

Research Article

Classification and Detection of Malaria from Parasitized and Uninfected Red Blood Cell Images Using Transfer Learning Based Ensemble Model

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Abstract

Malaria is a potentially lethal infectious disease caused by the Plasmodium parasite. The transmission of this disease to humans occurs via the bites of Anopheles mosquitoes that are infected with the pathogen. The impact of this disease on the health systems of vulnerable nations, especially in sub-Saharan Africa, is profound and catastrophic. Malaria infiltrates and reproduces within red blood cells, leading to their destruction and the release of harmful substances into the circulation. The parasite's capacity to adhere to and alter the surface of red blood cells might induce their adhesiveness, impeding blood circulation in crucial organs including the brain and spleen. Hence, it is crucial to employ effective methods for promptly identifying malaria in order to preserve patients' lives. The primary objective of this project is to establish a very effective model for the early detection of malaria. For the study trials, we utilized malaria pictures depicting both parasitized and uninfected red blood cells. We employed a transfer learning ensemble model, utilizing three distinct pretrained models: VGG16, Resnet-50, and Inception-V3. The models were trained with softmax activation, Adam optimizer with a learning rate of 0.002, categorical-crossentropy loss function, and accuracy matrices. Ultimately, in order to get an improved outcome, we combine all three models and obtain an accuracy rate of 98.6%. We evaluate our model using data that was not used throughout the training and validation procedure.

Keywords

Transfer Learning, Pre-trained Model, VGG, Resnet, Inception, Malaria Classification, Ensemble Model

1. Introduction

Malaria is a harmful disease caused by the Plasmodium parasite. The primary mode of transmission is through the bite of Anopheles mosquitoes that are infected [1]. The illness is attributed to many species of Plasmodium, including Plasmodium vivax and Plasmodium falciparum. These parasites infiltrate and proliferate within the erythrocytes of humans [2, 3]. Malaria continues to be a significant global health issue,

particularly in tropical and subtropical regions, impacting millions of people each year. Untreated individuals might have severe consequences and even fatality as a result of malaria. A delayed diagnosis of malaria might provide significant hazards, potentially resulting in the fatality of the individual. In 2019, the World Health Organisation (WHO) reported a total of 229 million cases of malaria infection, with

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Received: 23 April 2025; **Accepted:** 15 May 2025; **Published:** 21 July 2025



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409,000 fatalities attributed to the disease. The illness primarily affects children under the age of five, who constituted 67% of the total malaria fatalities in 2019. The African area bears the greatest burden, with 97% of the people afflicted by malaria [4]. The primary method for diagnosing malaria is by examination of microscopic slides [5]. However, an alternate option is the PCR test (polymerase chain reaction), which is more costly and mostly employed to confirm the species following the first microscopic diagnosis [6]. Malaria is frequently linked to poverty and is particularly prevalent in impoverished areas [7]. Consequently, the inspection of microscopic slides continues to be the most used approach for diagnosis. Yet, the effectiveness of this procedure is greatly dependent on the proficiency of the pathologists. The task of scrutinising several slides can be arduous, and the scarcity of proficient pathologists might result in erroneous diagnoses, particularly in healthcare facilities that are already overwhelmed. Computer-aided diagnosis (CADx) is a cost-effective and promising solution to address these problems. Therefore, we proposed a transfer learning approach to handle this problem. We proposed following work step to get a better result:

- 1) Getting a compatible dataset which can offer enough data also useful in handling.
- 2) Pre-process the data set for balancing both level data.
- 3) Find comfortable transfer learning model (VGG16, RESNET-50, INCEPTIONV3) and DNN classifier for better result.
- 4) Ensemble three transfer learning model to get best result from it.

We proposed an ensemble model having three well known transfer learning model to get better result instead of using single model.

2. Related Work

Recently, scientists have investigated the possibility of utilising automated image analysis methods to assist in the diagnosis of malaria. Several research have utilised machine learning algorithms and image processing techniques to differentiate between red blood cells that are infected with parasites and those that are not, based on their morphological features and staining patterns. This literary study emphasises the significance of ongoing research in this domain to create reliable and easily available diagnostic instruments that can assist healthcare professionals in rapidly and correctly detecting malaria infections. In their study, Vijayalakshmi et al. [1] utilised a transfer learning approach to identify the disease caused by the *Falciparum* malaria parasite. They applied a distinct Deep Neural Network (DNN) model for this purpose. The VGG-19 SVM model demonstrated superior performance compared to the CNN model. Nevertheless, the VGG-19 SVM project model yielded a performance score of 93.13%, which is deemed somewhat subpar. An improved feature extraction technique utilising histogram-based texture

characteristics was employed to identify the malaria parasite using picture data acquired from the Parasitology department at Gadjah Mada University. The obtained features were then entered into an Artificial Neural Network (ANN) [8] model. The training of the Artificial Neural Network (ANN) utilised the back-propagation technique, specifically designed for a multilayer perceptron [9]. The testing findings showed that the suggested Artificial Neural Network (ANN) attained an accuracy score of 87.8% with a calculation time of 0.55 seconds. Suraksha et al. [10] concentrated on categorising blood smear pictures of malaria parasites by utilising data from protozoal red blood cells acquired from the National Library of Medicine. In addition, a hybrid model [11] that combines a pre-trained VGG-19 and CNN is used. The VGG-19 CNN model has superior performance in comparison to other models, with an impressive accuracy rate of 96.02%. Nevertheless, there is a requirement for more improvements in performance. The work in question, documented in reference [12], introduced a segmentation approach specifically developed for the purpose of identifying microscopic pictures of the malaria parasite originating from the Eijkman Institute for Molecular Biology in Indonesia. The proposed technique earned a comprehensive metric score of 86%. Allassaf et al. [13] devised a distinctive approach known as IDTL-MPDC, which effectively identified malarial parasites in blood smear pictures. The DE algorithm attained a remarkable accuracy score of 95.86%, which has the potential for further enhancement. In their study, Masud et al. employed mobile clinical systems and deep learning techniques to accurately detect life-threatening cases of malaria in patients. The primary objective of their research was to employ a Convolutional Neural Network (CNN) architecture to efficiently and precisely detect malaria using a mobile application. The dataset utilised to assess their methodology is openly accessible on Kaggle and was acquired from Chittagong Medical College Hospital in Bangladesh, comprising of two hundred patient records. The proposed model attained a precision rate of 97.30% by evaluating the performance of a conventional CNN model utilising cyclical-SGD. Sriporn et al. [14] employed a Convolutional Neural Network (CNN) model to recognise and diagnose malaria using photographs of the condition. The study utilised a dataset acquired from the National Library of Medicine, comprising 151 patients with infections and 50 persons without infections.

3. Data

This work employed a benchmark dataset [15] comprising of pictures of red blood cells infected and uninfected with malaria parasites. The provided photos relate to each respective class. The collection has a total of 27,601 photos depicting cases of malaria. The dataset has been thoroughly equalised to allow empirical research.

4. Methodology

4.1. Data Preprocessing

We have a big dataset with almost 27k images which are in different sizes. We resize all the images according to our transfer learning model's required input size. For example, VGG16 expects an input image of 224x224 pixels. We also rescale all the images. We separate 100 images from both infected and uninfected level data for testing purposes. The rest of the data is split into 80% and 20% for training and validation cause. we used basic augmentation (Flip, Rotation) in training data.

4.2. Model Architecture

Transfer learning is a technique in which a neural network model is initially trained on a similar task, utilizing the model's weights and knowledge acquired from a vast dataset like ImageNet. This approach is versatile, enabling the direct utilization of pre-trained models as a preprocessing step for

feature extraction, and their integration into completely novel models. Our suggested approach utilizes three renowned models: VGG16, Resnet50, and Inception-V3. We import these models individually as base models, setting the include-top argument to False. The Imagenet weights are initialized with pre-trained weights that were learned on the ImageNet dataset. Additionally, the trainable property is set to False. The obtained output is sent into the Global Average Pooling technique, which is then followed by a basic Deep Neural Network (DNN) layer that serves as the classifier. We obtained our output layer by applying the Softmax activation function to our final dense layer. We compile models with Adam optimizer with a learning rate of .002, loss function categorical-crossentropy, accuracy metric is also specified to evaluate the model's performance during training and evaluation. We implemented identical procedures for each model and observed the outcome across 100 epochs. In order to obtain our ultimate intended outcome, we employ an ensemble of three distinct models and gather the desired result. Figure 1 illustrates the entirety of our workflow.

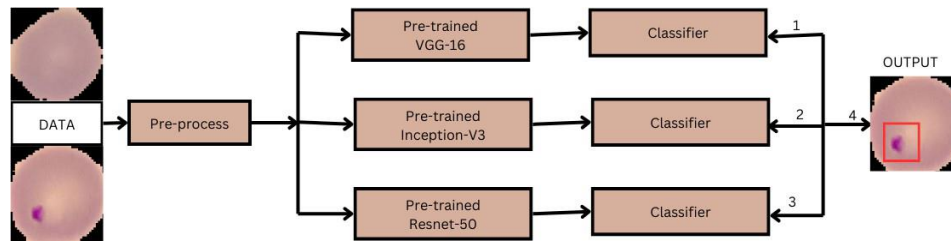


Figure 1. Proposed work flow.

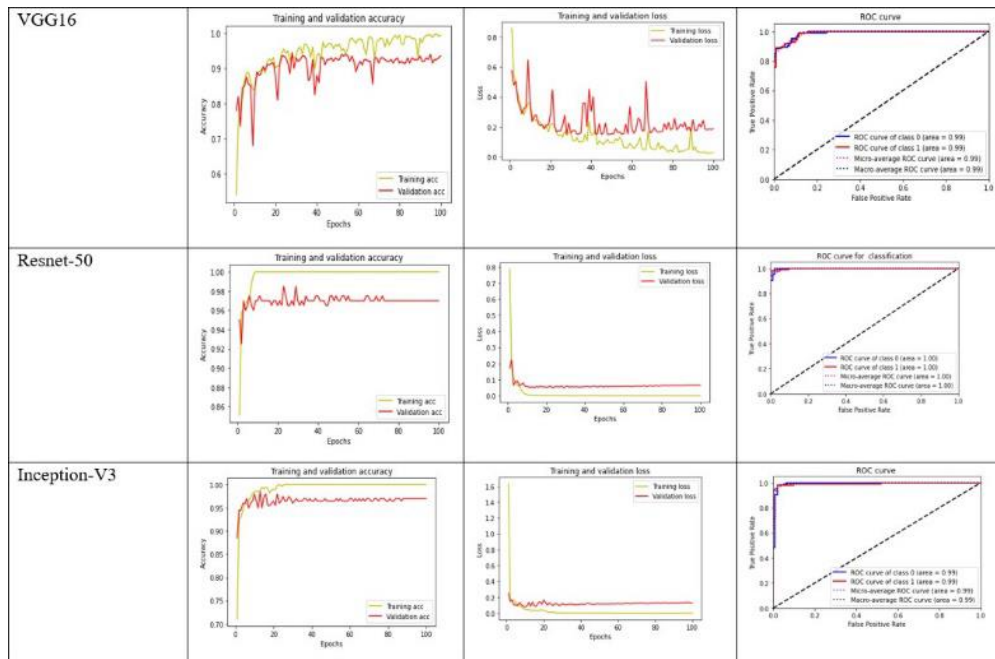


Figure 2. Train and Validation Accuracy, Loss and ROC curve.

4.3. Environment Settings

The study used accuracy (ACC), area under the curve (AUC), precision, recall, receiver operating characteristic (ROC) curve, F1 score, and kappa to assess the effectiveness of the malaria cell classification model. In this example, the training data is augmented by employing various techniques such as rotation, translation, scaling, flipping, and shifting. Every image in the training set is subjected to rotations of 90, 180, and 270 degrees to eliminate any background noise. The experiment was done on a PC with the following specifications: a 64-bit version of Windows 10, an Intel(R) Core(TM) i7 CPU 7710 operating at 2.67 GHz, 32 GB of RAM, and a 6 GB GPU. In addition, the solution leverages the two most renowned and widely used deep learning frameworks, namely Keras and Tensorflow.

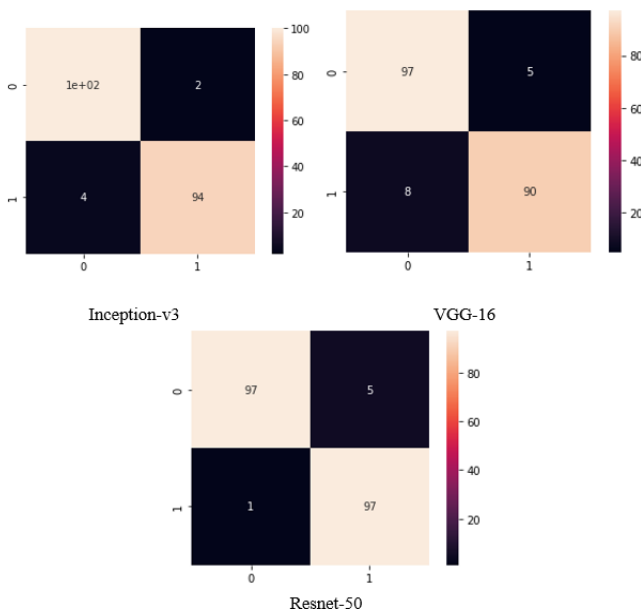


Figure 3. Confusion Matrixs.

$$Accuracy = \frac{TP + TN}{TP + FN + TN + FP}$$

$$Precision = \frac{TP}{TP + FP}$$

$$Recall = \frac{TP}{TP + FN}$$

$$F\ score = \frac{2 \times Precision \times Recall}{Precision + Recall}$$

5. Results and Discussion

In our proposed work we dealt with three transfer learning base pretrained models. We analyzed our three models sep-

arately. Table 1 shows the model accuracy, AUC, precision, recall, and F1 values. We trained our Three different pretrained models with 100 epochs and observed training and validation [Figure 2]. We analyze individual ROC curves too. we get 93% accuracy on the VGG model and get approximately 97% for both the resnet and inception models. then we combine three models to get the highest result which is the proposed result of 98.6%. This is the highest result from our model.

Table 1. Result analysis.

Model	ACC	AUC	Precision	Recall	F1
Inception-V3	97%	99%	97%	97%	97%
VGG-16	0.93%	98%	93%	93%	93%
Resnet-50	97%	99%	96.8%	97%	97%
Proposed	98.6%	99%	98%	98%	98%

6. Conclusion

The work presents an improved methodology for promptly detecting malaria and utilizes pictures of infected and uninfected red blood cells affected by malaria for the tests. We applied classical neural network approaches and different transfer learning techniques for comparison. Comparing between three different pretrained model with same parameters we get that inception model works better than two other model we used in our work. And to get a better result we proposed to ensemble three model by which we practically get the best result 98.6%. We faced some issue during our experiment specially mentioned issues are GPU power shortage and time consumption. If we trained our model on Better GPU powered device which will allow less time consumption and more epochs this will definitely upgrade our result. Furthermore, we recommend using a sophisticated pre-trained neural network structure to extract sophisticated information from malaria photos. Implementing this approach might improve the efficiency of malaria diagnosis by utilizing red blood cells.

Abbreviations

ACC	Accuracy
AUC	Area Under the Curve
ROC	Receiver Operating Characteristic

Conflicts of Interest

The authors declare no conflicts of interest.

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