CNN-Based Automated Malaria Parasite Detection From Microscopic Thin Blood Smears Images

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Abstract: Malaria is a deadly, infectious mosquito borne disease caused by plasmodium parasites. The detection of unicellular protozoan plasmodium parasite which is the cause of malaria takes light microscopic analysis by a skilled practitioner for the diagnosis of malaria. The standard method for diagnosing malaria using light microscopy involves preparing thick and thin blood smears that are stained and examined under a microscope. The major drawback of this approach is its dependence on skilled technicians, of which there is a critical shortage. In this aspect this results in a delay in an inaccurate diagnosis. A reliable alternative is required to enable routine access to high-quality diagnosis, which is currently not available. Deep learning is an artificial intelligence technique where the machine is train to mimic the thought process of a human brain. Our project mainly focusses on building a deep convolutional neural network (CNN) that can detect the malaria parasite infection from thin blood smear samples.

Keywords : CNN, Deep learning, Computer-aided diagnosis.

I.INTRODUCTION

Malaria is a serious and potentially fatal disease caused by parasites that are transmitted to humans through the bites of infected Anopheles mosquitoes. The disease is caused by the Plasmodium parasite and can result in severe fever and flu-like symptoms. There are five species of the Plasmodium parasite that cause malaria in humans, with P. falciparum and P. vivax being the most dangerous. P. falciparum is the deadliest parasite and is responsible for most malaria-related deaths, particularly in Africa. P. vivax is less deadly but can cause long-lasting infections and is prevalent in many parts of Asia and Latin America. Effective prevention measures such as bed nets, insecticide-treated clothing, and indoor residual spraying can help reduce the spread of malaria. Early diagnosis and prompt treatment with antimalarial drugs can save lives and prevent complications. Vaccine development efforts are also ongoing to further combat this deadly disease.It is preventable and curable. In 2021, there were an estimated 247 million cases of malaria worldwide. The estimated number of malaria deaths stood at 619000 in 2021. The WHO African Region carries a disproportionately high share of the global malaria burden. In 2021, the region was home to 95% of malaria cases and 96% of malaria deaths. Children under 5 accounted for about 80% of all malaria deaths in the region.

The standard diagnostic method for malaria involves examining blood smears for infected erythrocytes under a microscope. This requires qualified microscopists with experience and knowledge in the field. The quality of diagnosis using this method is dependent on the skills of the microscopists. Other diagnostic methods, such as rapid diagnostic tests, may be less dependent on the expertise of the operator. However, blood smear examination remains an important diagnostic tool for malaria.Automatic image recognition technologies based on machine learning and big data have been applied to both thick and thin malaria blood smears for microscopic diagnosis since 2005. In this work, we use a deep learning approach to detect parasite-infected red blood cells in thin smears. The model we are utilizing is a convolutional neural network (CNN), a specialized deep learning algorithm that has been developed specifically for analyzing 2D data, such as images.

II. Literature survey

[1] Adan Antonio Alonso-Ramirez proposed a CNN model that can classify malaria-infected red blood cells from uninfected ones, using two deep learning approaches without any preprocessing stage. The first approach uses Convolutional Long Short-Term Memory, while the second approach uses Convolutional Bidirectional Long Short-Term Memory architecture. They used a public dataset of parasitized and uninfected red blood cell images for training and testing the proposed models. The methods achieved an impressive accuracy of 99.89% in detecting malaria-infected red blood cells, without any preprocessing data. When evaluating the diagnosis of malaria, several factors are taken into consideration, including the expense associated with each test, the accuracy of the test in detecting the disease (measured by sensitivity and specificity), the amount of time it takes to administer each test, and the level of expertise required by the user to perform the test accurately. Computer-aided diagnostic (CAD) systems for malaria analysis have been developed to address these limitations. Deep learning approaches based on Artificial Neural Networks (ANN) have been used recently to make fast and accurate malaria diagnoses, employing public datasets. In this paper, the proposed methods include Overall flowchart, NLM-Malaria dataset, The CNN-LSTM architecture, The CNN-BiLSTM architecture. The model performance was evaluated using various metrics, including accuracy, precision, recall, F1-score, and confusion matrix, considering image size, data splitting for model training and testing, and processing time per data sample.

[2] P.A. Pattanaik proposed an advanced deep learning approach, called Multi-Magnification Deep Residual Network, for the classification of microscopic blood smear images in order to identify malaria using machine learning technologies. However, automatic segmentation of erythrocytes in these images is a challenging problem due to the scarcity of experts, low image qualities, slow manual process, and inefficient quality of diagnosis. To tackle these issues, the proposed MM-ResNet framework fully automatically classifies the microscopic blood smear images as infected or non-infected at multiple magnifications. This is the first application of MMResNet for malaria-infected erythrocyte identification in microscopic blood smear images. The proposed framework combines batch normalization and individual residual units to solve the problem of vanishing gradients, degradation, and low-quality images, resulting in an average accuracy of 98.08% in classifying infected or non-infected cells. The MM-ResNet architecture is based on the combination and consideration of shape, appearance features, and a cascade of boosting classifiers for multi-view analysis of microscopic blood smear images. The case study comparing different techniques highlighted the benefits of using MMResNet over other machine learning techniques. The widen consistent architecture and fixed depth improve performance across residual networks until a suitable number of residual functions and depth is achieved.

[3] Arindam B. Chowdhury developed a network that can count blood cells and detect malaria pathogens in blood samples. The system has an overall performance with a mean average precision of over 0.95 when compared with the ground-truth. The software is also designed to be ported to a low-cost microcomputer for rapid prototyping. To train the network, the author used different datasets including Original Medical Databases, Preprocessing Image Samples, Synthetic Dataset Creation, Partially Visible Cells, and Final Overview of the Created Dataset. The experimental results presented in the paper are compared with the ground truth data of the testing and validation datasets which are known to be 100% accurate. This system offers an affordable digital pathology solution capable of identifying malaria and providing a comprehensive blood cell count using a single blood smear image. The author's contribution includes the creation of a dataset of blood smear images that has a wide variation in the combination of blood cells, complete blood cell count, distribution of WBCs, and Malaria detection. The case of partially visible WBCs is handled separately to improve the accuracy of detection. The system's performance is tested on a compact off-the-shelf embedded platform like Raspberry Pi 3 and is cost-effective, with a performance relatively close to a human pathologist. The use of this system can enable cheaper and faster treatment of patients and users.

[4] In this paper, Sidharth S Prakash has developed a deep convolutional neural network that can predict the malaria parasite infection from thin blood smear samples. For this study, the dataset comprising of 24,960 images was obtained from the National Library of Medicine, with an equal distribution of images between the 'parasitized' and 'uninfected' classes. The neural network model has delivered an F1 score of above 94% for each of the parasitized and uninfected class. The proposed model does not intend to replace the expertise of medical professionals but rather act as a helping hand in the diagnosis of malaria. Moreover, the author plans to extend this study to predict the malaria parasite infection utilizing transfer learning techniques with pre-trained models like ResNet. The study is significant as it provides an automated and efficient way of detecting malaria in blood smear samples, which can significantly reduce the time and effort required for the diagnosis of malaria.

III. METHODOLOGY

Block diagram :

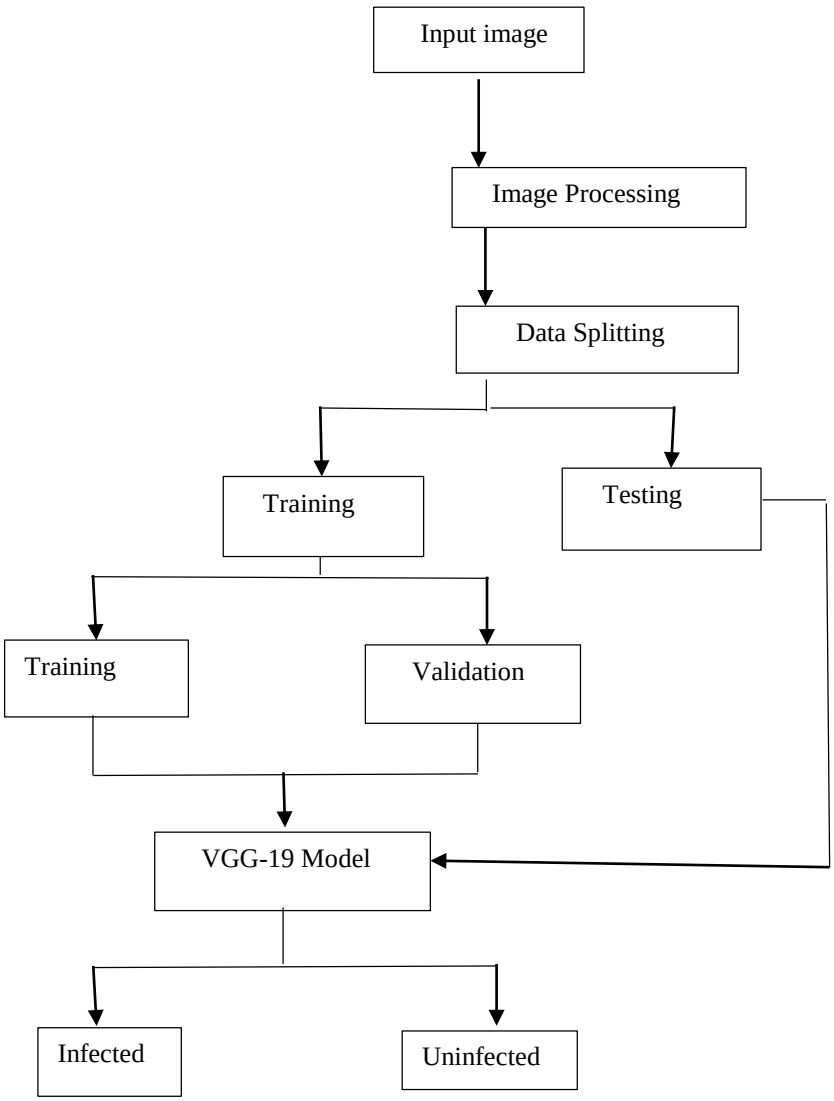

Fig-1: Block Diagram

Our malaria parasite detection model using VGG19 algorithm consists of a collection of a dataset from the NIH (National Institute of Health), followed by Data Preprocessing. The data set is divided into two parts in the ratio 70% and 30%. Here 70% is the training data set and the 30% is the testing data set. Then training is performed on the training data set to train the model which is made sure it is a validation set. Then the model is built using VGG19 algorithm. Then testing is performed and detection of the malaria parasite is obtained.

A) Data collection: This is the first module, which is concerned with data collection. A total of 27,560 PNG images of thin smear blood cells were collected for this study from the National Institute of Health (NIH) dataset. This dataset is classified as parasite and uninfected blood images in which 13,780 are parasite blood sample images and 13,780 are uninfected blood sample images. We used 70% of this data i.e. 19,292 images for training and remaining 30% of the dataset i.e. 8,268 is used for testing the model.

B) Data Preprocessing: The data requires special preprocessing to apply deep learning algorithms to them. The collected dataset from NIH website contains images of different dimensions. We are going to set all image dimensions to 225x225. The algorithm supports only 225x225 dimensioned images. The only preprocessing applied was calculating the mean RGB value of each pixel across the entire training set.

C) Deep learning model: The CNN consists of five layers such as input layer,convolution layer , activation layer , pooling layer and fully connected layer.

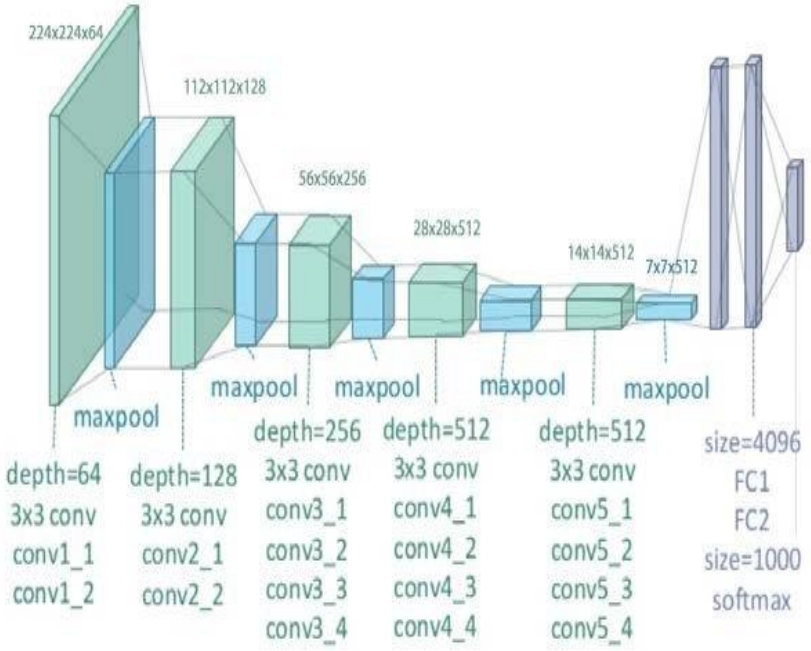

Fig 2: CNN Architecture

In this phase, a deep learning model is erected by learning and generalizing from training data, then applying that acquired knowledge to fresh and new data. This data is different from the training data. The model has never been seen before to make predictions. Webuild the model using VGG19 algorithm

- **VGG19**

  VGG19 is a variant of the VGG model, which is a popular Convolutional Neural Network used for image recognition and other computer vision tasks. It is a deep neural network that has 19 layers, making it a powerful model for image classification. VGG19 is one of several variants of the VGG model, including VGG-11 and VGG-16. The architecture of VGG19 consists of 16 Convolutional layers, 3 fully connected layers, and 5 max-pool layers.The layers in VGG19 model is as follows:

  - Conv3x3 (64)
  - Conv3x3 (64)
  - MaxPool
  - Conv3x3 (128)
  - Conv3x3 (128)
  - MaxPool
  - Conv3x3 (256)
  - Conv3x3 (256)
  - Conv3x3 (256)
  - Conv3x3 (256)
  - MaxPool
  - Conv3x3 (512)
  - Conv3x3 (512)
  - Conv3x3 (512)
  - Conv3x3 (512)
  - MaxPool
  - Fully Connected Layer (4096)
  - Fully Connected Layer(4096)
  - Fully Connected Layer (1000)
  - Soft Max

This network received a fixed-size (224 * 224) RGB picture as input, indicating that the matrix was shaped (224,224,3). The mean RGB value of each pixel, calculated throughout the whole training set, was the only preprocessing that was carried out. They were able to cover the entirety of the image by using kernels that were (3 * 3) in size with a stride size of 1 pixel. To maintain the image's spatial resolution, spatial padding was applied. Stride 2 was used to conduct max pooling over a 2 * 2 pixel window. Rectified Linear Unit (ReLU) is a type of activation function that is commonly used in neural networks to introduce non-linearity into the model.

There are mainly four layers in this network. They are:

a) Convolutional layers:

Convolutional layers extract features using filters and then learns from them. For this reason, these layers are also called as feature extraction layers.

The mathematical equation for convolution is given as:

b) Pooling layers:

The main of these pooling layers is to reduce the size of the volume when image size is too large. Pooling makes sure that the features can still be identified even if it is somewhat deformed or not, particularly comparable in multiple photos. In this model, we are using maximum pooling. While using max pooling, we choose a piece of the feature map that was produced in the previous stage and report the value that is highest or maximum there. By doing this, we maintain the image's characteristic while also removing more irrelevant data. The map we end up with is known as the pooled feature map.

c)Flatten layer:

The purpose of flatten layer is to flat the whole network by putting into vector form. The flatten layer transforms the entire pooled feature map matrix into a single column.

d)Fully connected layer:

Fully connected layers in CNN are those layers where all the inputs from one layer are connected to every activation unit of the next layer.

ReLu:

The Rectified Linear Units (ReLU) activation function is commonly used in neural networks to introduce non-linearity into the model. Mathematically it is given by

$$f(x) = \max(0,x)$$

D)Training and testing the model:

This step includes training the model. The model that is built using the above architecture and the custom-built layers is now trained with the training dataset available. During the training the model tries to recognize and understand the underlying features and patterns in the train dataset. The weights are assigned to the custom-built layers of the model during the training phase. These weights are used to classify whether the given image is affected with Malaria parasite is not. Thus, the built model is first compiled and then it is pipelined into the training phase using the ' model.fit ' function in the keras module.

IV. RESULTS AND DISCUSSIONS

The experimental findings and a discussion of the effectiveness of our proposed methodology are presented in this section. Figure 3a and 3b display the accuracy and loss graphs of the malaria parasite detection model. The accuracy graph shows the model's performance on both the training and validation sets, while the loss graph displays the model's training and validation loss over each epoch. Because of dropout regularisation, the model fits well and overfitting is therefore prevented.

To evaluate the performance of the malaria parasite detection classifier on the test data, a confusion matrix is used. A confusion matrix is a tabular representation that compares the actual class labels of the test data with the predicted class labels generated by the model. The confusion matrix on testing data is shown in Fig. 7. Other characteristics that can be determined using it include F1-score, recall , precision, and classification accuracy. A few terms are necessary to specify in order to calculate these parameters from the confusion matrix, such as

1. True Positive ,
2. True Negative ,
3. False Negative ,
4. False Positive

Precision (P) and recall (R) for the two-class classification are determined separately for each class based on-vs-rest, and the average of P and R is then used to determine the F1 score. F1 rating is the P and R's weighted harmonic means. The equations for calculating the above mentioned parameters are:

1. Accuracy = TP + TN / TP + TN + FP + FN
2. Precision = TP / TP + FP
3. Sensitivity = TP / TP + FN
4. Specificity =TN / TN + FP
5. F1-Score = $\frac{2 * P * R}{P + R}$

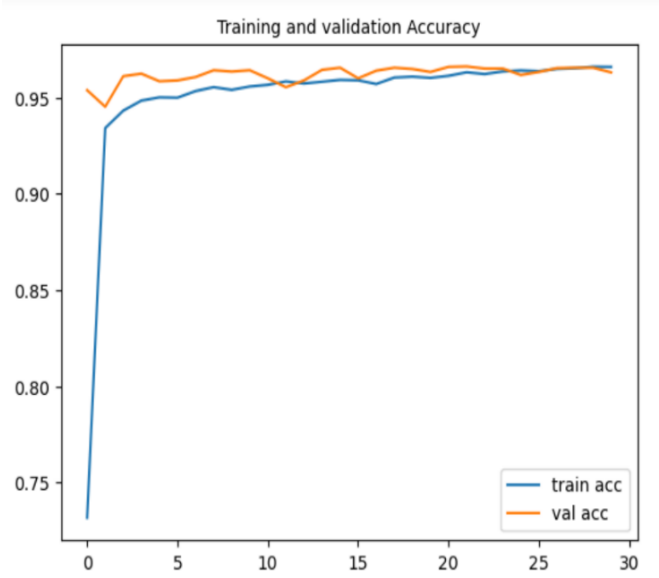

Fig-3a: Model accuracy graph

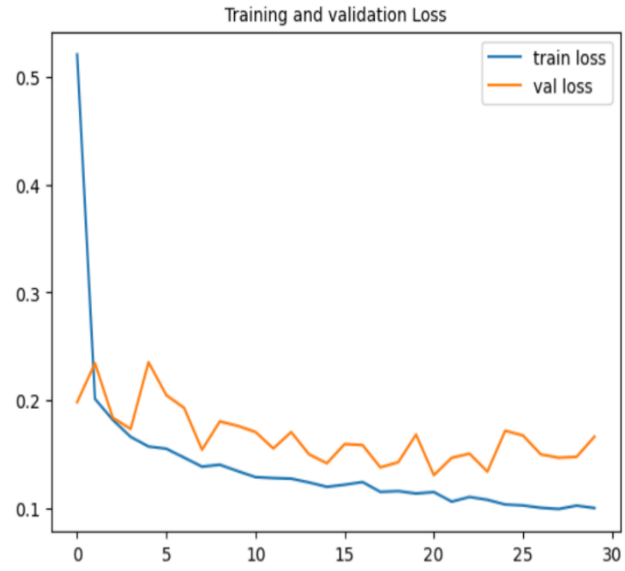

Fig-3b: Model accuracy graph

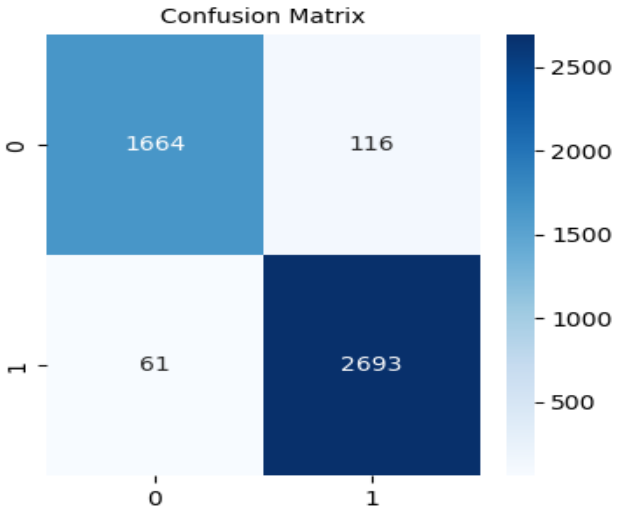

Fig-4: Confusion Matrix

Method	Accuracy	Sensitivity	Specificity	F1-Score
VGG19	96.09	93.48	97.78	96

Table-1: Performance

V.CONCLUSION

In summary, our designed convolutional neural network model is a suitable solution for malaria parasite classification. By employing the VGG19 architecture and training on a dataset of over 23,024 images, we achieved an accuracy of 96.09%, which outperformed the VGG-16 architecture and other similar studies. We found that both the architecture and the volume of training data can affect the performance of the model. This study has significant potential for use in clinical settings for accurate malaria diagnosis.

The future scope for this project is promising and has the potential to make a significant impact on the field of malaria diagnosis. Here are a few potential areas for future development:

1. Improving Accuracy: Although CNN-based models have shown promising results in malaria parasite detection, there is still room for improvement in terms of accuracy.
2. Real-time Diagnosis: CNN-based models can be used to develop real-time malaria diagnosis systems.

Overall, CNN-based automated malaria parasite detection holds immense potential for the future of malaria diagnosis, and research in this area can have a significant impact on improving healthcare outcomes.

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