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Deep Learning-Based Detection of Malaria Infection Through Blood Sample Analysis for Malaria Diagnosis

M. Raju[1*], Y. Naveen Reddy[1], M. Keerthi[1], A. Rishitha[1], D. Pavan[1]

[1]Department of Computer Science and Engineering, Sree Dattha Institute of Engineering and Science, Sheriguda, Hyderabad, Telangana, India

Abstract

Malaria, a life-threatening disease caused by Plasmodium parasites transmitted through infected mosquitoes, remains a significant public health concern in many regions worldwide. Early and accurate detection of malaria infection is crucial for timely treatment and disease management. The automated malaria detection system can be integrated into portable diagnostic devices, enabling healthcare professionals to perform rapid and accurate malaria tests in remote or resource-limited settings. The system can assist researchers and health organizations in tracking malaria prevalence and monitoring its spread, contributing to epidemiological studies and efficient resource allocation. Conventional methods for malaria detection involve manual examination of blood smears under a microscope by trained technicians. Although reliable, this process is time-consuming, labour-intensive, and dependent on the expertise of the microscopist. The regression-based examination of blood smears introduces the potential for errors, leading to false-negative or false-positive results. In recent years, deep learning-based approaches have shown promising results in automating the detection of malaria parasites through blood sample analysis. This work presents an advanced machine learning-based method for the automated detection of malaria infection, leveraging image processing techniques to achieve high accuracy and efficiency.

Keywords: Malaria disease, Deep learning, Image processing, Disease classification, Internet of Medical Things.

1. Introduction

Malaria infection is a widespread and potentially deadly disease caused by the Plasmodium parasite, transmitted to humans through the bite of infected female Anopheles mosquitoes. Diagnosis and monitoring of malaria often rely on the analysis of blood samples, which provides crucial insights into the presence and severity of the infection. When a blood sample is obtained from a patient suspected of having malaria, it undergoes a series of laboratory tests to confirm the diagnosis and assess the level of parasitic activity. The primary diagnostic method is the examination of a thin blood smear or a thick blood smear under a microscope. Thin blood smears are used to identify the Plasmodium species responsible for the infection, while thick blood smears are employed to quantify the number of parasites present in the blood. This information is vital for determining the severity of the disease and guiding treatment decisions. Additionally, molecular techniques like polymerase chain reaction (PCR) can be employed to confirm the presence of the parasite and, in some cases, differentiate between species with high accuracy.

Blood sample analysis also allows for the evaluation of other important parameters such as hematocrit levels, which help in assessing anemia, a common complication of malaria. Moreover, serological tests can be performed to detect specific antibodies against Plasmodium antigens, providing information about previous exposure to the parasite and aiding in epidemiological studies. The timely and accurate

analysis of blood samples is crucial in the management and control of malaria. Rapid and precise diagnosis enables healthcare providers to initiate appropriate treatment promptly, reducing the risk of severe complications and death. Furthermore, monitoring the parasite load in the blood over time allows healthcare professionals to gauge the effectiveness of treatment and make necessary adjustments. Therefore, blood sample analysis remains a cornerstone in the battle against malaria, contributing to both individual patient care and public health efforts to control and ultimately eliminate this devastating disease.

2. Literature Survey

There are several promising prior studies on the capabilities of ML-based techniques in detecting infectious diseases. For instance, using a machine learning framework, Colubri et al. [6] introduced an application that can predict the outcome of Ebola patients from early clinical symptoms. Smith and Kirby [7] described ML applications for analyzing different types of microbial image data, particularly progress in smear and plate interpretation. Another notable study on ML-based infectious disease diagnosis is that of Das et al. [8], who developed a computer-aided malaria parasite characterization and classification based on light microscopy images of peripheral blood smears collected from 600 patients using an ML approach. Their proposed ML scheme applying the Bayesian approach provides 84.0% accuracy and 98.1% sensitivity by selecting the 19 most significant features, and the support vector machine (SVM) achieved 83.5% screening accuracy and 96.6% sensitivity with the 9 most significant features [8].

Similarly, there are other studies that have applied various machine learning methods to detect malaria parasites. Bibin et al. [9] proposed a deep belief network (DBN)-based trained model to classify 4100 peripheral blood smear images into parasitic or nonparasitic classes. The proposed method showed an F-score of 89.66%, a sensitivity of 97.60%, and a specificity of 95.92% [9]. Gopakumar et al. [10] used a customized CNN model operating on a focus stack of images for automated quantitative detection of Plasmodium falciparum malaria in blood smears. The detection accuracy of the CNN model was 97.06% sensitivity and 98.50% specificity [10].

Yang et al. [3] developed a method using a deep learning algorithm to detect malaria parasites in thick blood smear images, run on a smartphone. They trained and tested a deep learning method using 1819 thick smear images from 150 patients [3]. The study results showed the effectiveness of the CNN model in distinguishing positive (parasitic) image patches from negative image patches, with performance metrics of accuracy (93.46% ± 0.32%), precision (94.25% ± 1.13%), and negative predictive value (92.74% ± 1.09%) [3]. Especially in the case of the COVID-19 pandemic, Dandekar et al. [11] applied the neural network module of ML to develop a globally applicable COVID-19 diagnosis model to analyze and compare the role of quarantine control policies globally across the continents of Europe, North America, South America, and Asia. Dandekar et al. [11] also hosted quarantine diagnosis results from 70 countries around the world on a public platform: https://covid19ml.org/ (accessed on 15 March 2023).

One example of a notable literature review source for ML-based infectious disease diagnosis is the work of Baldominos et al. [12]. The study performed a computer-based systematic literature review in order to investigate where and how computational intelligence (i.e., different types of machine learning techniques) is being utilized to predict patient infection [12]. Deep learning, a specific subset of machine learning, is a computational processing system composed of artificial neural networks, heavily inspired by how biological nervous systems process information and make decisions [13]. Deep learning allows for incrementally learning complex input data features by going through the architecture's hidden layers [14]. That is, as the input data pass through hidden layers, the complexity of the input data is computed

as a simpler and less abstract concept for the final output, which is the so-called nested hierarchical approach [15].

3. Proposed Methodology

The methodology leverages image processing and machine learning techniques to automate the detection of malaria parasites in blood sample images. It is a promising approach to improve the efficiency and accuracy of malaria diagnosis, particularly in resource-limited settings where access to skilled technicians may be limited. However, it's important to note that developing and fine-tuning the DLCNN model typically requires a substantial amount of labeled data and expertise in machine learning and image analysis. Additionally, the performance of the model should be rigorously evaluated to ensure its accuracy and reliability in real-world healthcare applications. Figure 1 shows the proposed system model. The detailed operation illustrated as follows:

Step 1: Image Processing: This is the initial step where you process the blood sample images. Image processing techniques may include preprocessing steps such as noise reduction, contrast enhancement, and image segmentation to isolate the relevant features (in this case, malaria parasites) from the background and other elements in the image. This step is essential for preparing the images for further analysis.

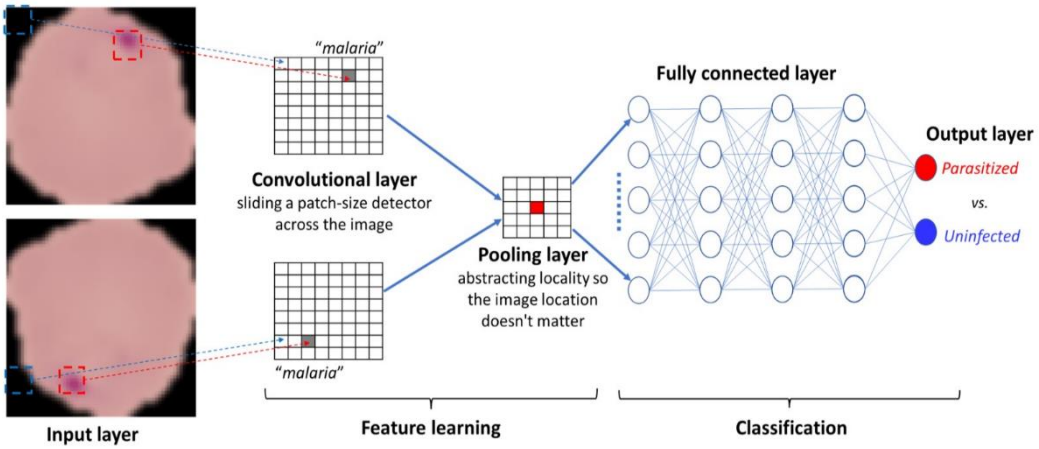


Figure 1: Proposed system architecture of malaria infection detection.

Step 2: DLCNN Building: After image processing, the next step involves training a machine learning model, specifically a DLCNN. In this step, you would typically use a labeled dataset of blood sample images, where each image is associated with a known diagnosis (e.g., whether it contains malaria parasites or not). The DLCNN is trained to learn patterns and features in the images that distinguish between infected and uninfected samples. This classifier can handle complex relationships in the data and can make predictions based on these learned patterns.

Step 3: DLCNN Prediction: Once the DLCNN model is trained, it can be used to predict whether new, unseen blood sample images contain malaria parasites or not. When a new blood sample image is input into the trained DLCNN, the model evaluates the image based on the patterns it has learned during training and produces a prediction. This prediction can help automate the process of diagnosing malaria from blood sample images, reducing the need for manual examination and potentially increasing the speed and accuracy of diagnosis.

3.1 DLCNN Algorithm

Deep neural network is gradually applied to the identification of malaria conditions. Deep neural network is designed by imitating the structure of biological neural network, an artificial neural network to imitate the brain, using learnable parameters to replace the links between neurons. Convolutional neural network is one of the most widely used deep neural network structures, which is a branch of feed forward neural network. The success of DLCNN network model also confirms the importance of convolutional neural network model. Since then, convolutional neural networks have developed vigorously and have been widely used in financial supervision, text and speech recognition, smart home, medical diagnosis, and other fields.

Convolutional neural networks are generally composed of three parts. Convolution layer for feature extraction. The convergence layer, also known as the pooling layer, is mainly used for feature selection. The number of parameters is reduced by reducing the number of features. The full connection layer carries out the summary and output of the characteristics. A convolution layer is consisting of a convolution process and a nonlinear activation function ReLU. A typical architecture of CNN model for malaria condition recognition is shown in Figure 2.

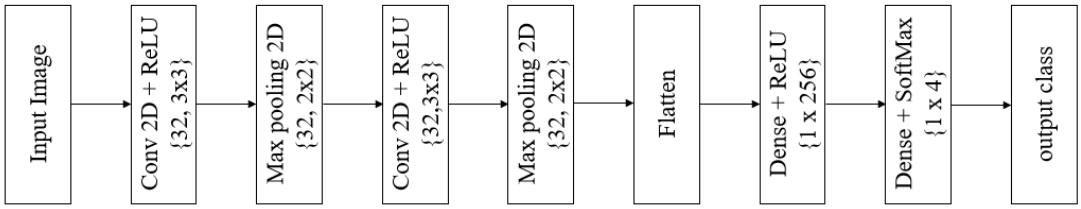


Figure 2: Proposed DLCNN

The leftmost image is the input layer, which the computer understands as the input of several matrices. Next is the convolution layer, the activation function of which uses ReLU. The pooling layer has no activation function. The combination of convolution and pooling layers can be constructed many times. The combination of convolution layer and convolution layer or convolution layer and pool layer can be very flexibly, which is not limited when constructing the model. But the most common CNN is a combination of several convolution layers and pooling layers. Finally, there is a full connection layer, which acts as a classifier and maps the learned feature representation to the sample label space.

Convolutional neural network mainly solves the following two problems.

1) Problem of too many parameters: It is assumed that the size of the input picture is $50 * 50 * 3$. If placed in a fully connected feedforward network, there are 7500 mutually independent links to the hidden layer. And each link also corresponds to its unique weight parameter. With the increase of the number of layers, the size of the parameters also increases significantly. On the one hand, it will easily lead to the occurrence of over-fitting phenomenon. On the other hand, the neural network is too complex, which will seriously affect the training efficiency. In convolutional neural networks, the parameter sharing mechanism makes the same parameters used in multiple functions of a model, and each element of the convolutional kernel will act on a specific position of each local input. The neural network only needs to learn a set of parameters and does not need to optimize learning for each parameter of each position.

2) Image stability: Image stability is the local invariant feature, which means that the natural image will not be affected by the scaling, translation, and rotation of the image size. Because in deep learning, data enhancement is generally needed to improve performance, and fully connected feedforward neural is difficult to ensure the local invariance of the image. This problem can be solved by convolution operation in convolutional neural network.

Convolution layer: According to the facts, training and testing of DLCNN involves in allowing every source image via a succession of convolution layers by a kernel or filter, rectified linear unit (ReLU), max pooling, fully connected layer and utilize SoftMax layer with classification layer to categorize the objects with probabilistic values ranging from [0,1].

Convolution layer as depicted in Figure 4.3 is the primary layer to extract the features from a source image and maintains the relationship between pixels by learning the features of image by employing tiny blocks of source data. It's a mathematical function which considers two inputs like source image $I(x, y, d)$ where x and y denotes the spatial coordinates i.e., number of rows and columns. d is denoted as dimension of an image (here $d = 3$, since the source image is RGB) and a filter or kernel with similar size of input image and can be denoted as $F(k_x, k_y, d)$.

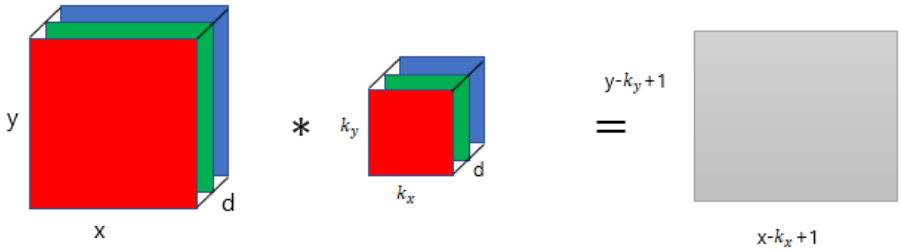
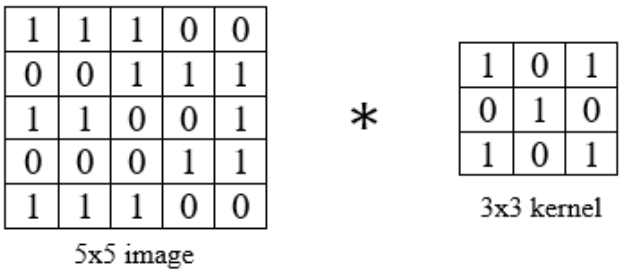
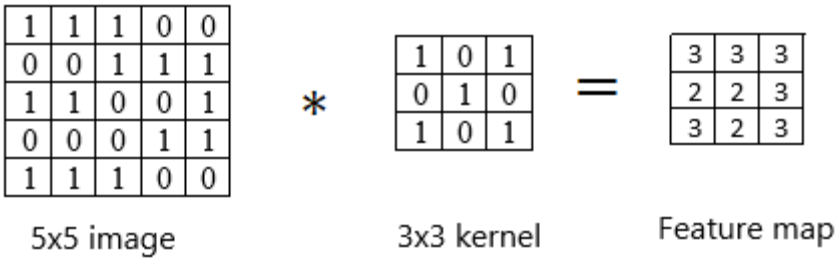


Figure 3: Representation of convolution layer process.

The output obtained from convolution process of input image and filter has a size of $C\left((x - k_x + 1), (y - k_y + 1), 1\right)$, which is referred as feature map. An example of convolution procedure is demonstrated in Figure 4(a). Let us assume an input image with a size of 5×5 and the filter having the size of 3×3. The feature map of input image is obtained by multiplying the input image values with the filter values as given in Figure 4 (b).



(a)



(b)

Figure 4: Example of convolution layer process (a) an image with size **5 × 5** is convolving with **3 × 3** kernel (b) Convolved feature map

ReLU layer: Networks those utilizes the rectifier operation for the hidden layers are cited as rectified linear unit (ReLU). This ReLU function $\mathcal{G}(\cdot)$ is a simple computation that returns the value given as input directly if the value of input is greater than zero else returns zero. This can be represented as mathematically using the function $max(\cdot)$ over the set of 0 and the input x as follows:

$$\mathcal{G}(x) = \max\{0, x\}$$

Max pooing layer: This layer mitigates the number of parameters when there are larger size images. This can be called as subsampling or down sampling that mitigates the dimensionality of every feature map by preserving the important information. Max pooling considers the maximum element form the rectified feature map.

SoftMax classifier: Generally, softmax function is added at the end of the output as shown in Figure 5, since it is the place where the nodes are meet finally and thus, they can be classified. Here, X is the input of all the models and the layers between X and Y are the hidden layers and the data is passed from X to all the layers and Received by Y. Suppose, we have 10 classes, and we predict for which class the given input belongs to. So, for this what we do is allot each class with a particular predicted output. Which means that we have 10 outputs corresponding to 10 different class and predict the class by the highest probability it has.

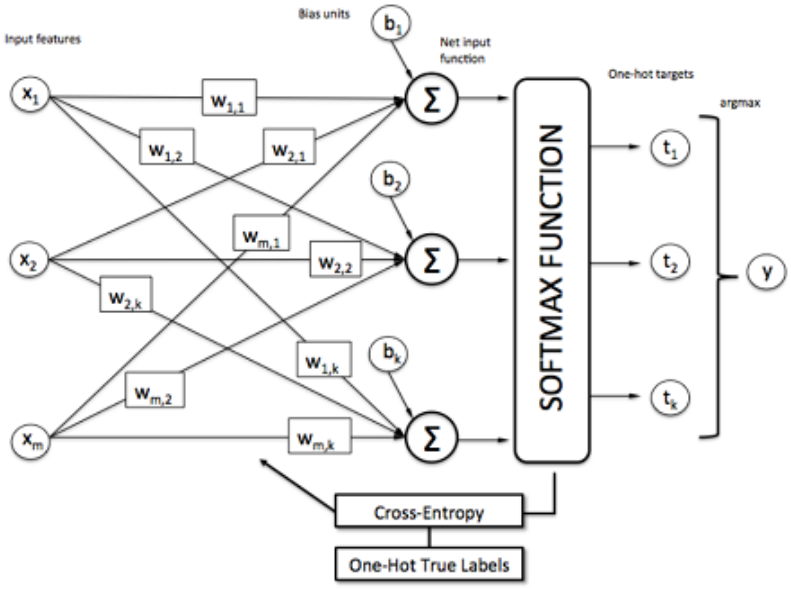


Figure 5: Malaria prediction using SoftMax classifier.

4. Results and Discussion

In Figure 6, a confusion matrix is presented, detailing the performance of the Gaussian naïve Bayes classifier. Confusion matrices are commonly used to evaluate the performance of classification algorithms by visualizing the counts of true positive, false positive, true negative, and false negative predictions. Figure 7 shows the confusion matrix of the CNN algorithm, offering a detailed breakdown of its performance similar to the one seen in Figure 6 but specific to the CNN model. In Figure 8, an accuracy and loss graph is presented, which is a common visualization used in deep learning to monitor the training process of neural networks. It likely shows the trend of accuracy and loss over the course of training epochs. Figure 9 compares the performance of the Gaussian naïve Bayes classifier and the CNN model through a graphical representation, likely indicating metrics such as accuracy, precision, recall, or F1-score.

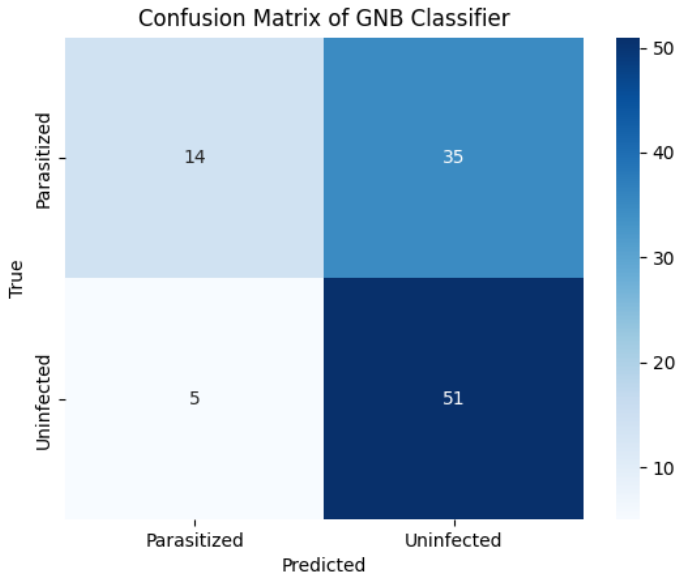


Figure 7: Confusion matrix of GNB Classifier.

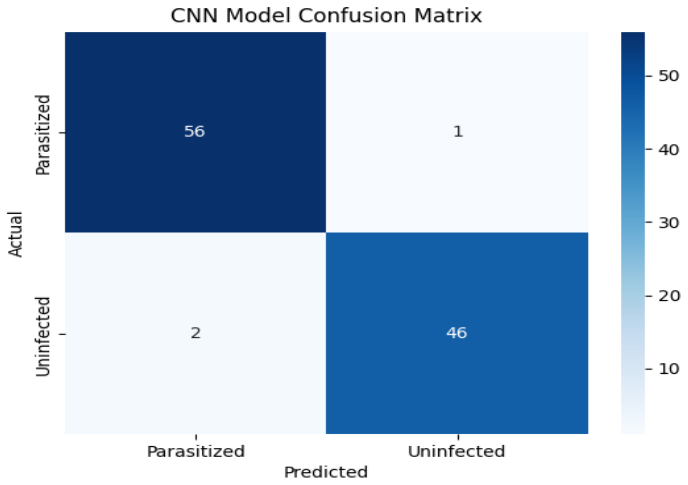


Figure 8: Confusion matrix of CNN Algorithm

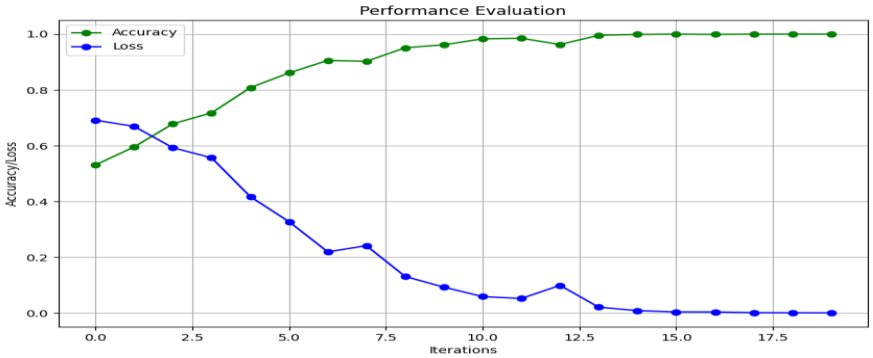


Figure 9: Accuracy and loss graph of CNN model

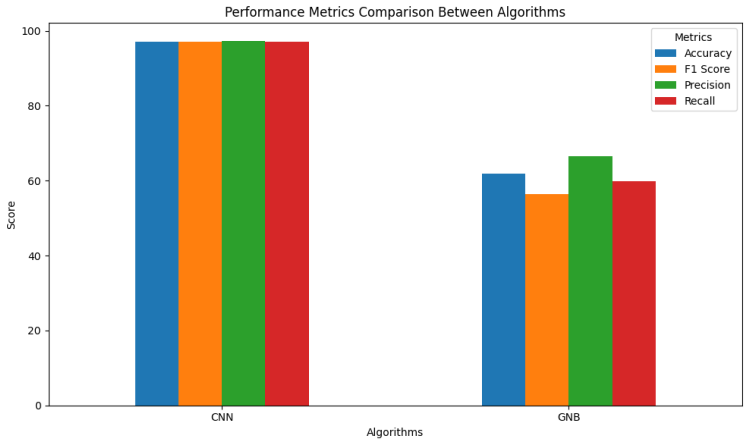


Figure 10: Performance Comparison graph of GNB and CNN Models

Figure 10 presents the predicted output using the CNN model, potentially showcasing examples of correctly and incorrectly classified images.

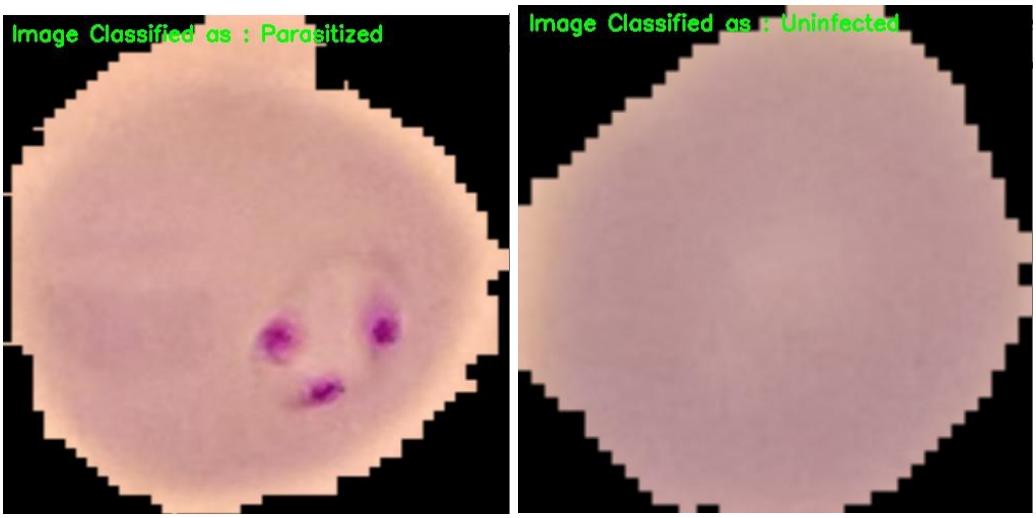


Figure 10: Predicted output using CNN model

Table 1 provides an overall performance comparison of the proposed machine learning models, including metrics such as accuracy, precision, recall, and F1-score. This table offers a summarized view of the models' performance across multiple evaluation criteria.

Table 1: Overall performance comparison of proposed ML models.

Model name	Accuracy (%)	Precision (%)	Recall (%)	F1-score
CNN	97.14	97	97	97
GNB classifier	61.23	66	59	56

5. Conclusion

In conclusion, the methodology involving image processing followed by DLCNN building and prediction for malaria diagnosis from blood sample images represents a significant advancement in the field of healthcare and disease management. This approach addresses critical challenges related to the

efficiency, accuracy, and accessibility of malaria diagnosis. By automating the analysis of blood sample images, it streamlines the diagnostic process, reducing the time required for diagnosis and treatment initiation. Additionally, it enhances diagnostic consistency, reduces the potential for human error, and offers scalability, making it suitable for both routine diagnostics and large-scale screening efforts. The integration of machine learning and image analysis technologies into healthcare systems holds promise for improving malaria control, early detection of outbreaks, and enhancing overall healthcare access. While there may be initial development costs, the long-term benefits in terms of improved healthcare delivery, reduced costs, and better disease surveillance make this methodology a valuable addition to the fight against malaria.

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