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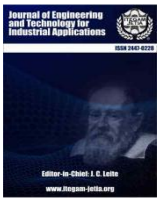

RESEARCH ARTICLE OPEN ACCESS

DEVELOPMENT OF MALARIA DIAGNOSIS WITH CONVOLUTIONAL NEURAL NETWORK ARCHITECTURES: A CNN-BASED SOFTWARE FOR ACCURATE CELL IMAGE ANALYSIS

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ABSTRACT

This study emphasizes that early diagnosis and treatment of malaria is critical in reducing health problems and mortality from the disease, especially in developing countries where the disease is prevalent. Malaria is a potentially fatal disease transmitted to humans by mosquitoes infected by a blood parasite called Plasmodium. The traditional method of diagnosis relies on experts examining red blood cells under a microscope and is inefficient as it is dependent on expert knowledge and experience. Nowadays, machine learning methods that provide high accuracy are increasingly used in disease detection. In this paper, a Convolutional Neural Network (CNN) architecture is proposed to distinguish between parasitized and non-parasitized cells. In addition, the performance of the proposed CNN architecture is compared to pre-trained CNN models such as VGG-19 and EfficientNetB3. The studies were carried out using the Malaria Dataset supplied by the National Institute of Health (NIH), and our proposed architecture was shown to function with 99.12% accuracy. The results of the study reveal that it is effective in improving the accuracy of cell images containing Plasmodium. In addition, a software that predicts whether cell images are noisy or not has been developed.

I. INTRODUCTION

Malaria is a disease that threatens health systems and affects millions of people, especially in developing countries [1]. Caused by Plasmodium parasites spread through mosquito bites, this disease can kill many people, especially children, if not treated in time. According to the World Health Organization (WHO), the majority of malaria cases occur in Africa and mortality rates are quite high. Children under five are particularly vulnerable to the disease [2]. Therefore, rapid and accurate diagnosis is crucial to prevent the spread of malaria and save lives.

Traditional methods of malaria diagnosis, such as microscopic examination and laboratory tests, are laborious and costly. Furthermore, as the clinical symptoms of malaria are non-specific, they can be confused with other diseases and lead to misdiagnosis [3],[4]. Therefore, early diagnosis and treatment are critical for assessing the severity of the disease and preventing fatal outcomes. However, factors such as limited resources, lack of information and insufficient scientific research pose serious challenges in malaria treatment, especially in developing countries [5]. At this point, computer-aided systems, artificial intelligence and open-source technologies are emerging as a unique tool to assist experts in the diagnosis and evaluation of malaria [6],[7].

Today, Deep Learning (DL) and Machine Learning (ML) techniques offer great potential in malaria diagnosis thanks to their ability to process large datasets, recognize complex patterns, and make rapid diagnoses [8]. Deep learning models are able to identify Plasmodium parasites in medical images, minimizing human error and speeding up the diagnosis process, thus providing an important second opinion in medical diagnosis processes and helping doctors. In this context, Computer Aided Diagnosis (CAD) and deep learning-based models in medical images have attracted much attention from researchers in recent years [9]. Such models can be trained on large datasets to recognize Plasmodium parasites, thus enabling faster and more accurate malaria diagnosis [10].

The aim of this study is to go beyond traditional malaria diagnosis methods and evaluate the performance of deep learning architectures in malaria diagnosis. A comprehensive review is presented on how these technologies can be used in clinical applications and how they can improve accuracy in malaria diagnosis. For this purpose, a cell image analysis application was developed with models trained on the dataset. This application aims to make a significant contribution to the early diagnosis and control of malaria by providing experts with a real-time and accurate diagnosis.

This paper aims to show how convolutional neural networks (CNNs), a deep learning architecture, can be used effectively and reliably in malaria detection from cell images and how a software application can support experts in diagnosis. This research demonstrates the potential of artificial intelligence in malaria diagnosis, providing a faster, reliable and cost-effective alternative to current diagnostic methods.

The rest of the paper is organized as follows: Section 2 is the literature review; Section 3 presents the dataset and methods used in the study; Section 4 presents the experimental results obtained; and Section 5 contains conclusions and general remarks.

II. LITERATURE REVIEW

Addressed the problem of misdiagnosis in malaria diagnosis in Nigeria and applied various machine learning models with age, gender and 15 symptom data of 337 patients. The Adaboost model showed the best performance with 98.2% accuracy and 96.6% precision; they concluded that this model can be used in decision support systems [11]. Aimed to overcome the limitations of traditional methods by using artificial neural networks and especially CNN for early diagnosis of malaria. With 1,920 blood smear images from 84 patients, CNN showed the highest success with 99.59% accuracy. The study reveals that CNN is an effective method for accurate diagnosis of malaria [12]. Developed an artificial intelligence-based system for the detection of malaria parasites with microscopic images. MobileNetV2 achieved the highest accuracy and ResNet152V2 achieved the lowest loss value. DenseNet121 provided the best results in terms of precision, recall and F1 score [13].

Developed a model using Inception and Capsule networks to detect malaria parasites from microscopic images. The system provides faster and more accurate results than conventional microscopy [14]. Used machine learning methods for malaria and breast cancer detection in this study. CNN, ResNet50 and VGG16 models were used for malaria detection and the highest accuracy was 94.73% with CNN. For breast cancer detection, the highest accuracy was found in ResNet50 with 95.53% in tests with the same models [15].

In this study, Anita et al. combined the Deep-CNN model with Random Forest (RF) for the detection of malaria parasites. By using Global Average-Pooling (GAP) layer and Canny edge detection, they better visualized the interference areas. Experimental results showed that the proposed model outperformed existing methods on malaria parasite datasets [16]. Alessandra et al. used machine learning to predict clinical outcomes in imported malaria patients. In their analysis, AST, platelet count, total bilirubin and parasitemia were associated with adverse outcomes. These parameters are not included in the WHO criteria for severe malaria. The study demonstrates the potential of ML algorithms to provide clinical decision support [17].

Developed a NASNet-based model for early diagnosis of malaria. The model combines NASNet and Random Forest methods for feature engineering, working with images of parasitized and healthy red blood cells. Support vector machines showed the best performance with 99% accuracy. This approach can help reduce mortality rates by improving malaria diagnosis [18]. Propose an IoT-based system for malaria detection. The system collects real-time symptom data with wearable sensors, processes the data using edge computing and cloud infrastructure, and analyzes it with machine learning. Four machine learning techniques were compared and Support Vector Machines (SVM) achieved 98% training accuracy, 96% testing accuracy and 95% AUC score with the highest accuracy. This system promises to accurately diagnose malaria cases [19]. Developed ML methods to predict clinical outcomes in imported malaria patients.

The study found that AST, platelet count, total bilirubin and parasitemia were associated with adverse outcomes, and aminotransferase and platelet were not included in the WHO criteria [20]. Propose a deep learning based method called EfficientNet for malaria detection. This approach detects malaria parasites using red blood cell images. Experiments showed that the proposed method is effective in malaria detection with 97.57% accuracy [21].

Succeeded in identifying malaria parasites in microscopic blood images with 96.73% accuracy using a CNN model called MozzieNet. Using data augmentation and hyperparameter optimization, the model demonstrated strong performance and was designed to help malaria diagnosis in remote areas [22]. According to [23] developed the miLab™ device, which achieved 98.86% accuracy in malaria diagnosis.

This device consistently prepared blood films with digital microscopy and detected malaria parasites with deep learning. It achieved 92.21% agreement in clinical tests. Evaluated the use of machine learning and deep learning methods in malaria diagnosis by reviewing 50 articles between 2015 and 2023. While most of the research focused on binary classification, multi-stage classification and dataset cross-validation were missing.

This study provides classification models that can accurately predict malaria types and recommendations for future research [24]. According to [25] improved the YOLOv5 framework, achieving 99.2% accuracy, 98.7% precision and 98.5% sensitivity in malaria diagnosis.

They replaced the C3 module with C3TR structure and improved PANet with Bi-directional Feature Pyramid Network, which outperformed existing methods. Developed MILISMA, a deep learning-based model, for the diagnosis of malaria anemia (SMA) in sub-Saharan Africa. The model detected morphologically altered red blood cells (RBCs), achieving 83% accuracy, 87% AUC and 76% precision-recall AUC. MILISMA helps to improve diagnostic and prognostic processes by identifying SMA-related RBC alterations [26].

III. MATERIALS AND METHODS

In this study, a model based on convolutional neural networks is proposed for the classification of malaria disease, consisting of two classes. The National Institutes of Health (NIH) in the United States provided an open-access dataset from which the photos used to validate the suggested method were taken. 27,558 cell pictures in all, including equal numbers of cells with and without parasites, are included in the dataset [27]. The Mahidol-Oxford Tropical Medicine Research Unit experts annotated every photograph included in the dataset.

The dataset is randomly divided into 80% for training and 20% for test samples of each class. Table 1 shows the distribution of images for each class for training, validation, and testing. Figure 1 shows randomly selected parasitized cell samples from the dataset, while Figure 2 shows images of unparasitized cell samples.

Table 1: Distribution of training, validation, and test sets.

Dataset Type	**Number of Parasitised Sample**	**Number of Unarasitised Sample**	**Total**
Training	8818	8818	17636
Validation	2205	2205	4410
Test	2756	2756	5512
Total Data			27558

Source: Authors, (2024).

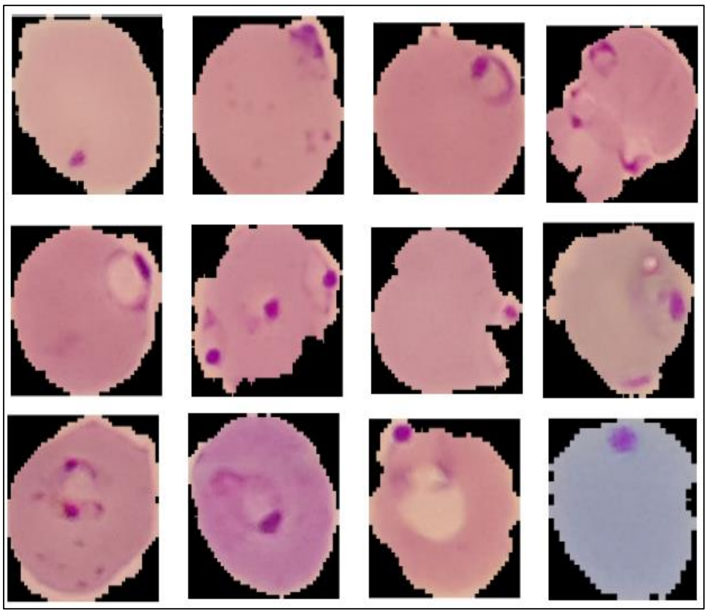


Figure 1: Parasitized cell samples.
Source: Authors, (2024).

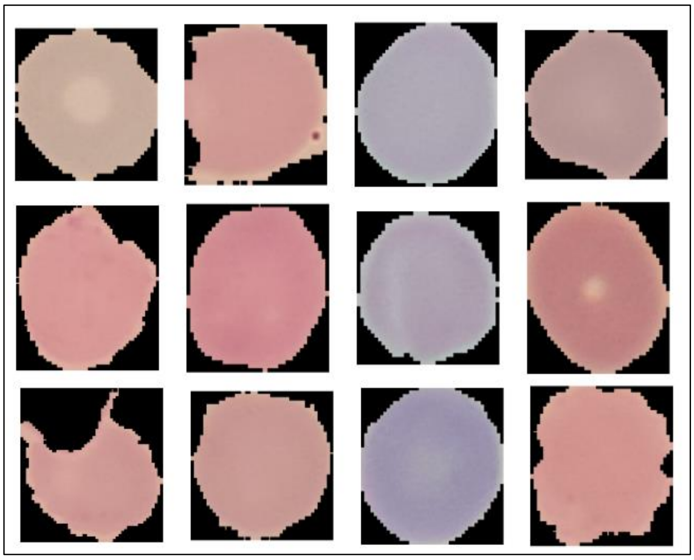


Figure 2: Unparasitized cell samples.
Source: Authors, (2024).

III.1 CONVOLUTIONAL NEURAL NETWORKS

Convolutional Neural Networks (CNN) are one of the deep learning models used in computer vision and pattern recognition. Basically, it is a specialized neural network architecture that can work effectively on visual data. CNNs consist of a series of convolutional layers that divide an image into small, overlapping regions and learn the features in these regions. These features represent specific patterns in the input images. The convolution and pooling layers create the feature maps and reduce their size. This allows the network to learn more complex features using fewer parameters in the learning process. CNNs are often successfully used in object recognition, face recognition, and other visual tasks [9],[28]. Figure 3 shows the architecture of a convolutional neural network.

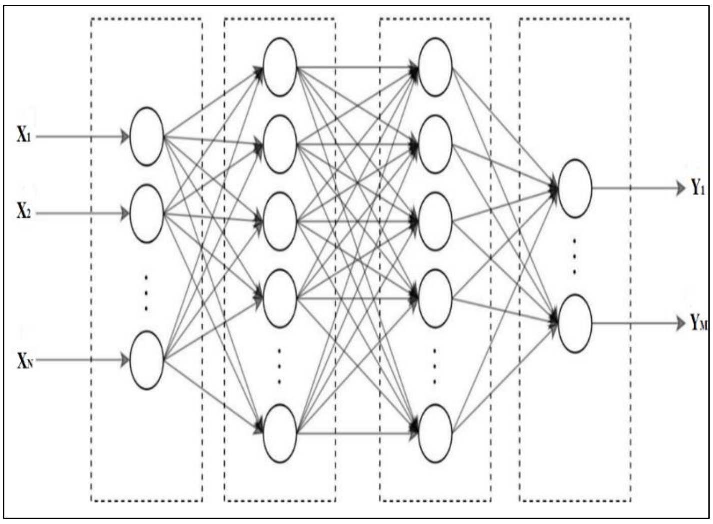


Figure 3: Convolutional Neural Network Architecture.
Source: Authors, (2023).

VGG19, developed by the Visual Geometry Group (VGG), is one of the most prominent convolutional neural network (CNN) models in deep learning. It was widely recognized for its impressive performance at the ImageNet Large Scale Visual Recognition Challenge in 2014. VGG19 has a deep architecture with a total of 19 layers. The main features of the architecture are a recurrent structure consisting of successive convolution layers followed by pooling layers. In particular, convolution layers with 3x3 filter sizes increase the ability to learn more complex features through the sequential use of small-sized filters. The VGG19 model has a structure that terminates with fully connected layers, which are used to classify the learned features. Furthermore, ReLU activation functions are generally preferred in VGG19. This model was one of the initial and referenced models in the deep learning community. However, due to its large parameter count and computational intensity, VGG19 has played a critical role in the evolution of deep learning architectures, although nowadays lighter and morescalable models have grown in popularity [29].

EfficientNetB3 is a high-performance neural network model designed for computer vision tasks in the deep learning domain. The EfficientNet series aims to provide efficient and scalable models, especially by using a scaling strategy that optimizes factors such as model size, depth, and width in a balanced way. EfficientNetB3 is a version that follows this strategy and has a larger size than previous EfficientNet models. The model includes specialized components such as convolution layers, mobile learning blocks, and expanding blocks. This enables the network to gain more learning capacity and extract visual features more effectively. EfficientNetB3 has achieved high accuracy rates on the ImageNet dataset and other visual recognition tasks. This model is considered an important step in the effort to optimize the size and performance trade-off of deep learning models [6].

III.2 PROPOSED MODEL

The three steps of the suggested method are feature extraction, data preparation, and classification. Figure 6 graphically depicts these phases. Preprocessing data is a useful tactic for enhancing image quality. Numerous noise sources, such as camera angle and microscope position, might contaminate images. To lessen picture noise, images were cleaned using a variety of techniques. In order to effectively categorize infected and non-infected photos for malaria detection, we have developed a CNN model. First, 4 convolutional layers with 2x2 filter sizes were used to process the 50 × 50 × 3 dimensional input images, followed by 4 maximum pooling layers of size 2x2. ReLU was chosen as the activation function. Finally, 1 Flatten layer, 2 Dropout layers, and 2 Dense layers were used to smooth the data. A Sigmoid activation function is applied to the output layer. It is seen that all of these parameters are trained. The block diagram of the proposed method is given in Figure 4.

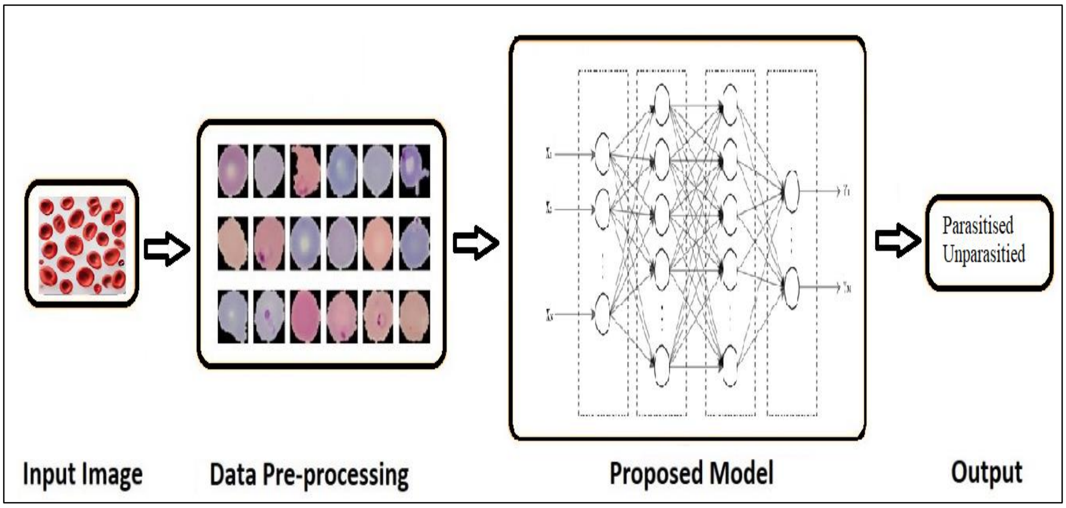


Figure 4. Block diagram of our proposed model.
Source: Authors, (2024).

The confusion matrix and classification assessment criteria derived from the confusion matrix are used to assess the classification performance of the suggested approach. The evaluation criteria consist of F1-score, recall, accuracy, and precision. The criteria are as follows: True Positive (TP), True Negative (TN), False Negative (FN), and False Positive (FP) numbers make up a confusion matrix. In this work, TP happens when a certain parasitic cell's class is accurately predicted by the classifier. When a cell picture is determined by the classifier to not be a member of a particular class of parasitic cells, TN happens. FP happens when a negative sample is mistakenly predicted as positive by the classifier. When a positive sample is mistakenly predicted as negative by the classifier, FN occurs.

The ratio of the number of test samples correctly classified according to each cell type to the total number of test samples is denoted by accuracy and calculated as in Equation (1).

$$\text{Accuracy} = \frac{TP+TN}{TP+FP+FN+TN} \qquad (1)$$

The ratio of the number of positive samples correctly classified by each cell type to the number of actual observed positive samples is denoted by recall, and calculated as in Equation (2).

$$\text{Recall} = \frac{TP}{TP+FN} \qquad (2)$$

The number of positive samples correctly classified by each cell type and the number of samples classified as positive samples are determined by precision and calculated as in Equation (3).

$$\text{Precision} = \frac{TP}{TP+FP} \qquad (3)$$

The F1-score corresponds to the harmonic mean of the precision and recall ratios. The F1-score takes a value between 0 and 1. The better performance of each cell classification model corresponds to a higher F1-score and is calculated as in Equation (4).

$$\text{F1} = 2\text{x}\frac{Precision\ x\ Recall}{\text{Precision}+\text{Recall}} \qquad (4)$$

IV. EXPERIMENTAL RESULTS

This chapter presents the results obtained using the materials and methods presented in the previous chapter. The study involves the classification of human red blood cell images as parasitized or unparasitized by the Plasmodium parasite. CNN architectures are used to detect whether the blood cell is parasitized or not. In this study, experiments were conducted with the pre-trained CNN architectures VGG-19, EfficientNetB3, and our proposed CNN model. The confusion matrices for each model as a result of the experiments are given in Figure 5-7 respectively.

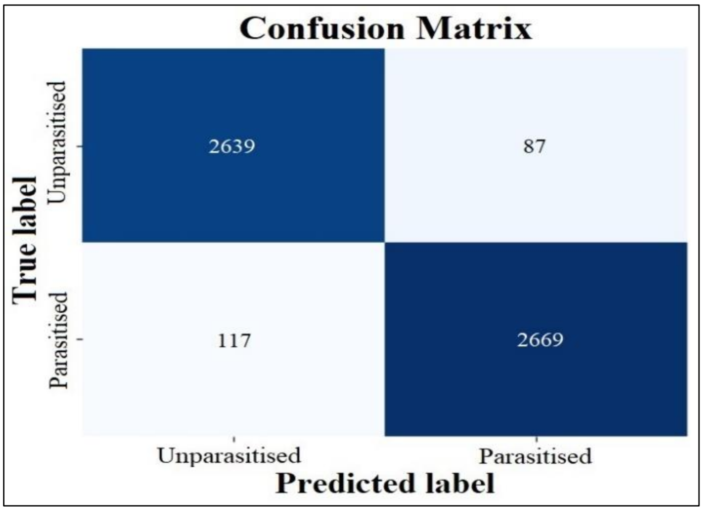


Figure 5: VGG19 Confusion Matrix.
Source: Authors, (2024).

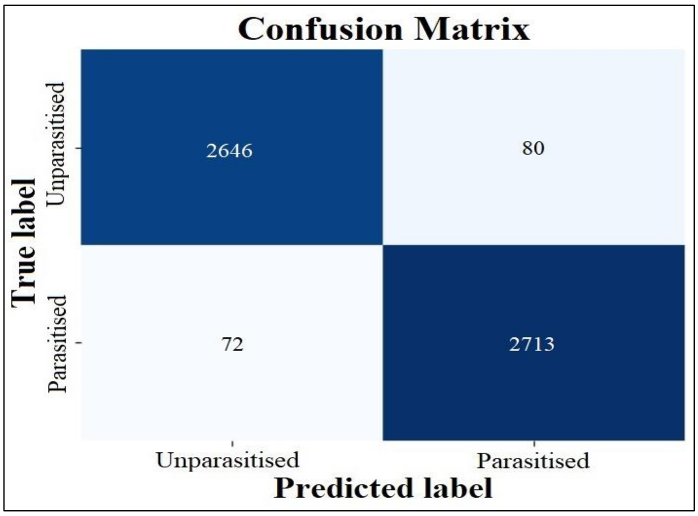


Figure 6: EfficientNetB3 Confusion Matrix.
Source: Authors, (2024).

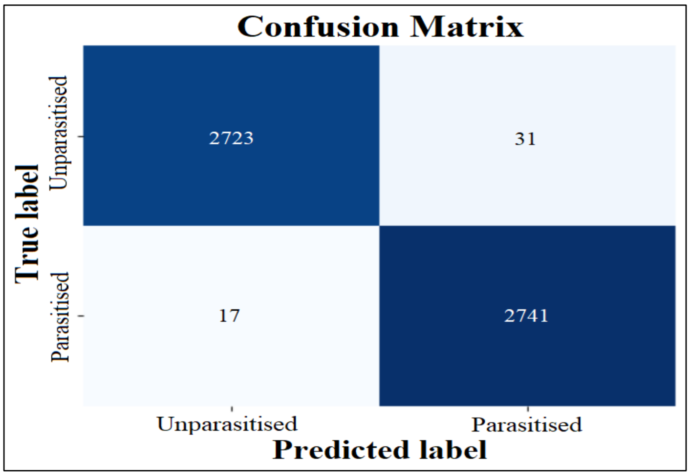


Figure 7: Proposed Model Confusion Matrix.
Source: Authors, (2024).

In this study, we conducted a comparative analysis to evaluate the performance of various deep learning-based classification methods for malaria cell categorization. The pre-trained architectures considered for evaluation include VGG19, InceptionResNetV2, DenseNet121, EfficientNetB3, and our proposed CNN model. Each model was fine-tuned and assessed using the National Institutes of Health open-access dataset, a widely recognized benchmark in the field of malaria diagnosis. The classification performance of the proposed image classification method is compared with pre-trained CNN-based methods in terms of accuracy, precision, recall, and F1-score as shown in Table 2.

Table 2: Comparison of the model results

Methods	**Accuracy (%)**	**Precision (%)**	**Recall (%)**	**F1 (%)**
VGG19	96,28	96,79	95,73	96,26
EfficientNetB3	97,23	97,70	97,33	97,20
Proposed Model	**99,12**	**98,87**	**99,37**	**99,12**

Source: Authors, (2024).

Table 2 compares the performance metrics of different deep learning models used for malaria diagnosis. This table shows that the proposed model has a significant advantage over popular pre-trained models such as VGG19 and EfficientNetB3 that have been previously used for malaria diagnosis. The performance evaluation is based on critical metrics such as accuracy, precision, recall and F-score. Firstly, it can be seen that the VGG19 model achieved 96.28% accuracy, 96.79% precision, 95.73% sensitivity and 96.26% F-score in malaria diagnosis. Although these results show that VGG19 performs well in malaria diagnosis, it still has some limitations. EfficientNetB3 outperforms VGG19 with 97.23% accuracy, 97.70% precision, 97.33% sensitivity and 97.20% F-score. EfficientNetB3, thanks to its advanced architecture, improved diagnostic accuracy and provided a more balanced performance. Although these two models have high accuracy in malaria diagnosis, they are still not competitive enough compared to the proposed model.

The proposed model achieved 99.12% accuracy, surpassing other models developed for malaria diagnosis. It also has extremely high values of 98.87% precision, 99.37% sensitivity and 99.12% F-score. These results show that the proposed model offers a more accurate and reliable performance in the diagnosis of malaria parasites compared to other models. The high sensitivity rate of the model (99.37%) reveals that it is highly successful in detecting true positive samples and minimizes the false negative rate. This is critical in a disease such as malaria that requires rapid response. The precision value of the proposed model (98.87%) shows that the false positive rate is low and the model avoids misdiagnosing healthy cells. This provides a significant advantage in reducing the false positive diagnosis rate in an infectious and widespread disease such as malaria, thereby reducing unnecessary treatment and resource utilization.

In conclusion, the proposed model outperforms other models in the literature with its high accuracy, precision and sensitivity rates in malaria diagnosis. Thanks to this superior performance, it offers a more reliable alternative in malaria diagnosis and enables earlier intervention by accelerating the diagnosis process. Especially in resource-limited regions, the rapid and accurate diagnosis of the proposed model has the potential to improve disease control and public health.

The comparative analysis revealed that our proposed CNN model outperforms all other architectures across key performance metrics, including accuracy, precision, recall, and F1-score. Specifically, the proposed model achieved an accuracy of 99.12%, which is significantly higher than the other models. Furthermore, our model maintained a compact architecture with only 620,441 parameters, demonstrating efficiency without compromising performance. The training-validation accuracy is shown in Figure 8, and the training-validation loss is shown in Figure 9 for 50 epochs. As the epoch value increases, the accuracy values in both the training set and the validation set increase. Simultaneously, the training and validation loss curves decrease as the epoch value increases. Figure 10 shows a screenshot where a randomly selected cell is predicted to be parasited or unparasited.

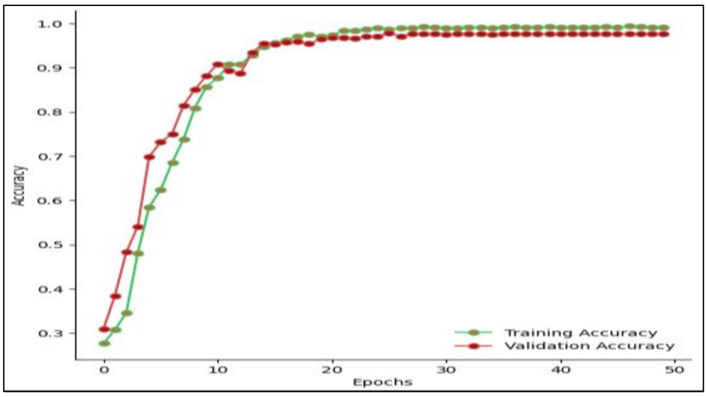


Figure 8: Training-validation accuracy curve.
Source: Authors, (2024).

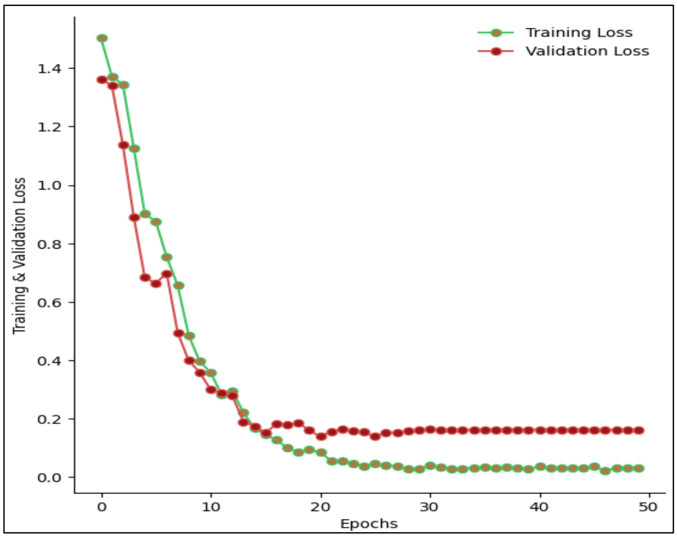


Figure 9: Training-validation loss curve.
Source: Authors, (2024).

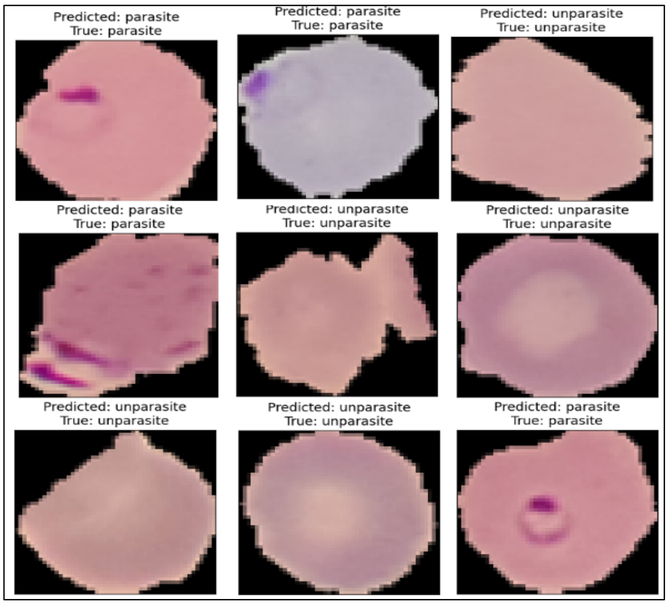
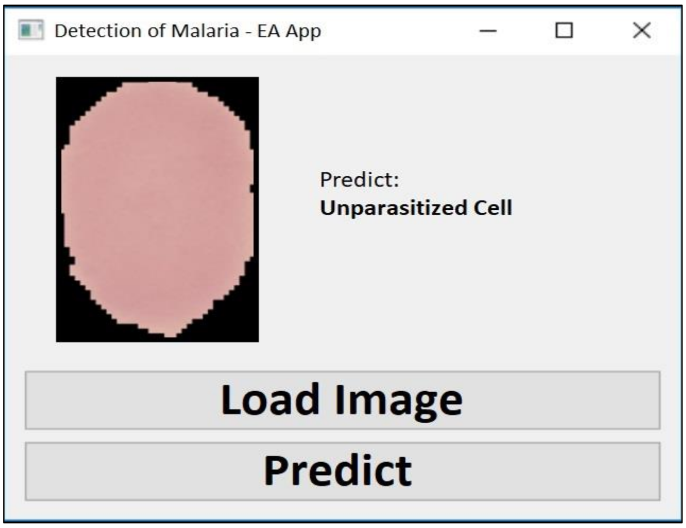


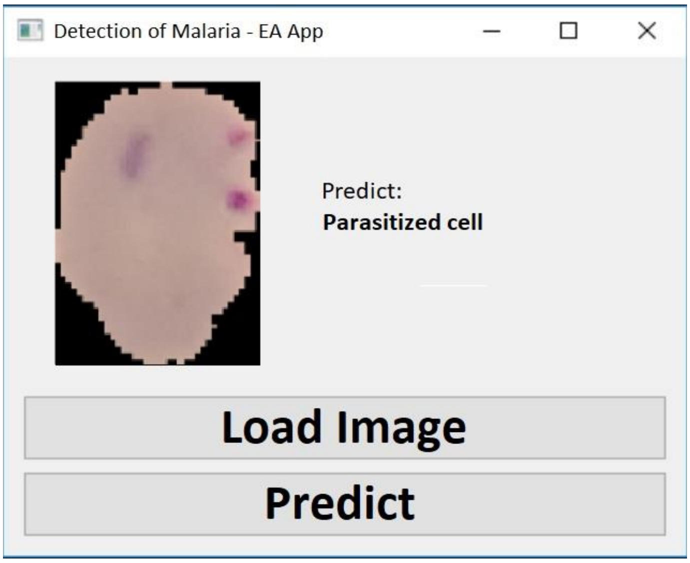
Figure 10: Estimation of the parasitic status of randomly selected cells.
Source: Authors, (2024).

The superior performance of the proposed CNN model underscores its potential as a reliable and efficient alternative for malaria diagnosis. This remarkable accuracy can significantly enhance diagnostic accuracy, particularly in resource-limited settings where timely and accurate diagnosis is crucial for effective treatment and control of the disease. The integration of our CNN model into a user-friendly software application further amplifies its impact, offering healthcare professionals a valuable tool for real-time malaria diagnosis. As such, our findings pave the way for advancements in malaria diagnosis through the fusion of artificial intelligence and medical science, marking a significant stride towards combating malaria and improving global health outcomes. A simple and fast to use desktop software that detects whether the cell is malarial or not when the blood cell image is uploaded has been realised. The application was implemented using Python programming language. The user can determine the status of the cell by uploading the blood cell image to the application and pressing the guess button. Figure 11 and Figure 12 show the screenshots of the application.



Predict:
Unparasitized Cell

Figure 11: Screenshots of the application showing predictions of actual cell images 1.
Source: Authors, (2024).



Predict:
Parasitized cell

Figure 12: Screenshots of the application showing predictions of actual cell images 2.
Source: Authors, (2024).

V. CONCLUSIONS

This study demonstrates the innovative potential of deep learning-based approaches in malaria diagnosis. Our CNN-based architecture, which was developed to overcome the difficulties of traditional diagnostic methods, has achieved a high accuracy rate of 99.12%, which is a remarkable achievement, especially in the rapid and reliable diagnosis of a common disease such as malaria. The 98.87% precision and 99.37% recall values of our model support its diagnostic performance and reveal that it has the capacity to produce high accuracy results by minimizing human error in the malaria detection process. These high-performance values demonstrate the applicability and effectiveness of CNN-based deep learning models in the diagnosis of a common and potentially fatal disease such as malaria. The developed software platform accelerates the diagnosis of malaria while at the same time minimizing the possibility of misdiagnosis by increasing diagnostic accuracy, thus enabling rapid and accurate diagnosis of malaria. The results of this study offer an innovative approach to malaria diagnosis that is independent of traditional methods and opens the door to a new era in healthcare by bringing artificial intelligence-supported solutions to the diagnostic process. Especially in diseases that threaten public health such as malaria, artificial intelligence applications for early diagnosis and treatment have great potential to improve health outcomes and reduce disease-related mortality rates. In this context, the convergence of AI and medicine is an important step that will shape the future of global healthcare.

VI. AUTHOR'S CONTRIBUTION

Conceptualization: Emrah ASLAN
Methodology: Emrah ASLAN
Investigation: Emrah ASLAN
Discussion of results: Emrah ASLAN
Writing – Original Draft: Emrah ASLAN
Writing – Review and Editing: Emrah ASLAN
Resources: Emrah ASLAN
Supervision: Emrah ASLAN
Approval of the final text: Emrah ASLAN

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