Revolutionizing Malaria Diagnosis: A Deep learning Approach for Accurate Parasite Detection in Blood Smear Images

[1]**Mr. N paparayudu,**[2]**Jadhav Mayuri,**[3]**Rohan raj,**[4]**Harshavardhan Reddy,** [5]**Avan**

[1]Assistant Professor, Dept. of IT, TKR College of Engineering and Technology, Meerpet, Hyderabad,

Paparayudu@tkrec.ac.in

[2,3,4,5]BTech Student, Dept. of IT, TKR College of Engineering and Technology, Meerpet, Hyderabad

jmayuri006@gmail.com, rohan.kattela@gamil.com, dhonakantirajureddy3742@gmail.com, 21K95A1203@gmail.com

Abstract: Malaria remains a significant global health challenge, particularly in regions with limited access to healthcare resources. Rapid and accurate diagnosis is crucial for effective treatment and disease management. In this study, we propose a novel approach leveraging deep learning techniques for automated parasite detection in blood smear images. Our model is trained on a large dataset of annotated blood smear images, incorporating state-of-the-art convolutional neural network architectures. Through extensive experimentation and validation, we demonstrate the effectiveness of our approach in accurately identifying malaria parasites within blood samples. The developed deep learning model exhibits high sensitivity and specificity, outperforming traditional methods and reducing the dependency on manual inspection. Moreover, our approach significantly reduces diagnostic time, potentially enabling faster triage and treatment decisions, particularly in resource-limited settings. Furthermore, we provide insights into the interpretability of our model, highlighting regions of interest within blood smear images and aiding in understanding the underlying characteristics of malaria parasites.

Keywords: Malaria Diagnosis, Deep learning, microscopic examination, blood smear images.

1. INTRODUCTION

Malaria is a disease caused by the bite of female Anopheles mosquito. Plasmodium parasite gets injected in the body due to the sting of a mosquito. There are several types of parasites out of which the two, P. falciparum and P. vivax carry the greatest risk; however, the most prevalent effect is of P. falciparum. According to the survey of the World Health Organization (WHO) in 2019, the globe had 228 million occurrences of the disease all over the

world [1]. There are about 300-500 million cases reported annually caused due to plasmodium parasites. WHO reported that around 405,000 people died of it, most of them children from sub-Saharan Africa. Malaria causes ailment and death in large numbers causing drastic effects on the national economy of a country. Malaria is a genuine purpose of worry for the poor countries as they are caught in the endless loop of ailment and destitution.

The blood sample examination is conducted for disease diagnosis and yields a reliable result. Thin blood smears help with recognizing the types of parasites inflicting the infection and thick blood smears assist in detecting the presence of parasites [2]. The accuracy of the analysis relies upon human skill and can seriously be influenced by the eyewitness fluctuation. In pathology labs, the blood samples are collected and the diagnosis of malaria infection is done by identifying the parasites in blood slides through a microscope by the experts. A chemical process is used in the detection of malaria parasites called Giemsa staining. In this process, the parasite in the blood sample is recognized and detected. In Giemsa staining, the red blood cells (RBC) and Plasmodium parasites are coloured. In the detection of plasmodium parasites, stained objects are required. [3]. To avoid false

results, these stained objects are analyzed further to determine whether they are parasitized or healthy. As per the WHO protocol, there are various techniques used in the detection of malaria that involve an intensive examination. In manual testing, the clinician needs to observe 5000 cells at 100X magnification and this process is time-consuming and exhausting. To make the diagnosis faster polymerase chain reaction (PCR) and rapid diagnostic test (RDT) came into consideration. These analyses are fast but less accurate. Detection of parasites from Giemsa blood samples needs trained and experienced technicians. By digitizing the process, the time consumed for screening reduces. This helps in improving the consistency in diagnosis. An automatic diagnostic process reduces diagnostic time; also, it can be used as a second opinion for the pathologists. Machine learning methods are used for medical data analysis. It can be used as a tool to monitor and detect malaria amongst people. Deep learning models use sequences of nonlinear processing unit layers to discover structural characteristics in the raw data. High-end features are abstracted from low-end features to assist with dynamic and non-linear decision-making processes in learning, resulting in end-to-end classification and extraction of features [4]. There are various layers in the

Convolutional Neural Network (CNN) wherein each layer of the CNN provides an activation function for the given image. The initial layers of CNN extract the primitive features like blobs, edges, and colours that are abstracted by the deep inner. Malaria is a life-threatening disease, which is caused by the bite of anopheles mosquitoes. It spreads plasmodium parasites in the human liver, affects the red blood cells and develops into life-threatening symptoms. According to the estimation of World Health Organization (WHO), in the year 2018, more than two hundred million cases of malaria have been reported and more than 90% of the cases are in the African region. To prevent, control and eliminate malaria, more than 3 billion dollars have been spent. Computer-aided diagnostic (CADx) tools have the potential to lessen the burden on healthcare staff by aiding in disease interpretation and diagnostic process using some machine learning (ML) algorithms applied to microscopic blood cell images. To overcome challenges of developing hand-engineered features that capture even the minute variations in the underlying data, deep learning (DL), also known as deep hierarchical learning, is widely used with significant success owing to its high accuracy. This paper, not being the subject's first study paper, several study papers have been released before, bearing

witness to automated diagnosis of malaria in blood smear images. Early detection of malaria is crucial to ensure appropriate diagnostic process and increase the chances of the patient being cured. Considering the severity of malaria by the number of deaths caused by this illness, accepting possible negligible mistakes caused while execution by an automated method is justifiable. Deep learning techniques have advanced over the years and have proven to be much better than traditional methods as they ease the feature extraction process. Hence, in this paper we further utilize deep learning as a method and propose an approach using a Convolutional Neural Network (CNN) for detecting malaria from microscopic cell images using image classification.

2. LITERATURE SURVEY

Alejandro israel et al. This work aims to classify malaria infected red blood cells from those uninfected using two deep learning approaches. Taking advantage of efficient deep learning approaches applied in computer vision field, the present framework proposes two deep learning architecture based on Convolutional-Recurrent neural Networks to detect accurately malaria infected cells. The first one implements a Convolutional Long Short-Term Memory while the second uses

a Convolutional Bidirectional Long Short-Term Memory architecture.

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Divyansh Shah et al. Malaria is one of the deadliest diseases across the globe. This is caused by the bite of female Anopheles mosquito that transmits the Plasmodium parasites. Some current malaria detection techniques include manual microscopic examination and RDT. These approaches are vulnerable to human mistakes. Early detection of malaria can help in reducing the death rates across the globe. Deep Learning can emerge as a highly beneficial solution in the diagnosis of disease. This model gives a faster and cheaper method for detecting plasmodium parasites. The custom convolutional neural network is primarily designed to distinguish between healthy and infected blood samples. The

proposed model consists of three convolutional layers and fully connected layers each.

Satabdi Nayak et al. With about 200 million global instances and over 400,000 fatalities a year, malaria continues an enormous strain on global health. Modern information technology plays a major part in many attempts to combat the disease, along with biomedical research and political efforts. In specific, insufficient malaria diagnosis was one of the obstacles to a promising mortality decrease. The paper offers an outline of these methods and explores present advancement in the field of microscopic malaria detection and we have ventured into utilization of deep learning for detection of Malaria Parasite. Deep Learning over the years has proven to be much faster and much more accurate as it automates feature extraction of the dataset. In this research paper, we investigated various models of Deep Learning and monitored which of these models provided a better accuracy and faster resolution than previously used deep learning models. Our results show that Resnet 50 model gave the highest accuracy of 0.975504.

3. PROPOSED SYSTEM

The proposed CNN model consists of three convolutional layers. There are 32

filters present in the first convolutional layer, 64 filters in the second convolutional layer, 128 filters in the third convolutional layer with each layer having kernel size of 3*3, and an activation function as ReLU. The sandwich design and appropriate initialization of weights performed by adam optimizer that improves the learning process of the model. The model incorporates three pooling layers. It consists of a pooling window having 2*2 pixels. Furthermore, the model has three fully connected layers that take the output of the previous layers and start classifying the images with labels. The initial two fully connected layers have ReLU as an activation function and a dropout of 50% to avoid overfitting. The output layer has Sigmoid as an activation function. We evaluated the execution of the CNN model by focusing on accuracy.

we investigate two training approaches and compare both based on performance and select the better approach. We further evaluate our proposed model on testing set using metrics like F1 Score, AUC Score, Specificity and Sensitivity.

The important contributions are:

1) Present a Convolutional Neural Network based approach for detection of malaria in cell images which outperforms the existing methods based on accuracy performance.

2) Perform a comprehensive evaluation of the proposed method using other performance metrics like F1 Score, AUC Score, Specificity and Sensitivity

VGG16 is a deep convolutional neural network architecture that was developed by the Visual Geometry Group (VGG) at the University of Oxford. It gained popularity due to its simplicity and effectiveness in various computer vision tasks, especially in image classification and object detection. Let's break down the architecture and functionality of each layer:

Input Layer:

Accepts the input image data. In VGG16, the input size is typically 224x224 pixels with three colour channels (RGB).

Convolutional Layers:

The convolutional layers form the backbone of the network. VGG16 consists of 13 convolutional layers stacked one after the other. Each convolutional layer performs a series of convolutions on the input image using learnable filters (kernels).

These layers are responsible for learning hierarchical features of increasing complexity as we go deeper into the network. The convolutional layers use

small receptive fields (3x3 kernel size) with a stride of 1 and 'same' padding, which means the spatial dimensions of the input and output volumes remain the same.

Max Pooling Layers:

After some of the convolutional layers, max-pooling layers are added to reduce the spatial dimensions of the feature maps while retaining important features. Max pooling is performed with a 2x2 window and a stride of 2. It selects the maximum value from each non-overlapping 2x2 region of the input.

Fully Connected Layers:

Towards the end of the network, there are three fully connected layers. Each fully connected layer connects every neuron in the previous layer to every neuron in its layer.

The fully connected layers in VGG16 have 4096 neurons each

Output Layer:

The final layer is a softmax layer that produces the probabilities for each class in the classification task. The number of neurons in the output layer corresponds to the number of classes in the dataset being used for training

SYSTEM ARCHITECTURE
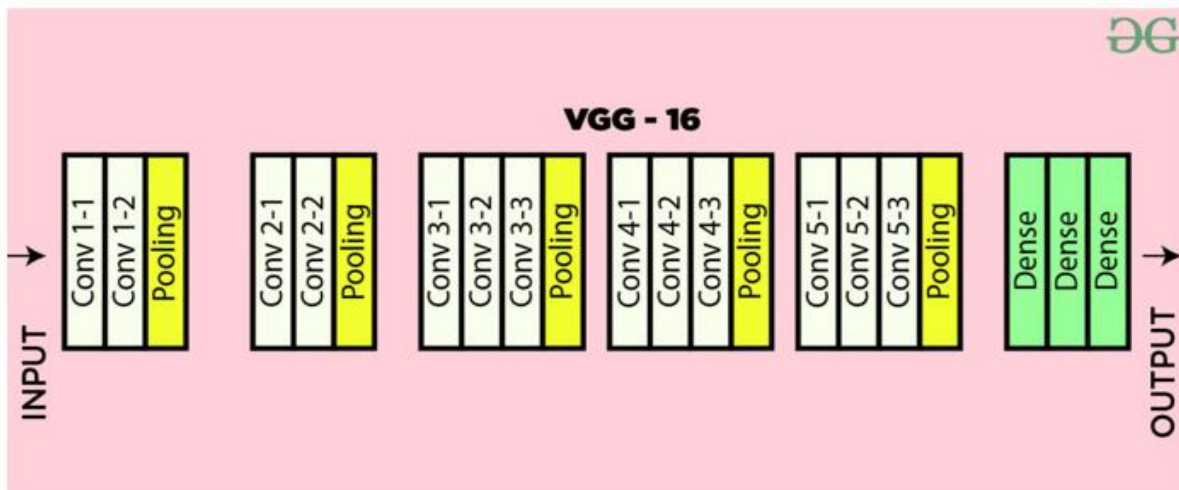
Fig.1 System architecture

For malaria parasite image classification, the VGG16 architecture can be employed with transfer learning. Transfer learning involves using pre-trained models, such as VGG16 trained on ImageNet, and fine-tuning them on a new dataset, like one containing malaria parasite images. Here's how VGG16 architecture can be adapted for this task:

Input Layer: The input layer would still accept images, typically resized to fit the VGG16 input size, which is 224x224 pixels with three color channels (RGB).

Convolutional Layers: The pre-trained convolutional layers of VGG16 act as feature extractors, capturing various patterns and features from the malaria parasite images.

Transfer Learning: Instead of training the entire network from scratch, the pre-trained VGG16 model's weights are often frozen, preventing them from being updated during training. This approach allows the model to retain the knowledge learned from ImageNet and focus on learning malaria-specific features.

Fine-Tuning Layers: While the convolutional layers are frozen, the fully connected layers at the end of the network are replaced or fine-tuned for the specific malaria classification task. This adaptation tailors the model's output to match the desired classes, such as "infected" or "uninfected" malaria cells.

Training: The adapted VGG16 model is then trained on the malaria parasite dataset, typically using techniques like gradient descent and backpropagation to optimize the model's parameters for accurate classification

Image Acquisition

The first step of the Malaria Parasite Classification is image acquisition. High-quality Malaria Parasite dataset used which are obtained from open Github repository.

The entire sample set is divided into three parts: training samples and validation samples in the training phase and testing samples in the testing phase. Moreover, the sample set is divided into positive and negative samples—a positive sample is an image showing patient behaviors, whereas a negative sample is a background image.

Annotated Dataset Collection

A Knowledge-based dataset is created by proper labeling of the collected images with unique classes.

Image Processing

The obtained images that will be engaged in a preprocessing step are further enhanced specifically for image features during processing. The segmentation process divides the images into several segments and utilized in the extraction of Malaria Parasite from dataset.

Feature-Extraction

This section involves the convolutionary layers that obtain image features from the resize images and is also joined after each convolution with the ReLU. Max and average pooling of the feature extraction

decreases the size. Ultimately, both the convolutional and the pooling layers act as purifiers to generate those image characteristics.

Classification

The final step is to classify images, to train deep learning models along with the labeled images to be trained on how to recognize and classify images according to learned visual patterns. The authors used an open-source implementation via the TensorFlow module, using Python and OpenCV including the Faster R-CNN model.

Deployment

The last step of machine learning life cycle is deployment, where we deploy the model in the real-world system.

If the above-prepared model is producing an accurate result as per our requirement with acceptable speed, then we deploy the model in the real system. But before deploying the project, we will check whether it is improving its performance using available data or not. The deployment phase is similar to making the final report for a project.

4. RESULTS AND DISCUSSIONS

Data Augmentation:

Data augmentation techniques are applied to the training set to increase dataset diversity and improve the model's generalization ability.

Augmentation techniques such as rotation, flipping, shifting, zooming, and changes in brightness or contrast are commonly employed.

Model Training:

The VGG16 model is trained on the pre-processed dataset using techniques such as transfer learning.

Transfer learning involves using the pre-trained weights of the VGG16 model (trained on ImageNet) as a starting point and fine-tuning the model on the malaria parasite dataset.

Evaluation Metrics:

Model performance is evaluated using metrics such as accuracy, precision, recall, and F1-score on the validation and test sets.

These metrics assess the model's ability to correctly classify infected and uninfected blood smears, providing insights into its effectiveness in malaria parasite detectio

Fig.2 malaria parasite detection

Fig.3 Anaconda activated

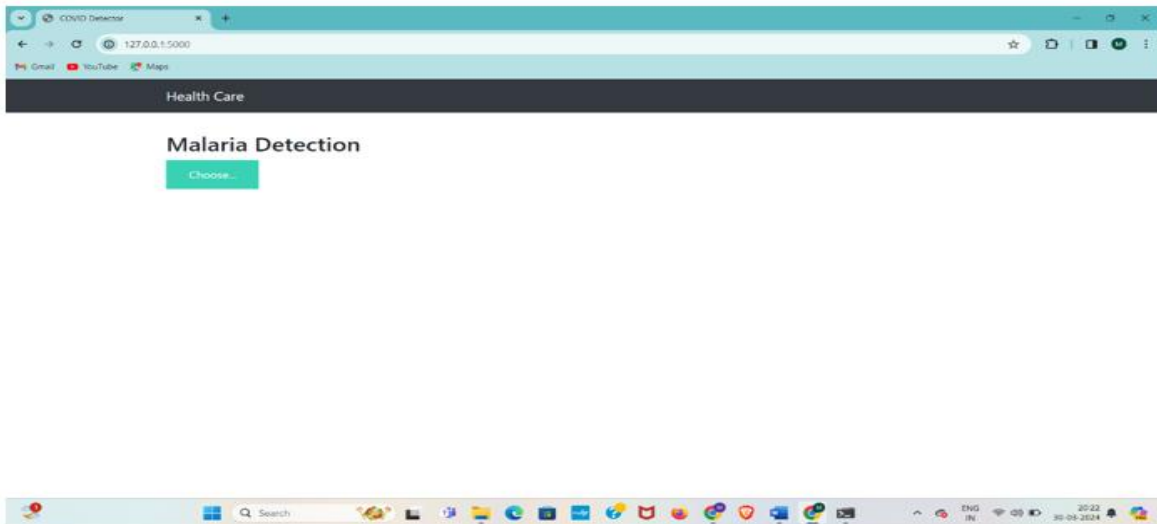Fig.4 Running using TensorFlow

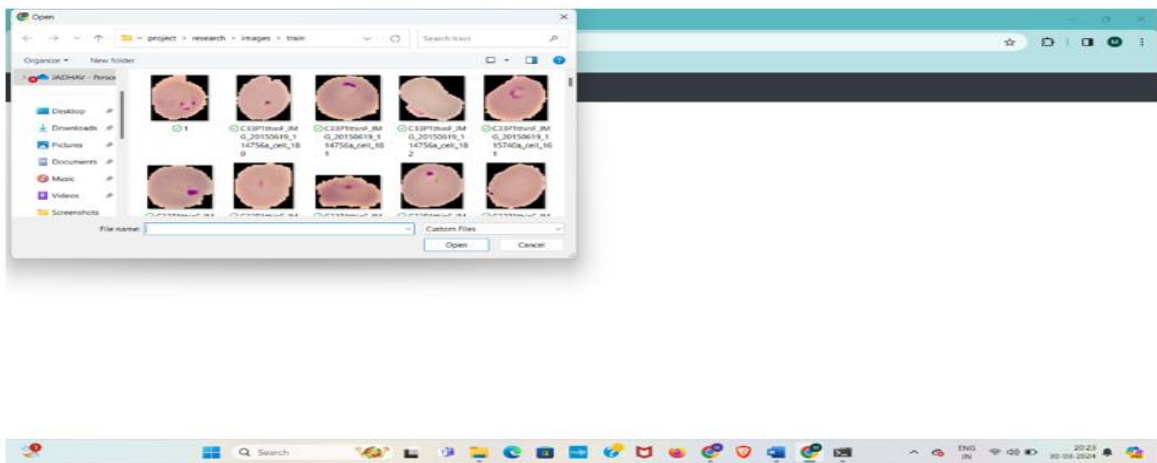Fig.5 Malaria detection process
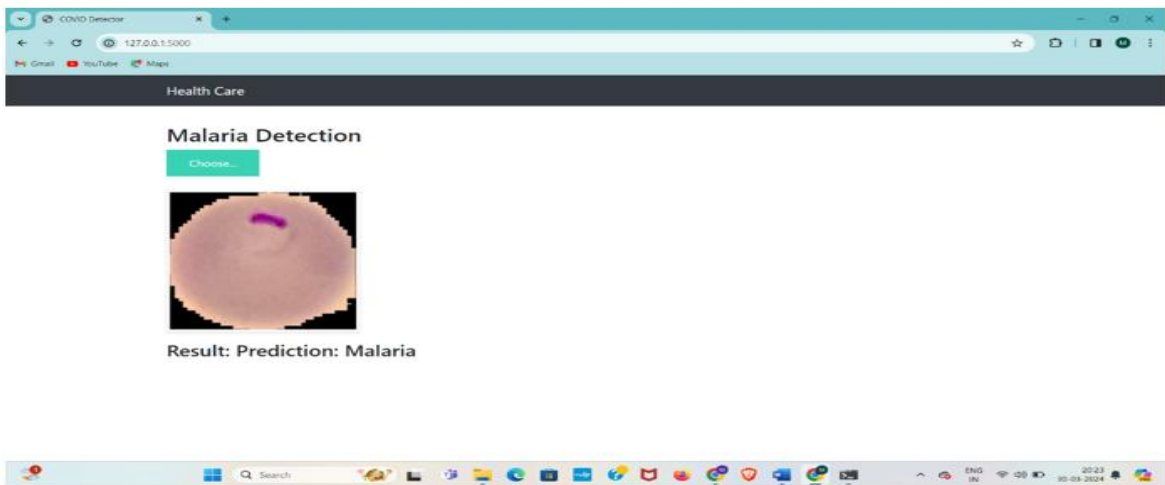

Fig.6 Malaria dataset uploaded

Fig.7 Prediction of malaria

5. CONCLUSION

As pathologists manually do the detection of malaria parasites using microscopes, there are chances of human errors and false detection of parasites that can cause further issues in the treatment of the patient. This system reduces the possibilities of human error in the detection of malaria parasites using image processing and deep learning methods. We developed an image classification model by using convolutional neural networks and labelled datasets. The proposed model yields an accuracy of ≈ 95%. The system is robust, and other factors do not affect it. We believe with more computing power the model can perform better than the present results. The model can further be expanded to diagnose other diseases from the blood samples.

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