et al.[13] Research computer vision, image processing, and deep learning to keep up with the latest developments in autonomous malaria detection data detection. This field is dynamic, and the past decade has produced much data. An intriguing new product has emerged from the lab, and deep learning methods have made significant strides in the digital realm. Thus, many classification systems would need to be updated. Deep learning makes classification characteristics difficult, making most human-made features could be more effective.

Research [14] introduces a CNN deep-learning blood malaria detection algorithm. A gadget spreads and lights blood samples. The created metaphors are focused on consuming a mirror and lens. The guesstimate and CNN models determine the sample's infection status. Researchers [15] use infected and uninfected samples for malaria testing. The 1000-epoch model was 97.1% accurate. Parasite species identification using deep learning models is tested in Research 17. VGG19, ResNet50V2, EfficientNetB3, and others are used to test a massive dataset with six classes. Through parameter tuning, deep learning models achieve 99% classification accuracy.

Using a deep CNN model, Soner et al. [16] identified malaria in cellular images. ANN, RNN, and CNN models were trained to identify malaria using 27,558 photos. Because the pictures had different sizes, the writers standardized them. Three convolutional layers preceded the CNN model's max pooling, flattening, hidden, and output layers. Verifying the findings using a binary loss function took 20 iterations and 64-bit batches. The CNN-trained model has 95% test accuracy and takes 10 minutes to train. We tested model accuracy with fivefold cross-validation. Nineteen researchers used 27,558 cell pictures to identify malaria. The writers standardized photo hues. CNN's six convolutional layers have 8,16,32,64,128, and 256 filters. Various deep learning algorithms were compared to rapid CNN. Many attributes employed SVMs to determine image infection. The feature bag SVM and suggested model are 85% accurate [17].

Twenty used two neural networks to categorize cellular pictures as infected or not. The proposed method [18] started with RBC segmentation, then data cropping and masking, and finally binary classification. They correctly identified 93.75 percent of red blood cell pictures. Another study [19] Utilized a customized CNN, a static VGG-19 CNN, and a refined CNN—all trained on 27,558 single-cell images with tenfold cross-validation. Bare, static, and fine-tuned CNNs had 94%, 92%, and 96% testing accuracy, respectively. Zhao et al. [20] created an automated smartphone app that accurately identified malaria from red cell images using Object recognition, convolutional neural network architecture, and low-resource image upscaling. They divided the balanced dataset into healthy and sick photos with 96.5% accuracy. The study [21] used ResNet50 and VGG16 CNN models to detect malaria in red blood cell pictures. VGG16 outperformed ResNet50 with 96.15 percent accuracy, 94.82 percent sensitivity, and 96.16 percent F1 score on 2,652 positive and 2,648 adverse outcomes. Malaria prediction was 95.23 percent accurate with a deep CNN model trained on mobile cell pictures [22]. Three pooling, convolutional, and fully linked 'ReLU' and 'sigmoid' layers were used.

Researchers found malaria in ultra-high-quality blood pictures 91% of the time in 2025 using a deep learning system [23]. Negi et al. [24] detected malaria in 2021 using Kaggle cell-image preprocessing and augmentation. Resizing, cushioning, and horizontally rotating photos increased data variety. Their accuracy reached 95.7% after 15 epochs, with a 0.31 decline. Emrah [22] used a CNN model with 20 weighted layers for malaria detection. Train and analyze 27,558 thin blood cell pictures, and the CNN model was 95.28% accurate. A substantial medical dataset shows that deep learning can detect malaria.

Maqsood et al. [25] tested many deep-learning models to find the best malaria detection model. An improved CNN model beats deep learning. Bilateral filtering and image augmentation show red blood cell traits before model training. CNN was generalized to avoid overfitting via image augmentation. The proposed method diagnoses malaria from tiny blood smears with 96.82% accuracy. All experiments used the standard NIH malaria dataset. The authors introduced a reinforcement learning-based "data augmentation convolutional neural network" [26]. The suggested DACNN model was tested using the DAGCNN and CNN models. DACNN outperforms previous image processing and classification research. The balanced class dataset classified malaria patient blood sample photographs with 94.79% accuracy. Implementing the recommended approach on blood smear images helps identify malaria parasites.

Malaria, a severe illness transmitted by infected female mosquitoes, can be identified using EfficientNet, a deep learning-based framework. For complex jobs, EfficientNet surpasses conventional methods by effectively extracting both low- and high-level information from images of red blood cells. Experiments show that EfficientNet is 92.57% accurate in detecting malaria from these images, making it a practical solution for medical healthcare staff. This innovative approach demonstrates the potential of deep learning in detecting malaria [27].

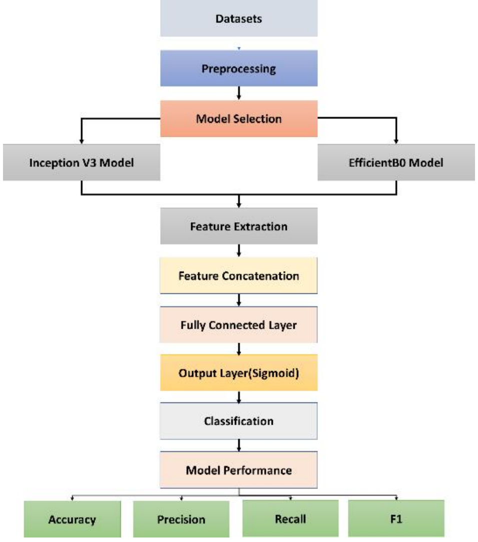
Hemachandran et al. [28] detected malaria using CNN, MobileNetV2, and ResNet50. Comparing created models revealed their superiority. Environmental factors affect malaria and transmission. ResNet50 identified malaria illnesses more accurately than other models. The National Institutes of Health website hosted 27,558 photos. This collection included 13,778 healthy and 13,780 parasitized cell pictures. The MobileNetV2 model outperformed its competitors in disease diagnosis with 97.06% accuracy.

It answers the limitations of traditional machine learning algorithms for automated malaria diagnosis. It presents a hybrid deep learning approach based on Inception V3 and EfficientNetB0 for feature extraction and achieves 94.27% accuracy on feature selection, outperforming the state-of-the-art. Unlike SVMs, Naive Bayes classifiers, and simple neural networks, this approach is superior in terms of accuracy, automation, and efficiency of malaria detection in resource-limited settings.

Research Design

The research design for this study includes data collection, preprocessing, model selection, and evaluation stages. Figure 1 outlines the end-to-end process flow:

Figure. 1 Proposed Model



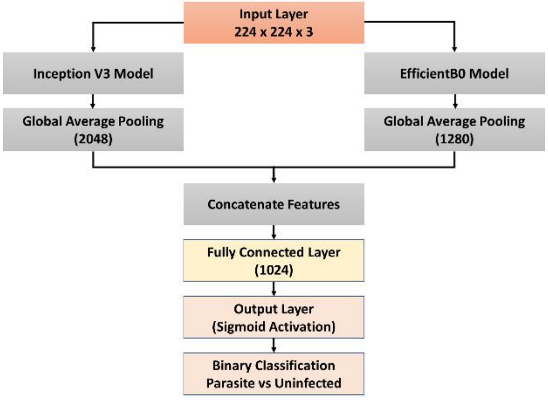
Data Acquisition and Preprocessing Techniques

Data for this study consists of blood smear images, classified into two categories: parasitized and uninfected. Images are preprocessed by resizing them to 224×224 pixels to ensure compatibility with the model architectures. Rotation, zoom, and flipping increase dataset diversity and prevent overfitting during training.

Model Architecture

A fusion-based neural network architecture was employed to maximize classification accuracy, combining Inception V3 [29] and EfficientNetB0 models as feature extractors. This architecture leverages the unique strengths of both models to capture a wide range of feature details and optimize performance. Figure 2 outlines the model architecture:

Figure 2. Proposed Model



To extract features from the image model, both Inception V3 and EfficientNetB0 have a Global Average Pooling layer feeding features into a branch and another branch that extracts features while shrinking the new feature dimensionality by feeding the features into a Global Average Pooling layer. Then, the outputs from both models are combined into one feature vector. For the classification part, first, we have concatenated the feature vector mentioned above and sent it to a Fully Connected Layer with one of 1,024 units and an Output Layer with a single sigmoid-activated neuron. The model architecture has an input layer with Image shape (224, 224, 3), and the Inception V3 gives feature maps of shape (5, 5, 2,048), yielding 21,802,784 parameters. The shape of the output of feature maps of EfficientNetB0 is (7, 7, 1,280) and 4,049,571 parameters. Once Global Average Pooling is applied to both models, feature maps have the shape of (2,048) for one case and (1,280) for the other. These are concatenated to form a feature vector with shape (3,328), which passes through a dense layer of size 1,024 (3,408,896 parameters) and into the output layer consisting of a single parameter (1,025). The final model has 29,262,276 parameters in total. With this architecture, feature patterns learned are compared to guide fast and automated decision-making, which can reveal essential insights for tasks such as disease management.

Model Training Procedure

The binary classification model was trained using a binary cross-entropy loss function and Adam optimizer. Training had ten epochs and 32 batches. We monitored and prevented overfitting with training and validation datasets.

Experimental Outcomes and Findings

Performance Evaluation Metrics

Accuracy, precision, recall, and F1-score metrics of the model classification were also evaluated. On 91 samples, 89% precision, 92% recall, and 91% F1 score were achieved in the model for the "Parasite" class. With 43 samples, the model's precision, recall, and f1 score were 91%, and 93%, respectively, for the "Uninfected" class. The accuracy of the model was 94.27%. The model exhibits balanced performance over classes, with the F1-scores in these high ranges showing that it can successfully classify 'Parasite' vs 'Uninfected' samples with strong classification results.

Training and Testing Loss Curves

We examined the loss curves for all ten epochs to assess model learning. Almost simultaneous falls in the training and validation loss curves indicate that the model learned well without overfitting. Aligned training and validation losses support the model's accuracy and robustness.

Figure 3. Training and Validation Accuracy Curves over 10 Epochs

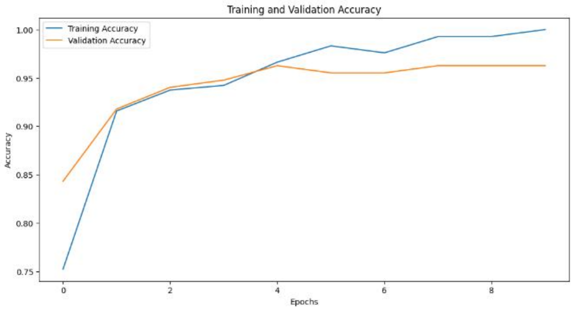
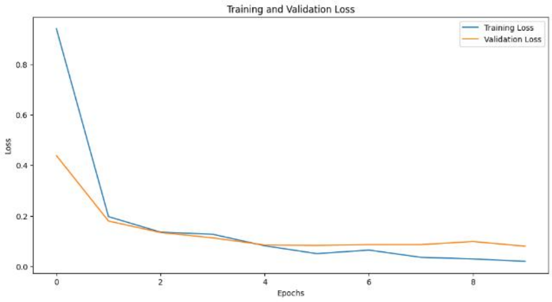


Figure 4. Training and Validation Loss Curves over 10 Epochs



Conclusion

This study employed a hybrid neural network model incorporating Inception V3 and EfficientNetB0 to identify malaria parasites in blood smear pictures. The model attained an accuracy of 94.27% in distinguishing between parasitized and uninfected samples by employing these two advanced approaches. The model's recall and precision indicate its efficacy. The method achieves a specificity of 89% for parasitized cells and 91% for uninfected cells, minimizing false positives and misdiagnoses. The model demonstrates a recall rate of 93% for uninfected cells and 92% for parasitized cells, effectively detecting malaria parasites. F1 scores of 91% and 94% signify balanced class performance and model reliability in real-world contexts, respectively. The model efficiently employs Inception V3 and EfficientNetB0 to capture characteristics across several scales. This combination enables the model to identify intricate cellular patterns and enhance malaria detection in resource-limited environments. Ultimately, our fusion-based neural network model illustrates the enhancement of medical diagnostics through deep learning architectures. Healthcare professionals in malaria-affected nations could gain from our AI-driven identification and treatment technologies owing to their precision, responsiveness, and specificity. This hybrid paradigm may facilitate AI-driven precision healthcare addressing future diagnostic issues.

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