Improving Malaria Detection with VGG19 Transfer Learning Model

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ORIGINAL RESEARCH

Abstract— The health challenge of malaria scourge particularly in sub-Saharan Africa, as a high mortality disease, has been of great concern to all and sundry. Reliable, quick and cost-effective diagnosis required for improved detection, treatment and prevention of the disease has been of major concern to researchers. Whilst microscopy and rapid diagnostic tests have performed appreciably well, they take time, require experienced personnel and sometimes give different results. Difficulty in obtaining large data of infected blood samples due to patients' confidentiality made adopting artificial intelligence (AI) and deep learning (DL) models for detection enhancement almost impossible. This study proposes an automated approach based on pre-trained DL technique known as transfer learning, namely: Visual Geometry Group 19-layer network (VGG19) convolutional neural network (CNN) architecture for malaria detection. A dataset of 27,560 blood smear pictures samples were sourced from Kaggle website and equally classified into infected and non-infected samples. Data resizing, normalisation, and increasing of the number of images by augmentation were carried out to improve the model performance. The model's performance effectiveness was verified using standard metrics of accuracy, precision, and recall with results of 98.63, 98.50 and 98.63 % obtained respectively. The results affirm the model could be used in clinics for accurate and effective detection of malaria with high prediction accuracy. It could also be built into an app on mobile devices for quick diagnosis of malaria-infested blood samples.

Keywords— Infected erythrocytes, Malaria detection, Plasmodium parasites, Transfer learning, VGGNet/VGG19 model.

1 INTRODUCTION

Majorly in tropical areas worldwide, malaria has posed great global health challenge to all age brackets of people. It has been responsible for high percentage of mortality. It is particularly caused by *Plasmodium* parasites, mostly: *Plasmodium falciparum* and *Plasmodium vivax,* in the red blood cells (Cowman et al., 2016, Alonso-Ramírez et al., 2024, WHO, 2023). Improved health care and control in this instance, requires administering the best forms of treatment for malaria infections, so that many lives could be saved globally. For this, early and accurate diagnosis has become very important.

Current methods used for the diagnosis of malaria parasites in blood cells include: microscopy, rapid diagnostic tests (RDT), and polymerase chain reaction (PCR). The microscopic examination of blood smears for infected erythrocytes by qualified microscopists has been the standard method for diagnosing malaria infections. Shown in Fig. 1 is a thin film smear of a malaria-infected blood showing infected and non-infected red blood cells and a normal leukocyte (Mbanefo & Kumar, 2020).

New upcoming methods include: loop-mediated isothermal amplification (LAMP), nucleic acid sequence-based amplification (NASBA), isothermal thermophilic helicase-dependent amplification (tHDA), nucleic-acid amplification based on saliva test, Plasmodium protein detection also based on saliva test, urine test, and transdermal hemozoin detection methods. Unfortunately, these methods are much more expensive and they provide less information than the microscopy method (Mbanefo & Kumar, 2020).

Regular and conventional methods of diagnosing malaria using microscopes to look at blood smears have to a large extent been often inadequate. This is because they are time-consuming, prone to error, and labour-intensive. The practice also usually suffers from shortage of well-trained personnel, thereby affecting the accuracy, reliability and effectiveness of the methods (Alonso-Ramírez et al., 2024).

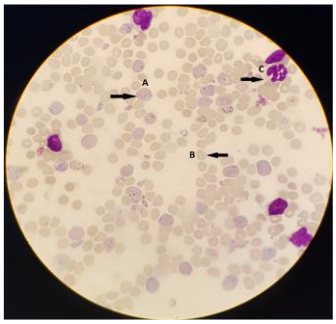

Fig. 1. Microscopy of a thin infected erythrocytes stained with Giemsa (Mbanefo & Kumar, 2020)

The field of artificial intelligence (AI) provides more advance approach and performance for diagnosis, treatment, therapeutic and surgical activities in various areas of medical science, with their potentials particularly seen in the automation of medical diagnostics (Dey et al., 2021, AL-Kafaf et al., 2024, Shameem & Malarvel, 2025). The use of machine learning (ML) and deep learning (DL) techniques have made considerable progress in training AI models for malaria detection which support timely and accurate detection of the disease (Qadri et al., 2023, Liang, 2016). Convolutional Neural Networks (CNN) was deployed in (Bouwmans et al., 2019, Benachour et al., 2025) to analyse blood smear images for malaria detection. Presented in Table 1 is performance

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comparison of the features of the traditional and AI-based malaria detection methods.

However, training AI models from scratch to achieve the expected high prediction accuracies for medical diagnosis and treatment requires a large amount of data, which we often do not have at our disposal due to confidentiality of patient medical information, and the difficulty of replication, comparison, and extension (Magotra & Rohil, 2022). Transfer learning makes use of pre-trained model which entails training a source task for the target task, by taking advantage of past knowledge obtained from the source task to improve generalisation. This is crucial in medical imaging, where annotated datasets are usually scarce because of patient privacy restrictions, costs, and the demand of resources to label (Soylu, 2022). The transfer learning approach allows us to take on new tasks for such medical diagnosis as malaria detection as it leverages on information from models pre-trained on big data. Majority of recent AI methods developed for malaria diagnosis prefer the approach of the use of transfer learning and pre-trained models for the development of the diagnosis models (Alnussairi & İbrahim, 2022, Jameela et al., 2022, Hemachandran et al., 2023, Siłka et al., 2023). Transfer learning therefore demonstrates the benefits of saving time, and reducing the cost of training the model and the risk of over fitting, a frequent problem with small training datasets.The approach as deployed in (Ramos et al., 2024) for identifying *Plasmodium* in microscopic images is shown in Fig. 2 using the pre-trained deep learning (CNN) architectures. This involves data pre-processing, and training and testing an ML model and analysing the results.

2 RELATED WORKS

Researches at improving malaria diagnosis have led to development of optimal, automated and innovative methods and approaches. Pre-trained models developed and/or deployed for this purpose include: DenseNet121, DenseNet169, DenseNet201, CNN, InceptionV3, VGG, ResNet50, EfficientNet-B1, EfficientNet-B7, MobileNet, and MobileNetV2 (Mujahid et al., 2024). High profile CNN architectures like VGGNet, ResNet, and Inception have shown particularly strong results in medical imaging due to their structural designs.

Oladele et al (2023) made use of the normal CNN model for classifying infected and uninfected malaria red blood cells and obtained a detection accuracy of 95.81%. In VGGNet, layers are arranged uniformly, such that its implementation is simplified, feature extraction is improved and tasks using very little data could run effectively (Oshoiribhor & John-Otumu, 2025). CNN architectures, ResNet and VGGNet, were studied and their performance compared for malaria detection in (Yang et al, 2021). At the time, computational demands of complex models made it difficult to deploy them in resource-limited settings. Shahin et al., (2025) developed an automated multi-model framework of DL and feature fusion for malaria detection using ResNet 50, VGG16, and DenseNet-201 for feature extraction. The results of their work showed accuracy, sensitivity, specificity, precision and F1-score of 96.47, 96.03, 96.90, 96.88 and 96.45 % respectively. In their work, Manning et al., (2022) developed a graphical user interface for segmentation of red blood cells and infected cells to enable users analyse the samples. They deployed classified cells data (two classes) on a Feed-forward Neural Network (FNN) model, and obtained detection accuracy of 92%. Madhu et al. (2023) developed an innovative inception-based capsule neural network approach for recognising parasitised and uninfected cells from blood image samples. They adopted the pre-trained InceptionV3 model, which assists in efficient representation learning for recognising malaria parasites. With a 50/50 dataset split, they achieved detection accuracy of 98.10%.

This study aims at improving, simplifying and automating malaria detection by applying transfer learning with a baseline VGGNet model, namely VGG19. In image classification tasks, due to scope and efficiency, VGGNet models are known and hence tailored for the task of detecting malaria-infected cells from blood smear image samples (Talla & Murthy, 2023).

3 METHODS AND MATERIALS

The research materials and methodology adopted for this study are discussed in the subsections of this section.

3.1 Data Acquisition, Selection and Pre-processing

This study made use of the NIH Malaria dataset accessed on the Kaggle platform at https://www.kaggle.com/datasets/iarunava/cell-images-for-detecting-malaria. As a public domain data from the United States National Institutes of Health (NIH) / National Library of Medicine (NLM), it is free to use for research, commercial, and educational purposes without restrictions.

The dataset consists of blood smear image collection of 27,560 pictures across two defined categories of blood samples, namely: parasites blood samples (shown in Fig. 3) non-parasites blood samples (shown in Fig. 4). To preserve objectivity in model assessment and training, equal numbers of images were assigned from both classes in its balanced image subset.

After acquisition of dataset, proper image pre-processing was done to keep the data elements consistent for the purpose of ensuring improved the model performance. The pre-processing consists of image dimension adjustment and pixel value normalization and augmentation to introduce the ability of generalization. Blood sample images were resized to 224×224 pixels because the VGGNet works with the standard input size of 224×224 pixels. The training of the VGGNet model was initially done with images of this same size making the transfer learning process easier and more efficient (Talla & Murthy, 2023).

A range normalization from 0 to 1 was implemented on pixel values to improve training efficiency instead of keeping the default scale of 0 to 255. Advantages offered by the normalization include:

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1. improving the convergence speed through distribution normalization of input data
2. fewer calculation overhead and system memory are required for the procedure
3. scaling of pixel values between 0 and 1 curtails high pixels from controlling model training.

Different data augmentation methods were used in order to enhance model generalization, performance and handling of new images. The methods apply variable transformations, which help the model develop more resilient features.

Table 1. Traditional vs. trained model based detection

Aspect	Traditional Methods	Trained Model Detection
Diagnosis accuracy	It depends on the skill of the technician.	It has a consistent high accuracy.
Speed	It is a slow multi-step process.	The application gives fast, almost instantaneous results.
Human error	High possibility of human error.	Human error is and minimized
Cost	Continuous maintenance costs for equipment and labor.	One time model training with low maintenance.
Clinical	Symptom-based and	Image-based and

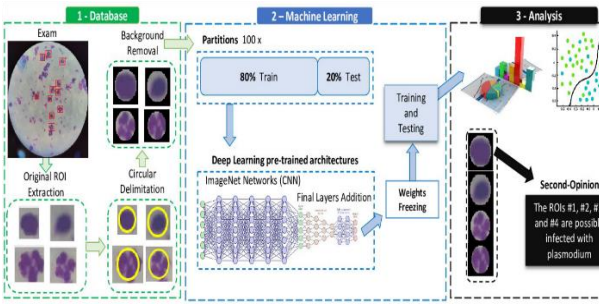

Fig. 2. Workflow for identifying Plasmodium-infected region of interest (ROI) (Ramos et al., 2024)

The model receives images at multiple angles through small rotational steps (+/-15 degrees) as part of orientation accommodation. The process of data augmentation includes horizontal image flips for appearance variation purposes. Slight modifications of the viewing scale using the "zoom" feature enable simulation of various magnification levels. The method adjusts brightness levels to create conditions similar to different lighting scenarios that occur during microscopy. The application of data augmentation during implementation made use of ImageDataGenerator from Keras, shown in Figure 5.

3.2 Malaria Detection Model Selection

In creating effective malaria detection systems, the CNN DL model was used for this study due to its proving to be highly effective at finding patterns within image contents (Gebrerufael et al., 2024). CNNs are extensively used for medical imaging classification applications because:

1. it automatically isolates essential image characteristics, namely: edges, textures and patterns during operation
2. the network reduces training complexity through convolutional and pooling layers, which decreases the number of trainable parameters making the system computationally efficient
3. it demonstrates high accuracy for medical diagnosis work alongside image classification and object detection operations.

The transfer learning process in medical imaging utilizes three main pre-trained CNN architectures, which include: ResNet, MobileNet and VGGNet (VGG16 & VGG19). Ahamed et al., (2025) performed a comparative study of VGG, ResNet and GoogLeNet models, assessing their performance, computational efficiency and convergence rate.

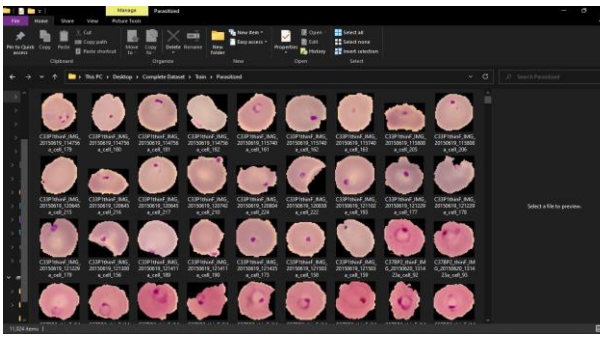

Fig. 3. Dataset containing parasitised images

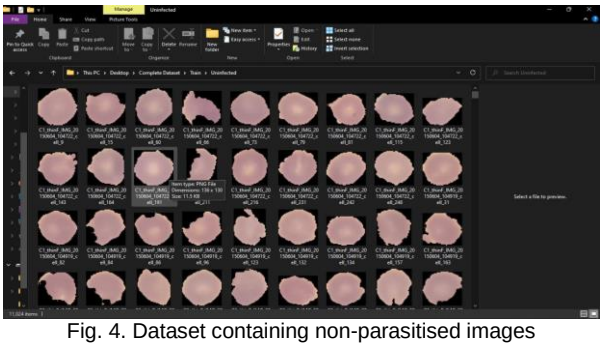

Fig. 4. Dataset containing non-parasitised images

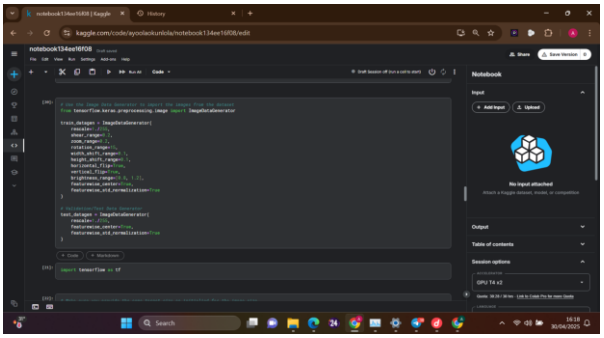

Fig. 5. Dataset augmentation

3.3 The VGGNet/VGG19 Architecture

Figure 6 shows the architecture of the VGG19 model as consisting 16 convolutional layers and three dense layers that are fully connected and the blocks classified into five separate classes followed by a max-pooling layer (Bamber et al., 2026). Figure 7 shows the convolutional layers of the VGG19 model.

The output function of each convolutional layer is given by Equation (1) (Nguyen et al., 2022):

$$C_j^l = \varphi\left(\sum_{i=1}^{M^{l-1}} C_i^{l-1} \times k_{ij}^l + b_j^{l-1}\right) \quad (1)$$

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where × as a convolutional function describes connection between weights of i^{th} and j^{th} features.

For this study, the Visual Geometry Group 19-layer network (VGG19) was chosen over other models because it offers the best performance metrics (Talla & Murthy, 2023). In computer vision, the VGG architecture is highly adaptive and ideal for transfer learning due to its efficient feature extraction proficiency (Zhang et al., 2023). The VGG architecture has the following key advantages that led to its selection:

1. a deep structural design consisting of 19 layers (16 convolutional layers alongside 3 fully connected layers) provides the model its capability to detect complex features
2. through ImageNet data set weights, the model is prepared with such learned features to be applied on malaria detection.

VGG19 is shown to have both high accuracy levels and competency for the malaria detection problem. Due to its versatility, the VGG19 model has been singularly deployed as a model for several classification and predictions of many medical issues, like in Jamshidi & Rostamy-MalKhalifeh (2024), Vetrithangam et al., (2023), Bi et al. (2024).

However, the process of achieving higher accuracy through VGG19 requires a costlier computational approach than lighter models such as MobileNet (Oshoiribhor & John-Otumu, 2025). The implementation of the VGG19 network was done with MathWorks on the MATLAB platform.

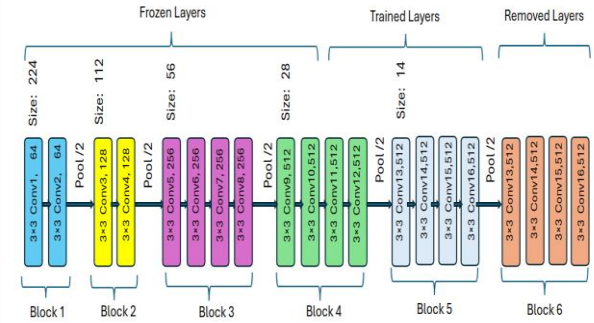

Fig. 6. VGGNet/VGG19 Model Architecture

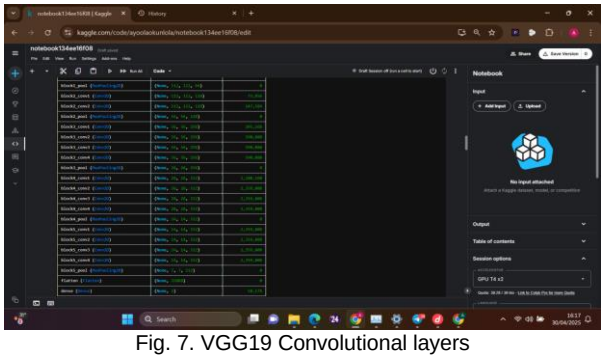

Fig. 7. VGG19 Convolutional layers

3.4 Evaluation Metrics

The model's performance measurement is carried out with the classification metrics used in this work, namely: Accuracy Score, F1-Score, AUC Score and Confusion Matrices from the sklearn. metrics module. These metrics are briefly discussed with their mathematical equations also given as follows (Bamber et al., 2026, Kadhim et al., 2023, Sinha & Gupta, 2023, Abbasi, 2021):

1. **Accuracy:** is the quantity of positive and negative predictions to the total number of prediction cases and given by:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (2)$$

However, as in most medical diagnosis, one is often dealing with imbalanced data, which may be misleading. Accuracy is not a good metric to assess a model's actual diagnostic reliability as there are far more uninfected than parasitized samples.

2. **Recall Sensitivity:** also known as the True Positive Rate (TPR), measures appropriate identification of the positive instances (parasitized cells) by the model, and given by:

$$Recall = \frac{TP}{TP + FN} \quad (3)$$

This is vital in malaria diagnostics as high sensitivity reduces the risk of false negatives and ensures timely and accurate treatment. As in [28], sensitivity is generally a major performance metric and crucial to building confidence in the model's potential to diagnose in the clinical setting.

3. **Precision:** measures the frequency of correct positive prediction by the model. As a crucial metric, the model minimises the number of FPs when the cost is high. It is given by:

$$Precision = \frac{TP}{TP + FP} \quad (4)$$

4. **Specificity:** is the model's capability of detect negative instances (uninfected cells). It is important because of the resulting reduction in false positives that lead to unnecessary treatments and resource wastage. It is given by:

$$Specificity = \frac{TN}{TN + FP} \quad (5)$$

5. **F1-Score:** accounts for situations of imbalanced dataset, as it balances precision and sensitivity. It serves as a more holistic view of model performance in datasets by balancing FNs against FPs. It is given by:

$$F1 - score = \frac{2 * Precision * Recall}{Precision + Recall} \quad (6)$$

6. **Receiver Operating Characteristic (ROC) Curve:** measures the discrimination power of the model between classes across different threshold settings. In diagnostic tasks, in particular, we are interested in how well the model distinguishes infected versus uninfected cells for all possible decision boundaries.

4 RESULTS AND DISCUSSION

Results obtained from training and evaluation of the VGG19 model for malaria detection are presented and discussed in this section. The model making use of high-level image features was trained for 30 epochs. The model performance is presented using accuracy, loss, precision, and recall metrics. Visual representations of these performance results are shown with plots to aid understanding how the model behaves. The results are discussed based on what was achieved in terms of attaining the objectives of the study and with regard to limitations encountered in the process of

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experimentation.

4.1 Training and Validation Accuracy

In training the model, the training accuracy is seen to increase as the epochs progress. Distinguishing features between parasitised and healthy blood cells are learned by the model. The accuracy improved over time, without any fluctuation, with steady progress demonstrated over the epochs as shown in Fig. 8 and the screen shot of the training and validation accuracy plot shown in Figure 9. The rate of improvement continued through 27 epochs at which the metrics became seemingly stable. The training accuracy rose from about 92.50% to the best value of 98.72% and the validation accuracy from about 92.00% to the best value of 99.35%. The gradual increase in validation accuracy, almost like the training accuracy, implies the model generalised quite well and was not really over-fitted.

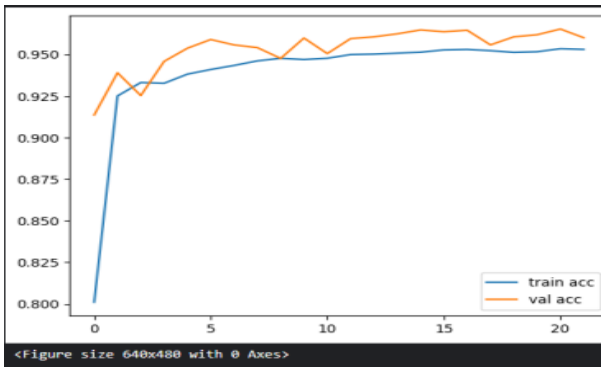

Fig. 8. Plot of the training and validation accuracy.

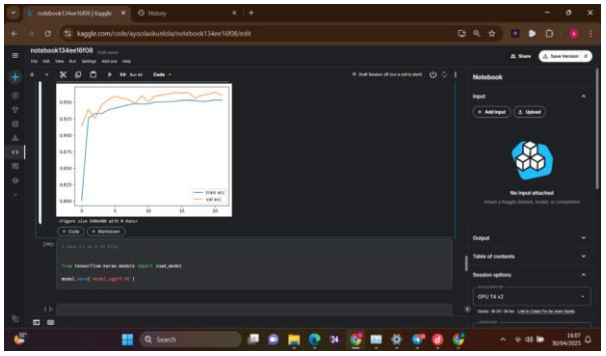

Fig. 9. Screen of the plot of the training and validation

4.2 Training and Validation Loss

In monitoring this loss to show the model optimising, the training loss consistently decreased throughout the process. This shows the model indeed started to learn to minimize the prediction errors. Also, the validation loss decreased during the course of the training, which shows consistency with the pattern of the training loss. Figure 10 shows the plot of the training and validation loss, while figure 11. is the screen shot of the plot of training and validation loss. The steady decrease in both losses infers that the model gradually reduces errors without over-fitting.

4.3 Observations from training

Learning curves of the model showed that the convergence would be smooth and often stabilize around 27 epochs.

1. Proper model regularization and data augmentation techniques prevented the model from showing severe over-fitting and provided no evidence for its occurrence.

Slight oscillations in the validation loss were observed but they all stayed within a reasonable range.

4.4 The Model's Performance per Epoch

The performance of the model across all the 30 training epochs, showing the accuracy, precision, and recall, was recorded for each epoch as shown in figure 12. Table 2 presents values of the training and validation accuracies, the precision and recall for each epoch.

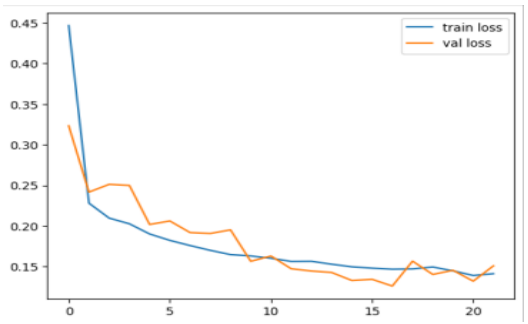

Fig. 10. Plot of the training and validation loss

Table 2. Performance Summary

Metric	Value (%)
Accuracy	98.63
Precision	98.50
Recall	98.63

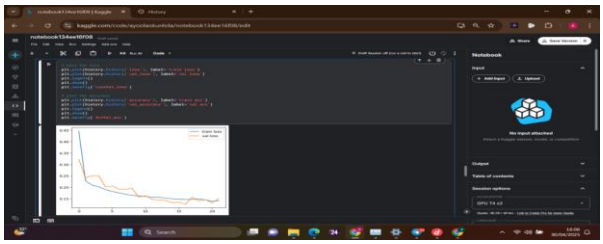

Fig. 11. Screen of the plot of the training and validation loss

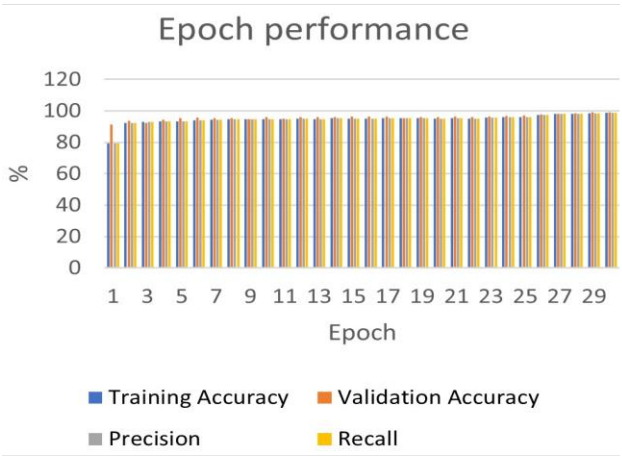

Fig. 12. Plot of the 30 training epochs showing performance parameters

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4.5 Interpretation of Metrics

1. Accurate model: the model makes the correct predictions most of the time.
2. High Precision: a sample is correctly predicted as infected, minimizing false positives (FP).
3. High Recall: the model identifies most of the infected samples, ensuring minimum number of false negatives (FN).

The malaria detection accuracy score of this study is compared with those of cited related works as presented in Table 3. The results show that transfer learning using VGG19 yields an effective malaria detection technique since it is able to achieve high performance with an appreciable size of dataset. Generalization capabilities of the model were excellent, over-fitting negligible, and diagnostic reliability strong. Future work in enlarging and diversifying the dataset and optimizing models will further make the system useful in true-world medical environments.

Table 3. Performance Comparison with cited related works

Ref.	Model deployed	Detection Accuracy in cited Related Works	Difference with the Accuracy (98.63%) of this Study
Mujahid et al., 2024	Efficientnet-B2 CNN model	97.57%	1.06%
Oshoiribhor et al., 2025	Pre-trained VGG16 CNN model	97.00%	1.63%
Shahin et al., 2025	ResNet 50, VGG16, and DenseNet-201 for feature extraction and feature fusion	96.47%	2.16%
Madhu et al., 2023	Neural networks based on Inception and Imperative Capsule networks	98.10%	0.53%
Talla & Murthy, 2023	Ensemble of pre-trained	96.94%	1.69%

5 CONCLUSION

This study used the VGG19 transfer learning model based on pre-trained deep learning for malaria detection from blood smear images dataset obtained from Kaggle. It indicates the importance of building a model that is accurate and efficient in predicting malaria infection, and summarizes the study's contributions in terms of achievements, and recommendations for additional work. It implemented a structured workflow process: acquiring data, pre-processing, training, evaluating data. It also showed that deep learning tools can work well in resource constrained settings and thus may be more accessible in malaria exposed regions. It positioned the model as a basis for a scalable deployment into future diagnostic systems. The result is a significant improvement over the current traditional microscopy-based methods, which are prone to human error.

This project contributes to the growing body of knowledge on AI in the area of health, and it ultimately provides a blueprint for future research and development for malaria detection like adding XAI tools such as GradCAM, SHAP, or LIME to get a visual understanding of what the model analyses when predicting.

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