Automated Malaria Parasite Detection Using Deep Learning Techniques

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ABSTRACT - Malaria is a global illness that has claimed the lives of millions of people. It is caused by Plasmodium parasites. A drop of the patient's blood spread out as a "blood smear" on a magnifying lens slide beneath a microscope can be used to identify malarial parasites. It is vital to apply deep learning algorithms to detect malaria parasites. In the proposed system, red and parasite cells from a peripheral blood smear images are separated using the segmentation process. In order to avoid the overfitting problem data augmentation method is used. Using Deep convolutional neural network model will extract the features from the given image then classify the features as either red blood cells or parasite cells. Using different combinations of the original images and augmented images to compare the classification accuracy associated with training and testing images. The proposed architecture is 98.7% accurate in identifying malaria and red blood cells, according to the testing data.
Keywords—Image processing, Deep Learning

I.   INTRODUCTION

Malaria is a serious fever infection caused by Plasmodium parasites, which are transferred to humans by mosquito bites from infected female Anopheles mosquitoes. Human malaria is caused by five parasite species, two of which, P. falciparum and P. vivax, are the most dangerous. P. falciparum is the most dangerous intestinal parasite and the most common on the African continent. In many countries outside of Sub-Saharan Africa, P. vivax is the most common malaria parasite. According to the latest World Malaria Report, 241 million malaria cases will be reported in 2020, up from 227 million in 2019. The estimated number of malarial deaths in 2020 remained at 6,27,000, an increase of 69,000 deaths over the previous year. While COVID-19 pandemic-related interruptions caused roughly 66 percent of these deaths (47,000), the remaining 33 percent of deaths (22 reflect a recent modification in WHO's malaria mortality calculation philosophy (independent of COVID-19 disturbances).

A drop of the patient's blood spread out as a "blood smear" on a magnifying instrument slide beneath a magnifying lens can be used to identify malarial parasites. The sample is dyed (typically with Giemsa stain) before analysis to give the parasites a unique appearance. Regardless, analysts developed a number of image processing algorithms that were integrated with machine learning algorithms for the early detection of malaria using blood smear images. Malaria analysis has been automated using deep learning techniques.

II.   LITERATURE SURVEY

Using a deep belief network, Dhanya bibin.et.al. [1] identified the presence of malarial parasites in human peripheral blood smear images (DBN). A trained model was used to classify 4100 peripheral blood smear images into the parasite or non-parasite classes in the framework of a DBN. The suggested DBN is pre-trained using the contrastive dissimilarity technique, which involves stacking restricted Boltzmann machines. Extract features from the images and populate the DBN's visible parameters to train the DBN. Finally, using a backpropagation technique that registers the likelihood of class names, the DBN is discriminatively calibrated. With an F-score of 89.66 percent, a sensitivity of 97.60 percent, and a specificity of 95.9%, the proposed system outperformed the competition.

Rajaraman, Sivaramakrishnan, et al. [2] performed numerous studies to analyze the weights, saliencies, class activation maps, and ROI localization in order to better understand the specific behavior of the customized CNN applied to the problem of distinguishing parasitized from uninfected cells in order to aid in malaria screening. Finally, a clinical dataset was used to validate the models' performance at the patient and cell levels, as well as to look for statistically significant differences in performance measures. The proposed system had a

cell level accuracy of 97.9 percent and a patient level accuracy of 95.1percent

Rahman, Aimon, et al. [3] conducted a series of studies to enhance malaria classification from segmented red blood cell smears using end-to-end deep learning. Data augmentation approaches used on the training set produced effective outcomes. Then, show how to use various network architectures, such as custom network architecture, fine tuning on pre-trained models, and extracting features using a convolutional network (CNN), and finally, a support vector machine classifier (SVM). TLVGG16 outperformed all other models with an accuracy of 97.77 percent using the proposed technique on the hold out test.

Nakasi, Rose, Ernest Mwebaze, and Aminah Zawedde [4] proposed an end-to-end machine learning strategy for trophozoites and WBC localization in thick blood smears for the measurement of malaria parasite density and integrated the model into a mobile smartphone detection app. The on-device inference strategy is based on a Faster R-CNN ResNet model with SSD MobileNet V2. The COCO dataset was used to pre-train all models for the purpose of object detection. Demonstrating that the proposed models can efficiently identify parasites and WBCs and count them for malaria parasitemia diagnosis in a fast, accurate, and consistent way. The proposed SSD model was also quantified and implemented in a mobile smartphone-based inference engine for real-time detection of malaria parasites and WBCs.

Plasmodium VF-Net is a system that assesses whether a patient is infected with the malaria parasite Plasmodium falciparum or Plasmodium vivax by computing image-level and patient-level infections [5]. Plasmodium VF-Net finds candidates for Plasmodium parasites using a Mask Regional-Convolutional Neural Network filters out false positives with a ResNet50 classifier, and identifies an infected patient based on patch-level probability aggregation and parasite levels. Finally, it obtains an overall accuracy of around 92 percent on a patient and image level when tested on 350 patients with 6000 photos.

Masud, Mehedi, et al. [6] described how deep learning architecture, such as the CNN, may be used to identify malaria in real time and with high accuracy from input images. In the categorization of malaria, an automatic learning rate finder, in combination with a commonly used regular usage such as batch normalization and dropouts, produces promising results. The suggested model outperforms customized and other CNN models (pre-trained such as VGG-16 and ResNet-50) in distinguishing healthy and infected cells with malaria. The model was integrated into an Android-based mobile application to make malaria detection easier and faster. In classifying parasitized and uninfected cell images, the proposed methodology has a 97.30 percent accuracy rate.

Abdurahman, Fetulhak, et al. [7] made use of YOLO models such as YOLOV3 and YOLOV4 are changed as YOLOV3-MOD1, YOLOV3-MOD2, and YOLOV3-MOD1 by increasing the feature size and adding more detection layers to improve the detection of small objects in microscopic images, such as malarial parasites. In small item detection, new anchor boxes are created using the K-means clustering algorithm. The proposed models YOLOV4-MOD, YOLOV3-MOD2, and YOLOV3-MOD1 achieved accuracy with mAPs of 96.32 percent, 96.14 percent, and 95.46 percent, respectively, for 608×608 input image resolution.

Sen Li.et.al. [8] suggested a deep learning technique for classifying malarial parasites of various stages in blood smear images using a deep transfer graph convolutional network (DTGCN). Unsupervised learning is used by the DTGCN model to transfer information learnt from source pictures containing discriminative morphological aspects of multi-stage malarial parasites, resulting in effective parasite recognition information. To identify multi-stage malarial parasites, the GCN algorithm is applied to segregate graph characteristics. The method achieved a precision of 96.1 % for parasitized images and 94.7 % for uninfected images in readily available microscopic images of multi-stage malarial parasites.

III.   PROPOSED METHODOLOGY

The proposed model of the system uses image processing and convolution neural network (CNN) to detect the malaria parasite and classify the image category as red blood cells and malaria parasite cells. Figure 1 shows the system model architecture; first step is to download the peripheral blood smear images as dataset.
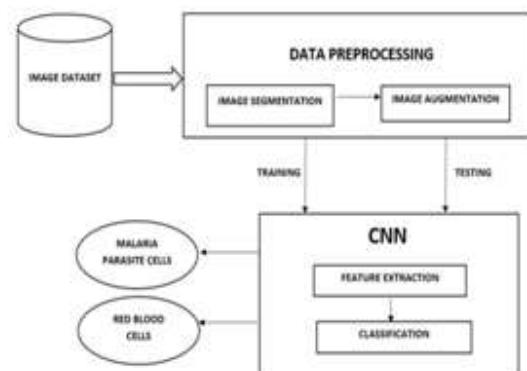

Figure 1

At pre-processing stage, segmentation of red blood cells and parasite cells from the blood smear image have been done. The segmented cell images are then passed to a data augmentation technique, which is used to significantly enhance the dataset's size. The trained model will extract features from the preprocessed image and classify the class as either red blood cells or parasite cells based on those features. The trained model will detect and classify the features using the validation data test.

A. DATASET ACQUISITION

From image preprocessing to evaluating the effectiveness of recognition algorithms, appropriate datasets are necessary at every stage of classification study. In total, 1328 peripheral blood smear images were acquired from the open dataset, along with an annotation file in. json format that included the image URL, image shape, channel, and checksum for security purposes. and where the objects are located with their coordinate points. 80% of blood smear image is taken for training and 20% for testing purpose
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B. SEGMENTATION PROCESS

The segmentation technique reduces the image's complexity, making subsequent processing or analysis of the image easier. In proposed method, image pre-processing involves extracting features from a peripheral blood smear image as red blood cells in figure 2 and infected (parasite) red blood cells in figure 3 using the coordinate points of features in the annotation file of all images.

Figure 2   Figure 3

C.AUGMENTATION PROCESS

Image data augmentation is a technique for artificially boosting the size of a training dataset by making enhanced copies of the dataset's images. Here, the dataset size is increased by rotating the images and flipping the images as horizontally and vertically. More datasets are used to train the deep learning model, which results in more accurate results.

D.CONVOLUTIONAL NERUAL NETWORK

The purpose of network training is for the neural network to learn the characteristics that distinguish one class from another. A convolutional neural network model was used to train the dataset. Image features are extracted and learned by the passing the input through convolutional layer, pooling layer and classification are done through flatten layer, fully connected layer and softmax layer, which identifies whether input is infected(parasite) or uninfected(red) blood cells. The figure 4 shows architecture of the proposed system, to classify the red and parasite cells from blood smear images
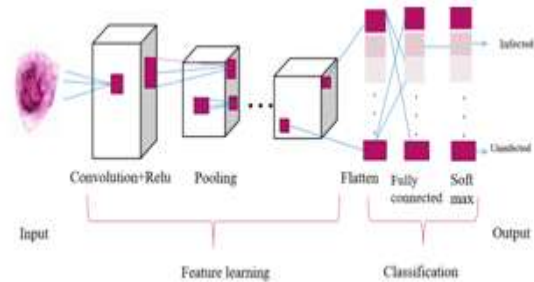
Figure 4

IV.RESULTS AND DISCUSSION

From figure 5, the accuracy of the classification of red and parasite cells from given peripheral blood smear images is 98.7%. The following figure 6 shows that prediction of red and parasite blood cells. The table 1 describes the comparison for existing and proposed methods.
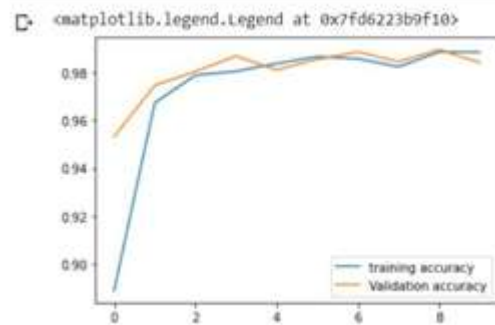
Figure 5

Figure 6

Ref.No	Methodology	Performance metrics
[1]	Deep Belief Network (DBN)	F-score- 89.66%, Sensitivity-97.60%, Specificity -95.9%
[2]	Customized CNN	Accuracy-97.9% at cell and 95.1% patient level images
[3]	TLVGG16	Accuracy - 97.77%
[4]	FasterR-CNN, SSD Mobile Net	F1 score: - Parasites: 0.789, WBC: 0.8426 Parasites:0.603, WBC: 0.7528
[5]	Mask R-CNN	Accuracy:92%
[6]	CNN	Accuracy:97.30%
[7]	YOLOV4-MOD, YOLOV3-MOD2, YOLOV3-MOD1	Accuracy:96.32%,96.14%, 95.46 %
[8]	Deep transfer graph convolutional network	Accuracy: 96.1% for parasitized 94.7 % for uninfected images
Proposed Method	Convolutional Neural Network	Accuracy – 98.7%

Table 1 Comparison table for existing and proposed methods

V.CONCLUSION

According to the World Health Organization, Plasmodium parasites infect around two million people each year, resulting in 300 to 500 million infection cases. Manual microscopy examination of peripheral blood smears is the gold standard and most often used diagnostic approach for malaria, although it cannot be recommended as a safe testing strategy. The goal of this research is to create an automated decision support system that can detect and classify malaria parasite cells and red blood cells from peripheral blood smear images using a deep learning architecture. The testing findings show that the proposed architecture detects malaria with a 98.7 percent accuracy rate. The proposed methodology could be developed into a mobile application to detect malaria parasite and red blood cells in peripheral blood smear images in the future, which will aid individuals in detecting malaria earlier.

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