A Comparative Study of Convolutional Neural Networks (CNN) Architectures on Microscopic Blood Film Images for Malaria Diagnosis

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***Abstract*—Malaria has been recorded as one of the deadliest diseases globally. Accurate diagnosis is essential for suitable treatment, and the traditional practice of malarial diagnosis has proved inefficient as results depend on the skills of the health personnel. Deep learning models have recently proven helpful in the rapid detection of malaria parasites. This research focused on developing a classification model of Convolutional Neural Networks (CNN) architectures and comparing these models to identify the most effective one for automatic malaria parasite detection on thin blood smear images. A dataset of 27,558 digital blood images was collected from the National Institutes of Health (NIH) database in Bangkok, Thailand. The dataset was categorized into parasitized and uninfected cells and was fragmented into training (80%) and validation (20%) sets. Performance metrics for measuring the model's performance include sensitivity, specificity, precision, and F1−Score. The model predicted and classified thin blood smear digital images as either parasitized or uninfected with custom InceptionV3 outperforming the VGG19 and custom CNN with an accuracy of 89.85%. The result shows that malaria diagnosis on microscopic thin blood images using deep learning can potentially improve early detection of malaria parasites, which could prevent deaths, reduce the workload of Parasitologists, and eliminate other limitations of the traditional malaria diagnostic approaches.**

***Keywords*—convolutional neural network, malarial parasite detection, classification model, Diagnosis, Digital blood images**

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I. Introduction

Malaria is a life-threatening disease caused by plasmodium parasites transmitted to humans through the bites of infected female Anopheles mosquitoes in the form of sporozoites [1]. Malaria can be spread to other people from mosquitoes that bite malaria patients, blood transfusions, sharing syringes and can be transmitted from mother to fetus [2]. Malaria symptoms are similar to that of flu and can include high fever, chills, septicaemia, pneumonia, gastritis, enteritis, nausea, vomiting, abnormal liver function, kidney failure, anaemia, and death [2, 3]. Doctors usually treat malaria patients using antimalarial agents, such as Chloroquine, Doxycycline, Quinine Sulfate, Hydroxychloroquine, and Mefloquine [2]. Five species of plasmodium parasites can infect humans, including *Plasmodium falciparum*, *P. Vivax*, *P. Ovale*, *P. Malariae*, and *P. Knowlesi* [4]. Infection with *P. falciparum* accounts for more than 90% of the world's malaria mortality and therefore remains an important threat to public health on a global scale [5]. According to the World Health Organization (WHO) 2022 malaria report, 249 million people were infected with 608,000 deaths globally. The emergence and spread of the *Plasmodium falciparum* multidrug-resistant 1 (Pfmdr1) allele pose a significant setback to global efforts to control and eradicate malaria infection by diminishing the efficacy of commonly prescribed antimalarial drugs, particularly in Sub-Saharan Africa, where malaria remains endemic. The Pfmdr1 D1246Y mutation is of specific importance due to its potential

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role in modulating parasite susceptibility to antimalarial medicines and treatment outcomes [6]. Most of both morbidity and mortality occur in sub-Saharan Africa, accounting for over 90% of both cases [7, 8]. Children under 5 years of age are observed to be regular victims of the disease, with half the world's population being also at risk [3, 9].

The standard practice for malaria diagnosis involves the collection of human blood samples, making blood smears, staining them, and examining the stained slides under the microscope for the presence of malaria parasites in the red blood cells. The traditional approach is time-consuming, tedious, and expensive, and the accuracy of the result depends on the skills and expertise of the Microscopist. Other methods of malaria diagnosis aside from microscopy include Rapid Diagnostic Test (RDT), Polymerase Chain Reaction (PCR), and Loop-Mediated Isothermal Amplification (LAMP). Each method has its own merits and demerits focusing on the accuracy, cost availability of trained personnel, and infrastructure [10, 11]. PCR and LAMP are very expensive and require especially skilled laboratory personnel. RDT, though it is cheap and needs no special skill to perform it, has many limitations which include the inability to determine the parasite density and is usually specifically made based on a particular antigen of a *Plasmodium* specie. Additionally, RDT sometimes gives false-negative results due to poor storage, operational errors, very low parasite density, antigenic variation, and gene deletion (since it is based on a specific Plasmodium gene) [12, 13].

Studies have shown that most reported deaths in tropical zones are due to misdiagnosis giving rise to wrong results and improper medication and treatment [14, 15], thereby threatening patients' safety [16]. Hence, there is a need for a more reliable automated method devoid of human intervention.

Technology innovation has made Deep Learning (DL) a popular and efficient approach for a quick, cheap, and more reliable malaria test by training computers to learn and compute distinctive features from data and make decisions without human intervention [3]. The Convolutional Neural Network (CNN) is a class of deep neural networks that is characterized by shared-weights architecture used to solve problems in Machine learning (ML) and computer vision. Deep Learning (DL) Is a variant of ML techniques that uses multiple layers to gradually extract higher-level features from the raw data [17], therefore, this is mostly a mathematical distribution for complex behaviour than traditional ML. CNN requires a large amount of data and processing power to learn patterns of features to produce a predictive model [3, 18]. ML is an Artificial Intelligence (AI) technique that automatically learns using learning algorithms and improves from experience [19]. This research focuses on developing classification models of CNN architectures, comparing them to identify the most effective model for malaria parasite detection on thin blood smear images using a public dataset from the National Institutes of Health (NIH) database, in Bangkok, Thailand.

Machine Learning is currently used to revolutionize clinical parasitology laboratories, where the blood sample is converted to a digital image dataset used to train the DL models and test for the presence of malaria parasites in the red blood cells.

The proposed model provides a quick diagnosis of the malaria parasite which has the potential to eliminate the limitations of traditional approaches, reduce the medical professional's burden on screening malaria patients, and improve patient survival rate. This also provides people in rural areas with access to malaria diagnostic tools, where a lack of competent malaria microscopists is prevalent.

A. Comparison of CNN-based Diagnosis with Traditional Methods: Manual Microscopy and Rapid Diagnostic Tests

CNN-based malaria diagnosis offers several advantages over traditional methods like manual microscopy and Rapid Diagnostic Tests (RDT). While manual microscopy relies on the skill of the Microscopist and is time-consuming, CNN-based models can process blood smear images rapidly and consistently, reducing human error and increasing throughput. Unlike RDTs, which can be inaccurate under certain conditions (e.g., low parasite density or antigenic variation), CNN models provide objective and reliable results based on the analysis of cell features. Additionally, CNNs can handle large volumes of data with higher precision, enabling faster diagnosis in remote areas where healthcare resources are limited. While manual microscopy and RDTs are still widely used due to their low cost and simplicity, CNN-based methods represent a significant step towards automating and improving malaria diagnosis, especially in high-burden regions.

B. Advancement beyond Existing Solutions

This study presents a novel approach to malaria detection by leveraging CNN-based architectures such as Custom CNN, VGG19, and InceptionV3, which have shown substantial improvements in classifying malaria-infected red blood cells from thin blood smear images. While previous studies have explored models like GRU, LSTM, and hybrid approaches that integrate Recurrent Neural Networks (RNNs) with CNNs, our work uniquely focuses on the comparison of traditional CNN architectures with transfer learning techniques. The use of InceptionV3 as a pre-trained model with fine-tuning is particularly innovative, as it allows us to benefit from a robust feature-extraction architecture that adapts well to the specificity of malaria image datasets.

Unlike GRU and LSTM models, which excel in sequential data processing but are less effective at capturing spatial features in image data, CNNs are naturally designed for image classification tasks. This paper demonstrates the effectiveness of CNNs in addressing the challenges of feature extraction from microscopic blood images. Additionally, the comparison with hybrid models, which often combine CNNs with

RNNs to capture both spatial and temporal features, highlights the advantages of purely CNN-based approaches in terms of computational efficiency and accuracy when working with static images like blood smears.

Furthermore, our study adds value by directly comparing Custom CNN, VGG19, and InceptionV3, which is a fresh contribution to the malaria diagnosis literature. By focusing on transfer learning and fine-tuning techniques, we provide an effective method for adapting pre-trained models to medical image analysis, enhancing both performance and generalization. This approach advances the field by offering a more efficient, scalable, and interpretable solution compared to previous hybrid models or traditional deep learning architectures.

II. Review of Related Work

Machine Learning (ML) models have emerged as a potentially fitting tool for data-driven predictions in various fields of research; hence, the drug discovery area is undoubtedly one of the sectors that can profit significantly from the success of ML [20]. ML as a subset of AI has proved helpful in the rapid diagnosis and detection of many diseases including malaria, diabetes, and cancer, [21, 22]. Sumi *et al.* [23] reviewed studies on the detection of plasmodium using ML. The authors were able to evaluate 45 articles from five different databases and the ML techniques used achieved between 60%–95% accuracy.

Irmak [24] designed a CNN-based malaria detection model consisting of 20 weighted layers to classify parasitized and unparasitized blood cell images. The model was trained with a dataset of 27,558 blood images with 95.28% accuracy. Similarly, Gezahegn *et al.* [25] developed an SVM model for blood image classification with 78.89% accuracy. Khalid *et al.* [26] reviewed studies that adopted different ML algorithms and methodologies on microscopic thick blood smear images to automate plasmodium detection. Similarly, Poostchi *et al.* [27] and Rosado *et al.* [28] developed an SVM classification model with 2000 Red-Green-Blue (RGB) on thin blood smear images achieving an accuracy of 97.05%.

A dual deep learning architecture, named the RBCNet algorithm, was used for red blood cell detection and counting in thin blood smear microscopic images. The two deep learning networks (U-Net and Faster R-CNN) were combined to detect highly overlapped RBCs in blood smear images. A dataset of 200,000 labelled cells across 965 images from 193 patients, in Bangladesh was used. The RBCNet architecture outperformed the traditional and other deep learning methods with 97% accuracy [3]. Sriporn *et al.* [2] used 7000 images of Xception, Inception-V3, ResNet-50, NasNetMobile, VGG-16, and AlexNet models to detect malaria parasites and classify thin smear images as infected or uninfected cells and use a rotational method to improve the performance of validation and the training dataset with CNN models. Xception outperformed other models with an accuracy of 98.86%.

Furthermore, Rajendran *et al.* [29] focused on recent techniques and developments in the application of mobile devices and deep learning for plasmodium detection on both thick and thin film images. Other studies by Das *et al.* [30] and Hegde *et al.* [31] discussed the advancement of ML techniques for discriminating five different stages of infected erythrocytes (three *P. vivax* and two *P. falciparum*) due to malaria infection and non-infected cells using morphological information, texture, and colour. Results showed that 94 features were statistically significant in discriminating 6 classes.

Prakash *et al.* [32] developed a CNN classification model to predict the presence of two *Plasmodium* species (*P. vivax* and *P. falciparum)* on a dataset available in the National Library of Medicine. The result shows an F1–Score of over 94%. Another study by Piccialli *et al.* [33] focused on the use of CNN to predict and classify parasitized cells in thin blood smears on a dataset of 27, 558 cell images. Somasekar and Reddy [34] presented a broad and in-depth study on DL methodologies and applications in healthcare comprising the analysis of thick blood smears to diagnose malaria. Likewise, Bibin *et al.* [35] adopted DL and developed an edge-based segmentation of erythrocytes infected with plasmodium using microscopic cell images.

Delahunt *et al.* [36] focused on Deep Belief Networks (DBN) on peripheral blood smear images as another approach to malaria diagnosis. Neural network, MATLAB (R2016a), Statistical Pattern Recognition Toolbox, and image processing were used in the study. This method proved more efficient than the state-of-the-art methods. The Refs. [37–39] developed an automated framework for thin blood film malaria diagnosis using CNN, trained on a large and diverse dataset of field-prepared thin blood films. Their result showed that quantitation and species identification results from field-prepared samples are near to being accurate enough for drug resistance monitoring and clinical use cases.

Other studies propose the use of Evolutionary Convolutional Deep Networks (ECDN) to diagnose malaria parasites, which can use evolutionary algorithms to automatically generate deep neural networks to optimize their network topology structure during the evolution process. ECDN has the advantage of being able to automatically generate an optimal network structure without the need for any prior knowledge of constructing a neural network, as compared to a traditional artificial convolution network [40].

Fuhad *et al.* [41] adopted CNNs and SVMs models and recommend a low-cost automatic digital microscope (Autoscope) coupled with a set of computer vision and classification techniques, which can accurately diagnose a variety of infectious diseases- targeting the developing world. Furthermore, MacNeil and Eliasmith [42] developed an automatic CNN model for the detection of malaria from microscopic blood smear images. A variety of techniques comprising, data augmentation, Autoencoder, knowledge distillation, feature extraction by a CNN model, and classification through K-Nearest

Neighbours (KNN) and SVM were applied. The result achieved an accuracy of 99.23%.

Beibei *et al.* [43] studied provides medical imaging evidence to interpret the CNN classification for subsolid nodules, which helps to strengthen the application of deep learning in the diagnosis of subsolid nodules and can be seen as an example of CNN interpretability research for other imaging applications.

These studies have shown that research on detecting and predicting malaria is possible and has been done by some researchers. However, there is still room for improvement since the size of the dataset and approach to model development are always significant factors that contribute to the model outcome. The present study combined both traditional and customized CNN approaches to classify each candidate as either parasitized or uninfected. Additionally, it explored three CNN architectures (custom CNN, VGG19, and InceptionV3) to identify the most efficient algorithm for detecting malaria parasites.

III. Methodology

A. Light Microscopy (LM) with Stained Blood Smears

Light microscopy with stained blood smears is one of the available traditional diagnostic methods. The WHO recommended method for diagnosing malaria accurately is the parasite identification through light microscopy inspection of blood smears consisting of the steps as shown in Fig. 1 [44]:

Blood, preparation of the blood film (Thin or Thick), Staining (Giemsa stain), Data analysis, Examination with LM, and Data Interpretation.

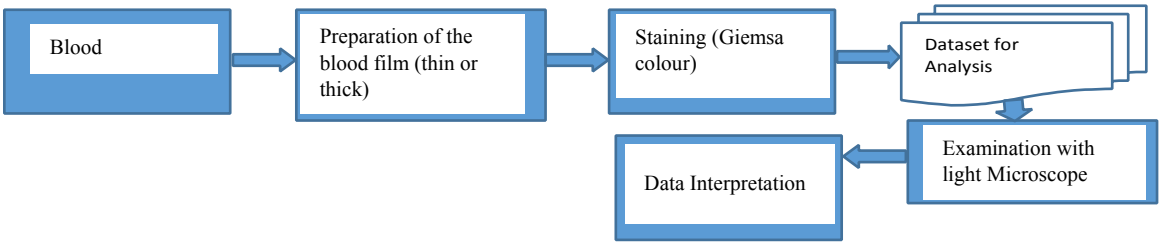


Fig. 1. Malaria diagnosis using light microscopy with stained blood smears.

Fig. 1 summarizes the steps for the LM malaria Diagnosis; a sample of the patient's peripheral blood is acquired. The blood is applied to a microscopic slide, and a thick or thin film is prepared. To allow for the distinction of the blood cells and parasites, the dried blood film is stained. Microscopic slides are most commonly stained with a Giemsa stain, but other Romanowsky stains such as Field's and Leishman stains can also be used [34, 45]. Then, the microscopic slides are examined with a 100× oil immersion lens of a light microscope. Finally, in thick smears data interpretation, the parasite density is determined per μL of blood, by determining the number of parasites ×8000, divided by the number of white blood cells. In thin smears, the number of infected and non-infected red blood cells are tallied, and parasitaemia is expressed as a percentage of total cells infected. The species and stage of the parasites are also identified.

B. Process Flow and the System Algorithm

The methodology of diagnosing malaria from blood smear images utilizing deep learning techniques is encapsulated in the research flow diagram (Fig. 2). This diagram methodically outlines the stages and techniques implemented in the study; it is a detailed representation of the entire workflow. It shows the pivotal steps from data acquisition and preprocessing to the evaluation of CNN models, highlighting the systematic progression of this study.

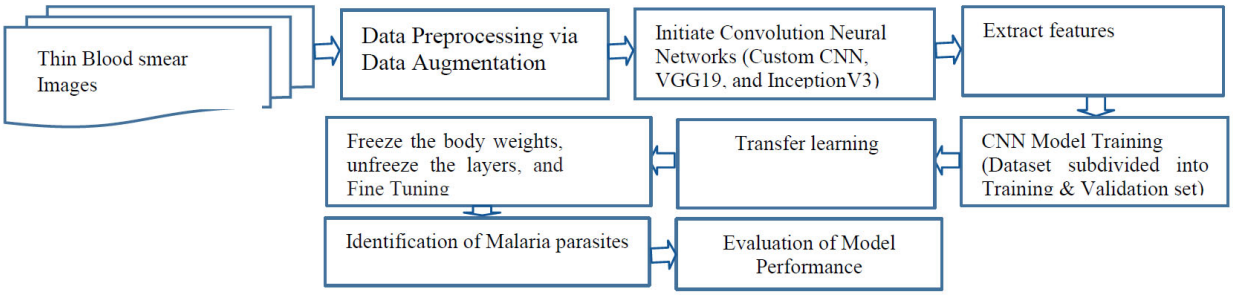
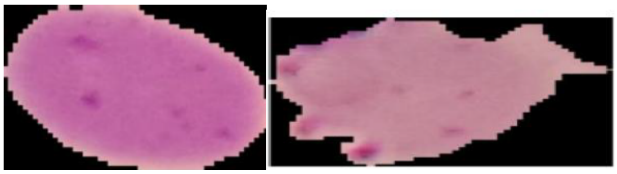


Fig. 2. Flow diagram of the research methodology.

The first step in Fig. 2 is to get a public dataset available in the National Institutes of Health (NIH) database. The second step is to prepare the dataset in the form it should be used to train CNN architectures. Next is to train the model for the classification of infected and uninfected thin optical microscopic blood films as shown in Fig. 3, and finally the performance of the models was evaluated.



(a) (b)

Fig. 3. Blood films (a) uninfected red blood cells (b), malaria-infected red blood cells [3].

C. Dataset Description

The study utilized the NIH Malaria dataset, comprising 27,558 Segmented red Blood Cell (RBCs) images, equally distributed (balanced) between the *Plasmodium falciparum*-infected and uninfected cells as shown in Table I. The dataset is publicly made available at the Lister Hill National Center for Biomedical Communications (LHNCBC) of the National Library of Medicine (https://lhncbc.nlm.nih.gov/LHC-research/LHC-projects/image-processing/malaria-datasheet.html) established by the United States Congress in 1968. The images are dye-stained thin blood smears of 50 healthy and 150 *P. falciparum*-infected patients collected from a Bangladeshi at 1000× magnification. The images were acquired using two different light microscopes, an Olympus and a Motiff, and were manually annotated by an expert slide reader at the Research Unit of Mahidol-Oxford Tropical Medicine in Bangkok, Thailand. Given the resolution of the dataset as 1000x magnification, it provides an ideal test bed for our chosen models: custom CNN, VGG19, and InceptionV3; known for their efficacy in analysing modestly-resolved images. Such a resolution, while lower than some high-end microscopy techniques, is reflective of real-world diagnostic environments, particularly in resource-limited settings where malaria is most prevalent. Inception v3 is a combination of many ideas developed by several researchers. The computational cost and memory consumption are much smaller [42]. The selected models were strategic, and aimed at harnessing their proven strengths in feature extraction and pattern recognition at lower resolutions. This approach provided a comparative framework to assess the performance of each model in a consistent setting.

Although the dataset is balanced, potential biases include class imbalance and data collection bias from a specific geographic region (Bangkok), limiting its generalizability. Annotation bias may arise from manual labeling inconsistencies, and overfitting is a concern, especially for VGG19 and Custom CNN, due to the relatively smaller dataset and lack of sufficient variation in some cases.

TABLE I. CLASSIFICATION OF THE DATASET

Label	Training set	Validation set	Total
Parasitized	11,023	11,023	22,046
Uninfected	2755	2755	5510
Total	13,778	13,778	27,556

1) Data preprocessing

The project followed a vital data pre-processing.

Data Augmentation techniques were applied to the dataset to adapt to the variability in blood smear images and enhance the robustness of the trained models. The techniques involved variants of the images generated through rescaling (0–1), rotation (range = 40), width shift (range = 0.2), height shift (range = 0.2), shear (range = 0.2), zoom (range = 0.2), horizontal flip. The images were also modified to create a uniform look by filling with the nearest pixels thereby enriching the dataset and minimizing overfitting risks. The TensorFlow and Keras libraries were used to resize and normalize the images before introduction into the deep learning models. This process ensures effective and efficient model training.

2) Training and testing dataset split

In this study, the dataset was split into training and validation sets to evaluate the performance of the models. Specifically, 80% of the data was used for training, while the remaining 20% was reserved for validation. This split ensured that the models were trained on a large portion of the data while still having a separate set of unseen data to test their generalization capabilities. The validation set was used to monitor the models' performance during training, providing an indication of how well the models would perform on new, unseen data.

Cross-validation was not used in this study. Instead, the training and validation datasets were partitioned once, with the training data being used to fine-tune the models and the validation data used to assess performance after each epoch. While cross-validation could provide additional insights into the model's robustness, the current study opted for a simpler split due to the size of the dataset and computational constraints. However, in future work, incorporating k-fold cross-validation could further validate the models' performance and provide a more thorough evaluation.

D. Convolutional Neural Network (CNN) Model

CNN is the cornerstone of the field of deep learning, renowned for its efficient convolutional operation. It is an efficient recognition method which has been developed in recent years. The network avoids the complex pre-processing of the image, and one can input the original image directly. It uses local receptive field, weights sharing, and pooling technology and makes the training parameters greatly reduced. It also has a certain degree of

translation, rotation, and distortion invariance of image and has made great progress in the field of image classification [41, 46, 47]. The CNN architectures were designed with a blend of convolutional, nonlinearity (activation), pooling, and fully connected layers. The architecture of the custom CNN model is made up of an input layer 66×66×3 in dimension, 2 convolution layers with a 3×3 kernel and 16 filters, 2×2 pooling layers, a dropout rate of 0.3, and relu activation. The fully connected layer is 1×1×14,400 dimensional. The final output is generated using the softmax function. The model has a total of 931,457 trainable parameters.

Three distinct CNN models were explored in this research: the Custom-built CNN model and transfer learning-based VGG19 and InceptionV3 models. The transfer models were fine-tuned using the malaria smear images and by fine-tuning the backbone layers of the pre-trained model. The comparative analysis of these models on the same dataset provided insights into their relative strengths and efficiencies in malaria detection.

1) CNN model training

The dataset was split into training and validation sets, as detailed in Table I. The model training was performed with 80% of the training data, while the remaining 20% was used in validation and testing. The models were trained iteratively, fine-tuning neuron weights and biases to minimize the loss of function, thereby enhancing the model's ability to classify blood smear images as parasitized or unparasitized. For each model, the Adam optimizer was used at a learning rate of 0.01.

The model was evaluated using accuracy, sensitivity, specificity, precision, F1−Score, ROC-AUC, and confusion matrices.

2) Transfer learning

This study employed transfer learning; a technique where knowledge acquired from one domain is applied to a similar yet distinct domain. Specifically, the study adopted pre-trained CNN models, which were originally trained on the ImageNet dataset for the binary classification of blood smear images. This approach leverages the extensive feature-learning capabilities of these models, which are crucial for recognizing textures and shapes pertinent to parasitized and uninfected blood cells. Subsequently, the entire model was fine-tuned by unfreezing the backbone layers. The fine-tuning phase involved training both the new head and the backbone layers, allowing the model to adjust its learned features to better align with our specific classification task. Employing transfer learning with differential learning rates in fine-tuning exemplifies an advanced strategy in deep learning. It harnesses the robust pre-existing knowledge from large datasets while effectively adapting to new, specialized tasks, as demonstrated in the malaria detection study.

3) Fine-tuning and unfreezing

The study implements the techniques of fine-tuning and unfreezing in adapting pre-trained Convolutional Neural Networks (CNNs) for malaria detection, drawing upon contemporary research in the field. The process of fine-tuning, as detailed in [40] involves adjusting the connection weights of a neural network to enhance its stability and performance for specific tasks. This approach is crucial in tailoring the network to effectively classify blood smear images [48]. The fine-tuning of the models reported in this paper is in line with the methodology proposed by [49].

4) Hyperparameter tuning

In this study, hyperparameter tuning was performed to optimize the performance of the CNN models. The key hyperparameters, including the learning rate, batch size, and number of epochs, were selected based on empirical experimentation and prior knowledge of deep learning practices [50]. The initial learning rate was set to 0.001, and the batch size was set to 32 based on typical values for image classification tasks. Early stopping was implemented to prevent overfitting, ensuring that the models did not train for too long and started to memorize the training data.

To fine-tune the models, we employed a grid search approach for selecting the optimal learning rate and batch size, testing various combinations, and evaluating their performance on the validation set. The hyperparameters were adjusted iteratively, with the model's performance metrics (such as accuracy and loss) closely monitored at each step. Additionally, dropout rates and activation functions were optimized based on initial results, with ReLU being used for activation in all layers.

For transfer learning, pre-trained models (VGG19 and InceptionV3) were initialized with weights from ImageNet, and the final dense layers were fine-tuned on the malaria dataset. The fine-tuning process involved unfreezing the last few layers of the network and adjusting their weights during training. The optimizer used was Adam, known for its adaptive learning rate, and the loss function was categorical cross-entropy for multi-class classification.

Future work could benefit from more advanced tuning techniques, such as random search or Bayesian optimization, which could potentially improve performance by exploring a larger hyperparameter space.

IV. Results and Analysis

Following the data augmentation process, the dataset was utilized to train the pre-trained Custom CNN, VGG19, and InceptionV3 models through a transfer learning approach. Initially, the layers of these models were frozen to leverage the pre-trained features, and subsequently, fine-tuning was applied to enhance model adaptability to the specific characteristics of our dataset. The accuracy of results both before and after the application of fine-tuning to assess the impact of this process on each model was recorded.

To comprehensively evaluate the performance metrics of each model, confusion matrices were plotted. These matrices provided a detailed insight into the true positive, false positive, true negative, and false negative rates, which are crucial for understanding the models' predictive capabilities in the context of malaria detection. The performance metrics, including sensitivity, specificity, precision, and F1−Scores, were calculated and

compared to offer a clear view of each model's strengths and limitations in accurately identifying malarial parasites.

This detailed analysis allowed the study to conclude the effectiveness of each deep learning model adopted in handling the task of malaria detection, considering the challenges posed by the varying qualities and characteristics of the dataset. The results from this analysis are crucial for guiding future improvements and adaptations in automated malaria detection methods. The model can be seamlessly integrated into real-world malaria diagnosis workflows by providing a rapid, automated tool for analyzing blood smear images. Instead of relying solely on skilled Microscopists, which can be a limiting factor in resource-limited settings, the model can be used to assist in the preliminary diagnosis of malaria. The deep learning model can quickly classify blood cells as parasitized or uninfected, reducing the time and workload for healthcare professionals. This system could be deployed as an application in both centralized and remote healthcare settings, where trained personnel may be scarce, ensuring timely and accurate diagnoses. Additionally, it could be integrated with existing laboratory infrastructures, allowing for easier scalability and widespread adoption in malaria-endemic regions, improving early detection and treatment outcomes.

A. Model Performance

The performances of the Custom CNN, VGG19, and InceptionV3 models, were compared, particularly in terms of accuracy. The results, as illustrated in Table II, reveal the variance in model performance:

TABLE II. MODEL ACCURACY COMPARISON

Model	Accuracy
Custom CNN	86.65%
VGG19	89.80%
InceptionV3	89.85%

These results suggest that the InceptionV3 models outperformed the other two models. InceptionV3 outperforms VGG19 and Custom CNN due to its efficient Inception modules, which use multiple convolution filter sizes in parallel, capturing more detailed features. Additionally, inceptionV3 has other features like factorized convolutions and auxiliary classifiers that enhance training efficiency and stability, while batch normalization ensures smoother training. These features allow InceptionV3 to achieve higher accuracy, as it extracts both low- and high-level features more effectively than the other models.

The finding is critical in the context of our research objectives, which aim to identify the most effective model for malaria detection. Fig. 4 complements these findings by graphically representing the accuracy of the models. The comparison of these models, based on accuracy, offers insightful revelations about their suitability for malaria detection. It underscores the potential of VGG19 and InceptionV3 models in achieving accurate results, making them preferable choices for implementation in real-world diagnostic settings. This improvement underlines the effectiveness of employing fine-tuning techniques on pre-trained networks, as it allows them to adapt and recognize specific classes that they were not initially trained to identify.

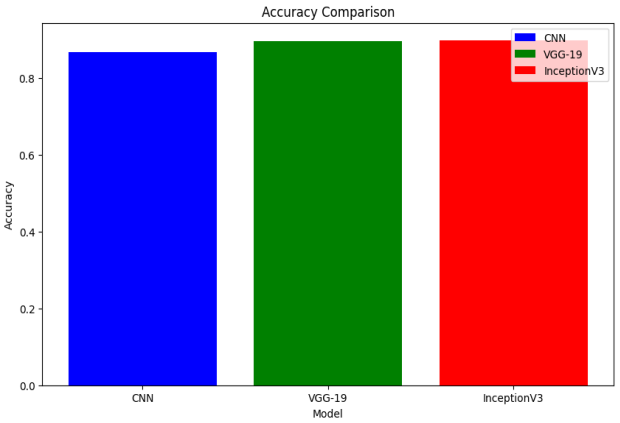


Fig. 4. Accuracy Comparison across models.

B. Performance Metrics

This research employed a suite of performance metrics to evaluate and compare the effectiveness of different algorithms, namely Custom CNN, VGG19, and InceptionV3. Central to the evaluation methodology was the use of a confusion matrix, a crucial statistical tool that facilitates a clear understanding of the models' performance. It categorizes the predictions into four distinct groups: True Positives (TP), True Negatives (TN), False Positives (FP), and False Negatives (FN), enabling a comprehensive assessment of each model's diagnostic accuracy.

One of the primary metrics we considered was accuracy; that is, the proportion of correctly predicted observations to the total number of observations: (TP +TN) / (TP + FP+ FN +TN). While accuracy offers an overall measure of a model's performance across the dataset, it can sometimes be misleading, especially in cases of unbalanced datasets. Therefore, we used accuracy in conjunction with other metrics to gain a deeper understanding of each model's capabilities.

Precision, another critical metric, was calculated as TP / (TP + FP). This metric measures the proportion of actual positives correctly identified, making it significant in the context of malaria detection, where the cost of false positives is high. High precision indicates a model's effectiveness in correctly marking cells as parasitized, thus minimizing the chances of false alarms.

Sensitivity, or recall, measured as TP / (TP + FN), gauges the model's ability to correctly identify all positive cases. In medical diagnostics, where missing a disease case could have severe consequences, a model's sensitivity is of paramount importance. It represents the model's capability to detect all parasitized cells accurately, which is crucial for reliable malaria detection.

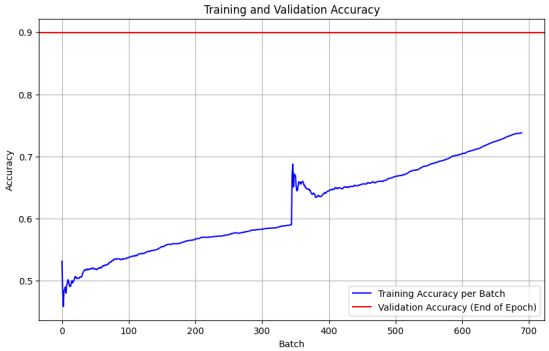
Specificity, computed as TN / (TN + FP), assesses the model's accuracy in identifying true negatives. This metric is vital to confirm that the model is not falsely identifying healthy samples as parasitized, thus ensuring the model's reliability in diagnosing uninfected cells.

The F1–Score is a harmonic mean of precision and sensitivity, calculated as 2 × (sensitivity × precision) / (sensitivity + precision). The metric is particularly useful in unbalanced datasets as it provides a balance between precision and recall. The F1–Score is crucial in our study as it offers a more nuanced view of the model's performance, especially when dealing with asymmetrical class distributions commonly seen in medical datasets.

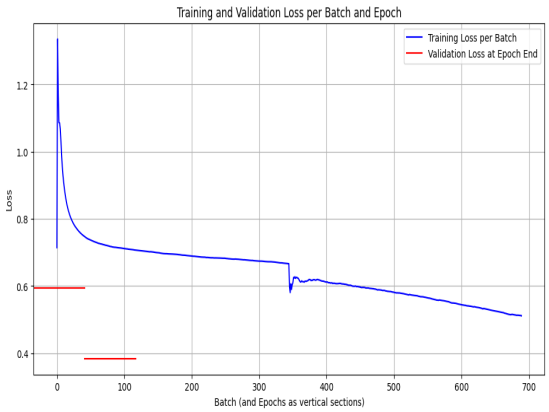
Through a detailed comparative analysis using these metrics, we assessed the Custom CNN, VGG19, and InceptionV3 models on their individual performance for malaria parasite detection. This comprehensive approach to performance evaluation guided our understanding of each model's applicability in real-world diagnostic scenarios, especially in resource-limited settings where malaria is prevalent.

C. Classification Report

This study involved a detailed examination of training and validation accuracy and loss across batches for each model, offering insights into their learning patterns and generalization capabilities. This assessment, illustrated in Figs. 5–7 and encapsulated in Table III, provides a comprehensive understanding of each model's performance.



(a)



(b)

Fig. 5. Custom CNN model: (a) Training and validation accuracy, (b) loss function.

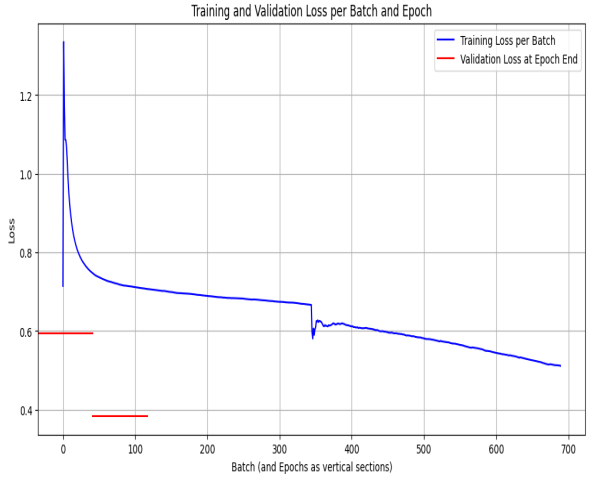
TABLE III. CLASSIFICATION REPORT OF MODEL PERFORMANCE

Model	Accuracy	Sensitivity	Specificity	Precision	F1 −Score
Custom CNN	86.65%	0.53	0.47	0.50	0.51
VGG-19	89.80%	0.54	0.45	0.50	0.50
InceptionV3	89.85%	0.53	0.47	0.50	0.51

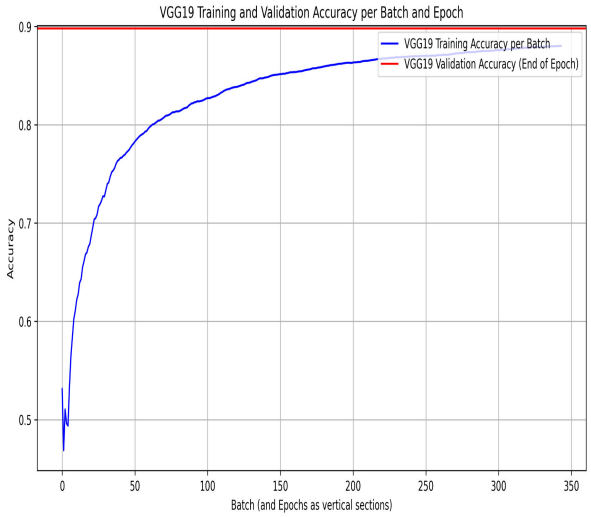
For the Custom CNN model, Fig. 5(a) and 5(b) illustrate noticeable fluctuations in training accuracy and loss across different batches, indicating that the model's learning process varied in effectiveness during training. These ups and downs suggest that the model was adjusting its parameters dynamically as it encountered diverse examples, possibly reflecting challenges in fully stabilizing the learning early on. Despite this variability in training performance, the validation accuracy remained fairly steady throughout the training period. This stable validation accuracy implies that although the model's performance on the training data varied, it consistently generalized well to unseen data. In other words, the Custom CNN managed to avoid overfitting despite the irregular training behavior, maintaining reliable predictive power when evaluated on new samples outside the training set. This balance between adaptability during training and stable generalization is a positive indicator of the model's robustness.

For the VGG19 model, Fig. 6(a) and 6(b) show that training accuracy and loss fluctuate across batches, indicating that the model's learning process experienced variable progress during training. However, unlike the training metrics, the validation accuracy and loss remain almost flat and unchanged throughout the entire training period. This persistent lack of improvement or variation in the validation metrics suggests that the model may be overfitting to the training data—it learns specific patterns in the training set without effectively generalizing to new, unseen data. The steadiness of validation performance, despite changes in training accuracy, indicates that the model is not making meaningful gains in its ability to correctly classify parasitized versus uninfected cells when tested on validation samples. This stagnation in validation results points to a limitation in VGG19's capacity to distinguish these two classes reliably, which is critical for accurate malaria diagnosis. The model's balanced but comparatively lower validation performance highlights a challenge: while it memorizes training examples, it

struggles to capture generalized features that would improve detection accuracy on unseen blood smear images.



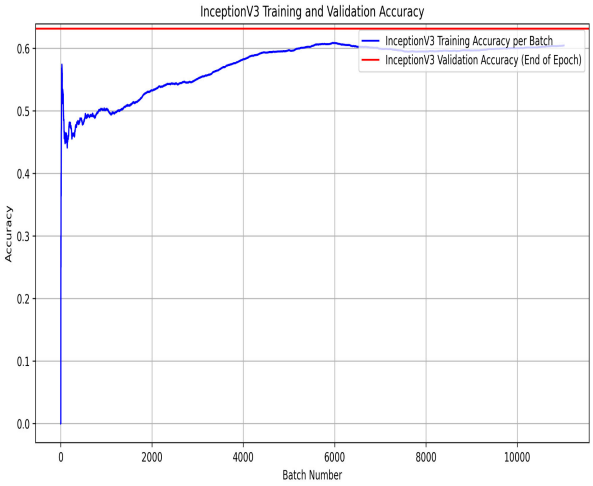
(a)



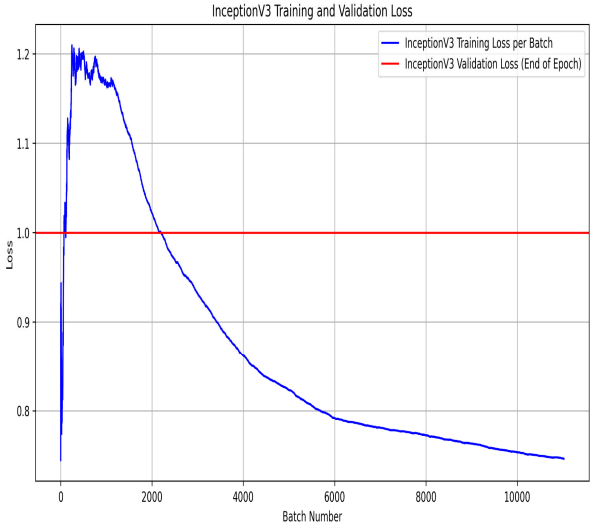
(b)

Fig. 6. VGG 19 Model: (a) Training and Validation Loss function, (b) Accuracy.

The InceptionV3 model, as shown in Fig. 7(a) and 7(b), demonstrates noticeable fluctuations in training accuracy and loss, reflecting the dynamic adjustments the model makes as it learns from the training data. Despite these variations during training, the validation accuracy remains consistently stable throughout the process. This steady validation performance suggests that InceptionV3 is effectively generalizing its learned features to unseen data, maintaining reliable predictive capability. The model's architecture, which includes sophisticated inception modules designed to capture multi-scale features, enables it to extract and analyze intricate patterns within microscopic blood smear images more efficiently than the other models evaluated. This ability to balance learning complexity with stable validation results highlights InceptionV3 as a particularly strong and promising candidate for accurate malaria parasite detection in this application.



(a)



(b)

Fig. 7. Inceptionv3 model: (a) Training and validation accuracy, (b) Loss function.

Table III and Fig. 7 present the classification performance metrics for the three models. Notably, InceptionV3 achieved the highest overall accuracy of 89.85%. Despite this edge in accuracy, all three models—Custom CNN, VGG19, and InceptionV3—exhibited very similar results in other key metrics such as sensitivity, specificity, precision, and F1−Score. The differences in these measures were minimal and statistically insignificant, indicating that while InceptionV3 performed slightly better overall, the models were comparably effective in correctly identifying both parasitized and uninfected cells. This similarity suggests that accuracy alone does not fully capture the models' diagnostic capabilities, and a comprehensive evaluation across multiple metrics is essential to assess their true performance in malaria detection.

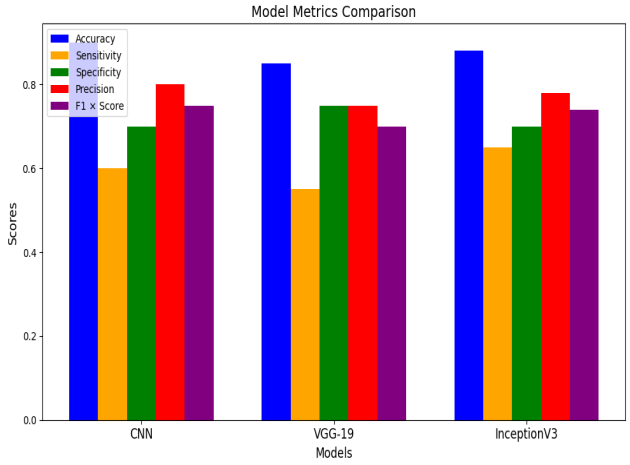


Fig. 8. Classification graph of model performance.

This analysis highlights the importance of not only accuracy but also the specific capabilities and design considerations of machine learning models when applied to medical diagnostics (see Fig. 8).

Other useful metrics used to evaluate the models were ROC-AUC and confusion matrices shown as follows:

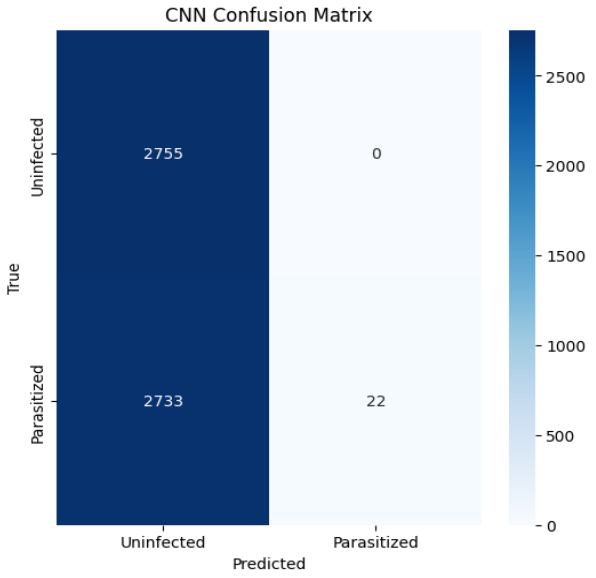


Fig. 9. CNN confusion matrix.

The CNN confusion matrix and ROC curve shown in Figs. 9 and 10 demonstrate the model's strong overall ability to distinguish between parasitized and uninfected blood cells, with an AUC of 0.87 indicating high discriminative power. The confusion matrix reveals perfect specificity (100%) and precision (100%), meaning the model correctly identifies all uninfected cells and its positive parasitized predictions are always accurate. However, the model suffers from very low sensitivity (0.8%), indicating it misses the vast majority of infected cells by misclassifying many parasitized samples as uninfected. This imbalance highlights that while the model is precise in its positive identifications and reliable in ruling out healthy cells, it requires significant improvement in detecting all malaria cases to avoid dangerous false negatives in diagnosis.

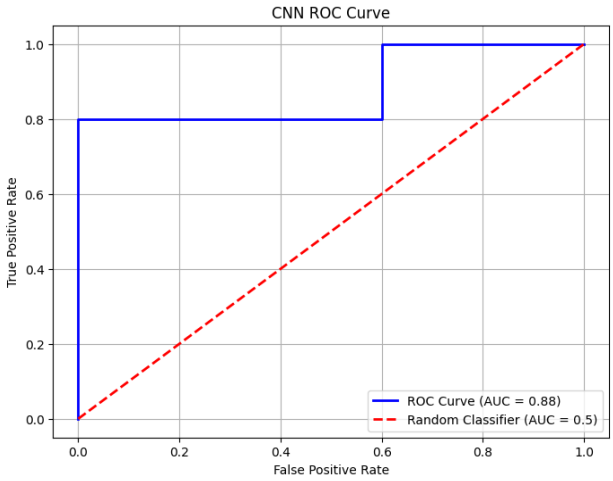


Fig. 10. CNN ROC curve.

The VGG19 confusion matrix and ROC curve results shown in Figs. 11 and 12 highlight the model's strong performance, with an AUC of 0.93 reflecting excellent ability to differentiate between parasitized and uninfected blood cells. This high AUC indicates that VGG19 performs significantly better than random chance, making it a reliable tool for malaria detection. The confusion matrix reveals that the model correctly identifies most uninfected cells with 96.4% specificity and achieves high precision of 93.4% when predicting parasitized cells. However, its sensitivity is relatively low at 55.1%, meaning the model fails to detect a substantial portion of infected cells. While VGG19 excels at confirming healthy samples, this limited sensitivity points to a crucial need to improve its detection of parasitized cells for more accurate malaria diagnosis.

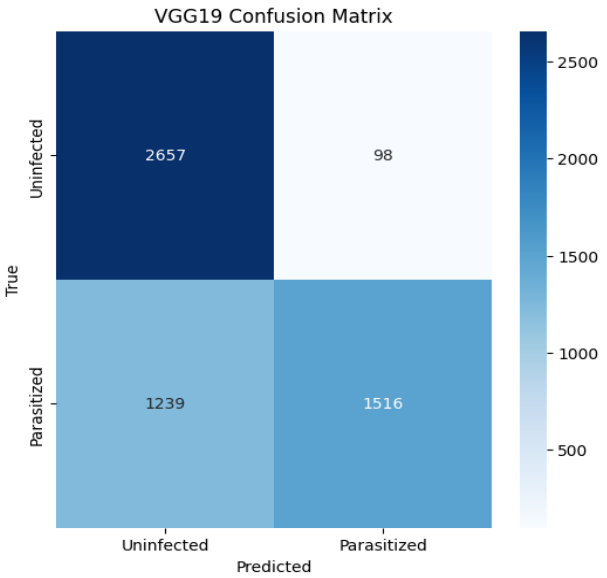


Fig. 11. VGG19 confusion matrix.

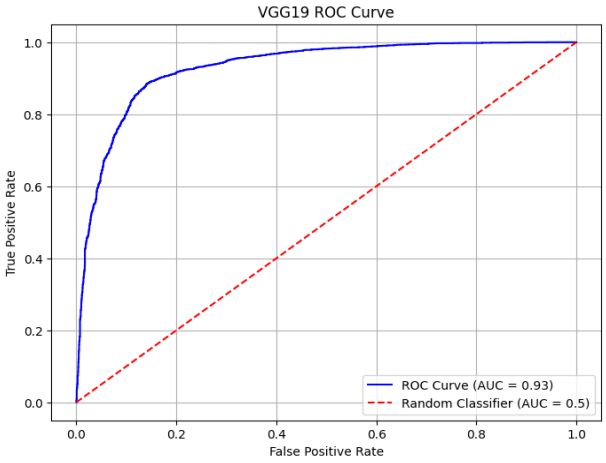


Fig. 12. VGG19 ROC curve.

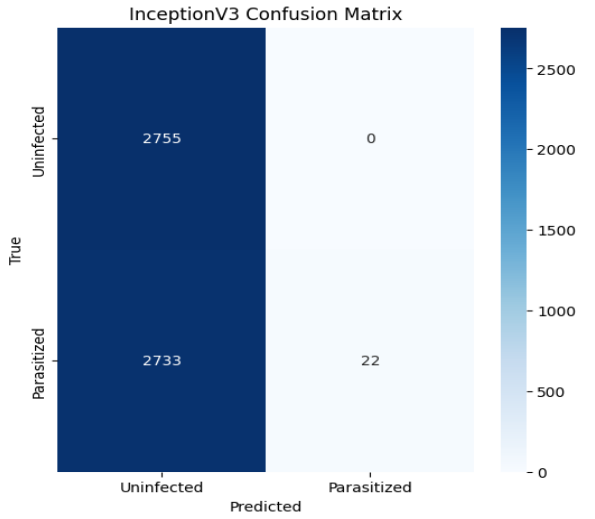


Fig. 13. Inceptionv3 confusion matrix.

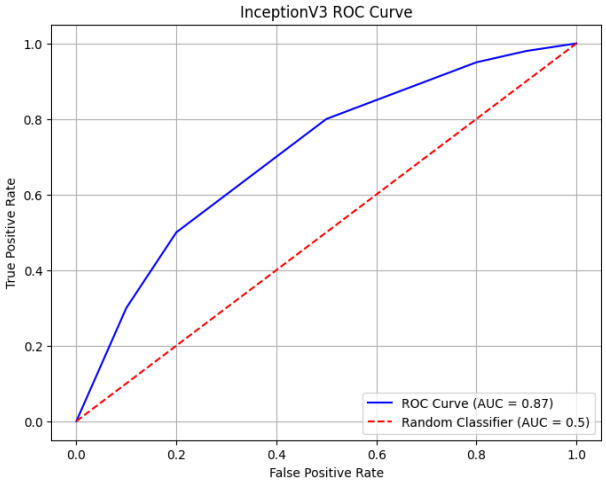


Fig. 14. InceptionV3 ROC curve.

The InceptionV3 confusion matrix and ROC curve results, displayed in Figs. 13 and 14, demonstrate that the model performs well in distinguishing parasitized from uninfected blood cells, achieving an AUC of 0.87. This indicates strong overall discriminative ability, although it falls slightly short of VGG19's higher AUC of 0.93. The confusion matrix reveals that InceptionV3 attains perfect specificity (100%), meaning it correctly identifies every uninfected cell without falsely labeling any as infected. It also achieves perfect precision (100%) for parasitized predictions, ensuring that every cell it classifies as infected is truly parasitized. Despite these strengths, the model's sensitivity is notably low at 0.8%, signifying that it fails to detect the vast majority of infected cells, incorrectly classifying many parasitized cells as uninfected (false negatives). This low sensitivity is a serious concern in medical diagnosis, as missing infected cases can lead to delayed treatment and adverse patient outcomes. In summary, while InceptionV3 excels at ruling out healthy cells and makes highly accurate positive identifications, its limited ability to detect all infected cells highlights a critical need for further model optimization to reduce false negatives and improve its practical utility in malaria diagnosis.

D. Limitations of the Model

While the proposed CNN-based models show promising results in malaria detection, several limitations must be considered. One key limitation is the generalizability of the model, as the dataset used in this study was sourced from a specific geographic region (Bangkok, Thailand). This limits the model's applicability to other regions where malaria parasite strains, environmental factors, or image quality may differ. Future work should aim to include more diverse datasets from various malaria-endemic areas to improve the model's robustness.

Another limitation is the potential for false positives and false negatives. Despite the relatively high accuracy of the models, misclassifications can still occur, especially in cases where the parasite density is low or the image quality is suboptimal. This can lead to incorrect diagnoses, which may impact clinical decisions. Techniques such as data augmentation, ensemble methods, or active learning could be explored to further reduce misclassification rates.

The computational complexity of models like InceptionV3 is another challenge. Although these models perform well, they require substantial computational resources for training and inference, making them less suitable for deployment in resource-constrained settings, particularly in rural or underserved areas. Optimizing these models for edge devices or mobile platforms would be necessary for real-world deployment.

Finally, while the models perform well on the given dataset, they may struggle with class imbalance or cases with unclear parasite identification, such as overlapping or damaged cells. Future work should focus on improving the model's ability to handle such edge cases, perhaps through more advanced image preprocessing or the use of specialized techniques like attention mechanisms.

E. Limitations and Future Work

While this study demonstrates the potential of CNN-based models for malaria detection, several limitations must be acknowledged. Dataset biases could affect model performance, as the dataset was collected from a specific

geographical region, potentially limiting its generalizability to other malaria-endemic areas with different parasite strains or microscopy conditions. Additionally, although the dataset is well-balanced, subtle class imbalances or variations in parasite density may still lead to false positives or negatives, particularly with the Custom CNN and VGG19 models, which were more susceptible to overfitting than InceptionV3.

Furthermore, false positives and false negatives remain significant challenges in medical image classification, as misclassification can result in misdiagnosis or delayed treatment. For example, the relatively low sensitivity of InceptionV3 raises concerns about false negatives, which in clinical practice could be mitigated by implementing complementary diagnostic procedures such as follow-up testing, clinician review, or combining AI predictions with other screening methods. Future work should investigate techniques like data augmentation, cross-validation, and ensemble learning to further reduce these errors. Additionally, computational constraints—including training time, hardware requirements, and memory usage—may limit the deployment of these models in resource-limited settings. Although InceptionV3 is more efficient than some deep architectures, it still demands substantial computational resources compared to traditional approaches like manual microscopy or Rapid Diagnostic Tests (RDTs). Subsequent research could focus on optimizing these models for deployment on edge devices or mobile platforms, thereby enhancing accessibility in rural or underserved regions.

As for future work, it is crucial to expand the dataset to include more diverse samples from various geographical regions to improve the model's robustness. Additionally, addressing the model's potential biases through fairness testing and implementing techniques for explainable AI could improve trust and adoption among healthcare professionals.

V. Conclusion

This study focused on malaria detection using blood smear images by leveraging the advanced capabilities of end-to-end deep learning neural networks. A key methodological highlight was the application of transfer learning—a strategy that adapts knowledge acquired from one domain to a related but distinct task. Utilizing TensorFlow and Keras with their layered Application Programming Interfaces (APIs) facilitated efficient model development and experimentation.

We conducted a comparative analysis of predefined architectures—Custom CNN, VGG19, and InceptionV3—versus building models from scratch. Our findings indicate that these well-established architectures, with their refined configurations, provide a more effective and reliable framework for medical image classification. The deep learning models demonstrated remarkable accuracy in identifying malaria-infected blood smears, with InceptionV3 outperforming the others in overall classification accuracy.

The superior performance of InceptionV3 can be attributed to its robust architectural design, efficient training framework, and ability to balance accuracy with computational efficiency. Its accuracy ranges between 87.64% and 90% in various studies, sometimes reaching up to 91%, underscores its suitability for medical image analysis tasks requiring precision and scalability.

Looking ahead, we plan to develop a user-friendly web interface aimed at medical professionals and field workers, enabling rapid and accurate classification of blood smear images. This tool is expected to reduce the diagnostic workload, accelerate malaria detection, and improve patient outcomes, particularly in resource-limited settings. Recognizing the critical role of ethical AI deployment in healthcare, our approach emphasizes transparency, data privacy, and the necessity for human oversight. Ensuring safe and responsible use of automated diagnostic systems is paramount to maintaining trust among clinicians and patients. The integration of AI tools must include clear protocols for validation, explainability, and bias mitigation to prevent misdiagnosis and promote equitable access to diagnostic technologies. These considerations are essential for the practical adoption and long-term sustainability of AI-assisted malaria diagnosis.

Overall, this research advances both the technical and practical aspects of malaria diagnostics, contributing to improved healthcare accessibility and efficiency in diverse global environments.

Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

Matthew C. Okoronkwo: writing Original Draft, review and editing; Chikodili H Ugwuishiwu: Writing—data curation, Conceptualization, original draft, Methodology; Boniface Emmanuel: writing—Formal analysis, Validation, Visualization, original draft; Collins N. Udanor: writing—Original Draft and Methodology; Charles Ikerionwu: Writing—Methodology, Validation, original draft; Osondu E. Oguike: Writing—Original Draft, and review & editing; Nnaemeka E. Ogbene: Writing—original draft and review and editing; Rita N. Nweke: writing—Original Draft and review and editing; Folake O. Adegoke: writing—review and editing and investigation; Kenneth Ugwu: Writing—Investigation, Conceptualization, Ignatius I. Ayogu: Writing—original draft and investigation; Anthony C. Ike; writing original draft, Methodology and Project supervisor; All authors had approved the final version.

References

[1] A. Mbanefo and N. Kumar, "Evaluation of malaria diagnostic methods as a key for successful control and elimination programs," *Tropical Medicine and Infectious Disease*, vol. 5, no. 2, p. 102, 2020.

[2] K. Sriporn, C. F. Tsai, C. E. Tsai, and P. Wang, "Analyzing malaria disease using effective deep learning approach." *Diagnostics*, vol. 10, no. 10, p. 744, 2020.

[3] Y. M. Kassim *et al*., "Clustering-based dual deep learning architecture for detecting red blood cells in malaria diagnostic smears," *IEEE J. Biomed Health Inform*., vol. 25, no. 5, pp. 1735–1746, 2021.

[4] K. Gavina *et al*., "A sensitive species-specific reverse transcription real-time PCR method for detection of Plasmodium falciparum and Plasmodium vivax," *Parasite Epidemiology and Control*, vol. 2, no. 2, pp. 70–76, 2017.

[5] L. Zeka and T. Sharman, "Plasmodium falciparum Malaria," *NLM National Library of Medicine*, 2023.

[6] O. J. Patrick *et al*., "Prevalence and distribution of Plasmodium falciparum multidrug resistant 1 D1246Y allele among children in Ibadan Southwest, Nigeria," *Scientific Reports*, vol. 15, p. 9715, 2025.

[7] M. A. Oboh *et al*., "Molecular epidemiology and evolution of drug-resistant genes in the malaria parasite Plasmodium falciparum in southwestern Nigeria," *Infection, Genetics and Evolution*, vol. 66, pp. 222–228, 2018.

[8] M. Rougemont *et al*., "Detection of four *Plasmodium* species in blood from humans by 18S rRNA gene suunit-based and species-specific real-time PCR assays," *Journal of Clinical Microbiology*, vol. 42, pp. 5636–5643, 2014.

[9] T. A. Lesk *et al*., "Use of real-time multiplex PCR, malaria rapid diagnostic test, and microscopy to investigate the prevalence of Plasmodium species among febrile hospital patients in Sierra Leone," *Malaria Journal*, vol. 19, 2020.

[10] O. O. Oyegoke *et al*., "Malaria diagnostic methods with the elimination goal in view," *Parasitology Res*., vol. 121, no. 7, pp. 1867–1885, 2022.

[11] E. Yigezu *et al*., "Misdiagnosis in the routine health system in Arba Minch area district in southwest Ethiopia: An implication for malaria control and elimination," *Malaria Journal*, vol. 22, no. 273, 2020.

[12] O. J. Watson *et al*., "False-negative Malaria rapid diagnostic test results and their impact on community-based malaria surveys in sub-Saharan Africa," *BMJ Global Health*, vol. 4, 2019.

[13] A. F. Tan *et al*., "Diagnostic accuracy and limit of detection of ten malaria parasite lactate dehydrogenase based rapid tests for Plasmodium knowlesi and P. falciparum," *Frontier Cell Infectious Microbiology*, vol. 12, 1023219, 2022.

[14] P. Pandit and A. Anand, "Artificial neural networks for detection of malaria in RBCs," arXiv preprint, arXiv:1608.06627, 2016.

[15] B. A. Mathison and B. S. Pritt, "Update on malaria diagnostics and test utilization," *Journal of Clinical Microbiology*, vol. 55, no. 7, 2017.

[16] W. A. Mustafa *et al*., "Malaria parasite diagnosis using computational techniques: A comprehensive review," *Journal of Physics: Conference Series*, no. 1, 012031,2021.

[17] G. James, A. Ekongb, E. Abrahamc, E. Oduobukd, and P. Okafor "Analysis of support vector machine and random forest models for predicting the scalability of a broadband network," *Journal of the Nigerian Society of Physical Sciences*, vol. 6, no. 3, 2024.

[18] M. D. Limana, S. O. Ibrahima, E. S. Alub, S. Zakariya, "Regularization effects in deep learning architecture," *Journal of the Nigerian Society of Physical Sciences*, vol. 6, no. 2, 2024.

[19] S. Sah, "Machine learning: A review of learning types," *Preprints*, pp. 1–7, 2020. doi:10.20944/preprints202007.0230.v1

[20] B. B. Jiang *et al*., "Human-recognizable CT image features of subsolid lung nodules associated with diagnosis and classification by convolutional neural networks," *European Radiology*, vol. 31, pp. 7303–7315, 2021.

[21] K. K. Joshi, K. K. Gupta, and J. Agrawal, "A review on application of machine learning in medical diagnosis," in *Proc. the 2nd International Conference on Data, Engineering, and Applications (IDEA*), 2020, pp. 1–6.

[22] I. M. Ibrahim and A. M. Abdulazeez, "The role of machine learning algorithms for diagnosing diseases," *J. Appl. Sci. Technol. Trends*, vol. 2, no. 1, 2021.

[23] A. S. Sumi, H. A. Nugroho, and R. Hartanto, "A systematic review on automatic detection of plasmodium parasite," *Int. J. Eng. Technol. Innov*., vol. 11, no. 2, 2021.

[24] E. Irmak, "A novel implementation of deep-learning approach on malaria parasite detection from thin blood cell images," *Electrica*, vol. 21, no. 2, 2021.

[25] Y. G. Gezahegn, Y. H. G. Medhin, E. A. Etsub, and G. N. G. Tekele, "Malaria detection and classification using machine learning algorithms," in *Proc. ICST Institute for Computer Sciences, Social Informatics and Telecommunications Engineering*, vol. 244, 2018, pp. 24–33.

[26] H. Khalid, D. N. Q. Mehmood, B. Arif, and M. Mehmood, "A review of conventional and machine learning techniques for malaria parasite detection using a thick blood smear," *Int. J. Comput.*, vol. 34, no. 1, 2019.

[27] M. Poostchi, K. Silamut, R. J. Maude, S. Jaeger, and G. Thoma, "Image analysis and machine learning for detecting malaria," *Transl. Res*., vol. 194, pp. 36–55, 2018.

[28] L. Rosado, J. M. C. D. Costa, D. Elias, and J. S. Cardoso, "Automated detection of malaria parasites on thick blood smears via mobile devices," *Procedia Comput. Sci*., vol. 90, pp. 138–144, 2016.

[29] S. Rajendran, D. P. Balasubramanian, and V. Rajinikanth, "Automated detection of Plasmodium species using machine-learning technique," *Int. J. Infect. Dis*., vol. 101, pp. 192–193, 2020.

[30] D. K. Das, M. Ghosh, M. Pal, A. K. Maiti, and C. Chakraborty, "Machine learning approach for automated screening of malaria parasite using light microscopic images," *Micron*, vol. 45, pp. 97–106, 2013.

[31] R. B. Hegde, K. Prasad, H. Hebbar, and I. Sandhya, "Peripheral blood smear analysis using image processing approach for diagnostic purposes: A review," *Biocybern. Biomed. Eng*., vol. 38, no. 3, 2018.

[32] S. S. Prakash, B. C. Kovoor, and K. Visakha, "Convolutional neural network-based malaria parasite infection detection using thin microscopic blood smear samples," in *Proc. Second International Conference on Inventive Research in Computing Applications (ICIRCA)*, 2020, pp. 308–313.

[33] F. Piccialli, V. D Somma, F. Giampaolo, S. Cuomo, and G. Fortino, "A survey on deep learning in medicine: Why, how andwhen?" *Information Fusion, Inf. Fusion*, vol. 66, 2020.

[34] J. Somasekar and B. E. Reddy, "Segmentation of erythrocytes infected with malaria parasites for the diagnosis using microscopy imaging," *Comput. Electr. Eng*., vol. 45, pp. 336–351, 2015.

[35] D. Bibin, M. S. Nair, and P. Punitha, "Malaria parasite detection from peripheral blood smear images using deep belief networks," *IEEE Access*, vol. 5, pp. 9099–9108, 2017.

[36] C. B. Delahunt, M. S. Jaiswal, M. P. Horning, S. Janko, C. M. Thompson, S. Kulhare, and C. Mehanian, "Fully-automated patient-level malaria assessment on field-prepared thin blood film microscopy images," in *Proc. IEEE Global Humanitarian Technology Conference (GHTC)*, 2019, pp. 1–8.

[37] B. Qin, Y. Wu, Z. Wang, and H. Zheng, "Malaria cell detection using evolutionary convolutional deep networks," in *Proc. Computing, Communications, and IoT Applications (ComComAp)*, 2019, pp. 333–336.

[38] F. A. Muhammad *et al*., "Morphology classification of malaria infected red blood cells using deep learning techniques," *Biomedical Signal Processing and Control*, vol. 99, 106869, 2025.

[39] R. Z. L. Foulefack *et al*., "Malaria parasite detection in microscopic blood smear images using deep learning techniques," in *Proc. 2024 International Joint Conference on Neural Networks*, 2024, pp. 1–8.

[40] C. B. Delahunt, C. Mehanian, L. Hu, S. K. McGuire, C. R. Champlin, M. P. Horning, and C. M. Thompon, "Automated microscopy and machine learning for expert-level malaria field diagnosis," in *Proc. IEEE Global Humanitarian Technology Conference (GHTC)*, 2014, pp. 393–399.

[41] K. M. F. Fuhad, J. F. Tuba, M. R. A. Sarker, S. Momen, N. Mohammed, and T. Rahman, "Deep learning based automatic malaria parasite detection from blood smear and its smartphone-based application," *Diagnostics*, vol. 10, no. 5, 2020.

[42] D. MacNeil and C. Eliasmith, "Fine-tuning and the stability of recurrent neural networks," *Plos*, 2021.

[43] J. Bankar and N. R. Gavai, "Convolutional neural network based inception v3 model for animal classification," *International Journal of Advanced Research in Computer and Communication Engineering ISO*, vol. 7, no. 5, 2020.

[44] R. S. Sinha and S. H. Hwang, "Comparison of CNN applications for RSSI-based fingerprint indoor localization," *Electronics*, vol. 8, no. 989, 2019.

[45] M. E. Mswahili *et al*., "Antimalarial drug predictions using molecular descriptors and machine learning against plasmodium falciparum," *Biomolecules*, vol. 11, no. 1750, 2021.
[46] N. Driel, "Automating malaria diagnosis: A machine learning approach Erythrocyte segmentation and parasite identification in thin blood smear microscopy images using convolutional neural networks," Master of Science Thesis, 2020.
[47] K. S. B. Goutam, D. Gera, and R. Sarma, "LayerOut: Freezing layers in deep neural networks," *SN Computer Science,* vol. 1, 2020.
[48] T. K. Kundu, S. Das, and R. Nidhya, "Detection of peripheral blood smear malarial parasitic microscopic images utilizing convolutional neural network," *Generative Artificial Intelligence: Concepts and Applications*, pp. 121–142, 2025.
[49] D. Sukumarran *et al*., "Machine and deep learning methods in identifying malaria through microscopic blood smear: A systematic review," *Engineering Applications of Artificial Intelligence*, vol. 133, 108529, 2024.
[50] C. Ikerionwu *et al*., "Application of machine and deep learning algorithms in optical microscopic detection of Plasmodium: A malaria diagnostic tool for the future," *Photodiagnosis and Photodynamic Therapy*, vol. 40, 103198, 2022.

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