

Survey of Malaria Detection using Deep Learning

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Abstract-Malaria is a deadly mosquito-borne parasitic disease caused by the parasites that are transmitted to people through the bites of female Anopheles mosquito. The current malaria detection techniques include manual microscopic examination, rapid diagnostic tests (RDTs) which are vulnerable to human mistakes. The insufficient diagnosis of malaria was one of the obstacles, hence, the modern information technology plays a major role in many attempts to combat the disease. Early detection of malaria can help in reducing the death rates across the globe. Deep learning, therefore, emerges as a highly beneficial solution in the diagnosis of the disease. This model gives a faster and cheaper method for detecting the parasites (Plasmodium). The custom convolutional neural network is primarily designed to distinguish between healthy and infected blood samples. This model consists of three convolutional layers.

Keywords-Malaria, deep learning, convolutional neural network, plasmodium.

I. INTRODUCTION

Malaria is a disease caused by the bites of female Anopheles mosquito. Plasmodium parasite gets injected in the body due to the sting of the Anopheles 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. 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. 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. To avoid false results, these stained objects are analysed 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. 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 innerlayers of CNN to create high-level features that give a more affluent image representation.

II. RELATED WORK

Numerous research projects around the world have been undertaken to implant deep learning models for clinical use. Some of the research conducted on this work is, a CNN based Deep Learning model AlexNet designed by Alex Krizhevsky [12] in 2012 that subsequently increased the performance of CNN in categorizing natural images. Many CNNs like GoogLeNet, VGGNet, and ResNet established considerable improvements in attaining ILSVRC annual challenges. Xception, a model designed by [10] used depth-wise separable convolutions that outpaced the Inception-V3 model on the ImageNet in the classification of data.

In 2016, Huang [6] proposed a model wherein each layer of the model is connected to the entire next layer by using network architecture and was named as Densely Connected Convolutional Networks (DenseNet) which is a variant of CNN. The model has had a lot of improvements using significantly fewer computations and parameters making a state-of-art model.

CNN provides a promising result that gets accompanied by the availability of large amounts of data. Transfer Learning (TL) approach is implemented where DL models are either fine-tuned or utilized as feature extractors in visual recognition assignments. The results published in Razavian et al. (2014) [13], made a point that CNN trained on huge datasets may serve as feature extractors for a wide range of computer vision tasks that lead to improved performance compared to revolutionary methods [14]. Researchers across the world have started to apply DL models in a variety of medical image analyses and understanding tasks that yields promising results [15].

There are various models developed consisting of a large number of layers providing accuracy in the range of 90- 95%. We find potential in focusing on the number of layers in the model along with the images in the training and testing dataset which will result in getting noteworthy accuracy. This imparts motivation to present a system with an adequate number of layers in the model that gives exceptionally good results.

III. WORKING

This work aims to build a system for the detection of malaria parasites in blood samples. The system intends to distinguish between healthy and parasitized blood samples. The work consists of image recognition and image classification that requires a systematic sequence of multiple events to attain the target. The model was built in Python 3.7.x and Visual Studio Code IDE. The method involved in solving such a problem usually is as follows. The acquired images go through several pre-processing techniques. The pre-processing is done to make images more suitable for the subsequent process. Pre-processing techniques involve resizing reduction in noise, and image contrast. Image size normalization is essential for maintaining the spatial resolution of images from multiple sources. The proposed model is depicted in below mentioned Fig. 1

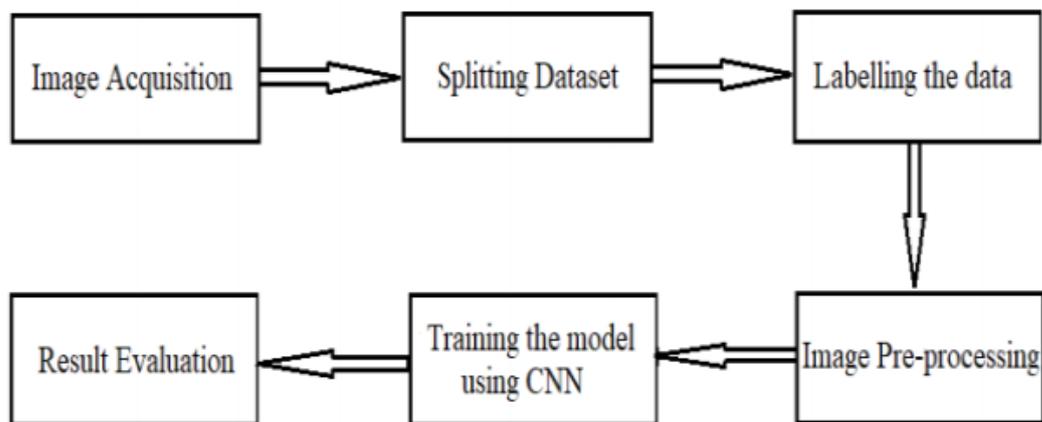


Fig. 1. Block Diagram

Features are categorized by using an appropriate classifier and then are placed in various classes. Suitable parameters are selected which appropriately describes the image. Features are deduced from images or quantities like histograms and signatures. In Fig. 2 images are labelled as parasitized (0) samples and uninfected (1) samples. These labels are later used in the model for predicting the output.

Further, the images are split into train and test dataset. The training dataset consists of 5000 images and the testing dataset consist of 1000 images. Later the CNN model is trained, and the output of the model is predicted. These outputs from the model help to determine the infected and healthy blood samples. Pre-processing is required on the images to maintain uniformity in the dataset. In Fig. 3, image pre-processing is done on the images by using ImageDataGenerator. It helps in providing more variations in images and focusing on required parameters.

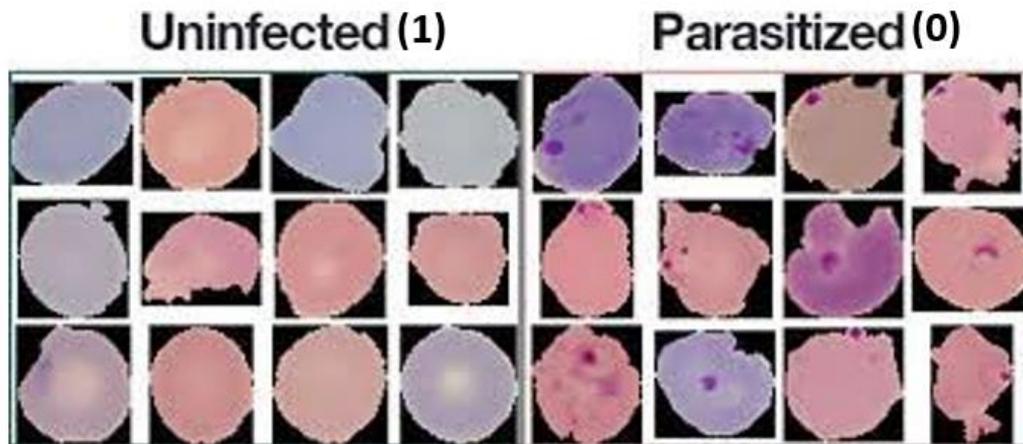


Fig. 2. Labelled Dataset

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train_datagen = ImageDataGenerator(rescale = 1./255,
                                   shear_range = 0.2,
                                   zoom_range = 0.2,
                                   horizontal_flip = True)
    
```

Fig. 3. Code snippet for image pre-processing

Using ImageDataGenerator, the images are rescaled to ensure that pixel values of all the images are between 0 and 1 irrespective of their RGB coefficients. The sheer range is used to focus more on the desired features of an image by neglecting unwanted surroundings. Here, the sheer range is considered to be 20%. Similarly, zoom range and horizontal flip are selected to provide more variations in the images helping in enhancing the quality of dataset which yields better results.

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 and the output layer have Sigmoid as an activation function.

V. CONCLUSION

As the detection of malarial parasites are done manually by pathologists 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 malarial parasite detection by using image processing and deep learning methods. We developed an image classification model by using convolutional neural networks and labelled datasets. The model can further be expanded to diagnose other diseases diagnosed from the blood samples.

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