Review On Image Processing Based Automatic Detection Of Malaria

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***Abstract*— Malaria is a disease caused when a female Anopheles mosquito bites. There are over 200 million cases recorded per year with more than 400,000 deaths. Current methods of diagnosis are effective; however, they work on technologies that do not produce higher accuracy results. Henceforth, to improve the prediction rate of the disease, modern technologies need to be performed for obtain accurate results. Deep learning algorithms are developed to detect, learn, and determine the containing parasites from the red blood smears. This chapter shows the implementation of a deep learning algorithm to identify the malaria parasites with higher accuracy. Design propose system a new and highly robust deep learning model based on a convolutional neural network (CNN) which automatically classifies and predicts infected cells in thin blood smears on standard microscope slides. This study proposes a new and robust machine learning model based on a convolutional neural network (CNN) to automatically classify single cells in thin blood smears on standard microscope slides as either infected or uninfected. . A convolutional neural network (CNN) architecture, which has 20 weighted layers is designed and proposed to identify parasitized microscopic images from uninfected microscopic images. A total of 27,558 thin blood cell images were used to train and test the CNN model, and 95.28% overall accuracy was obtained. The experimental results on large clinical dataset show the effectiveness of the proposed deep-learning method for malaria disease detection**

Keywords—CNN,Deep Learn,Maleria etc

I Introduction

Cognitive computing replicates the way humans solve problems while artificial intelligence and machine learning techniques search for creating novel ways for solving problems that humans can potentially do better. A substantial amount of research has been done during the last decades using machine learning algorithms for cost-effective solutions to support healthcare professionals in reducing diseases. Malaria disease originated from Plasmodium parasites through mosquito-borne infection. Malaria is very common over the world mainly in tropical regions. When infected female Anopheles mosquitoes bite a person, the parasites enter into the blood and begin damaging red blood cells (RBC) that carry oxygen. Flu virus is the malaria's first symtoms. symptom. The symptom generally starts in few days or weeks. Most importantly, the lethal parasites can stay alive more than a year in a person's body without showing any symptoms. Therefore, a late treatment can cause complications and even death. Hence, many lives can be saved through early malaria detection. Almost 50% of the population in the world is in danger from malaria. There are more than 200 million malaria cases and 400,000 deaths reported every year due to malaria. In practice, to identify malaria, microscopists inspect blood (thick and thin) smears for disease diagnosis and calculate parasitemia. Microscopy examination is used as one of the prime standards for the diagnosis of malaria [1, 2] to identify the existence of parasites in a blood drop from thick blood smears. However, thin blood smears are used for distinguishing the species of parasite and the development of malaria stages. Examination through a microscope is commonly used since it is cheap but time-consuming. The examination accuracy relies on the quality of blood smear and a skilled person who is expert in the classification and examination of uninfected and parasitized blood cells. Malaria is a disease activated by a type of microscopic parasite transmitted from infected female mosquito bites to humans. Malaria is a fatal disease that is endemic in many regions of the world. Quick diagnosis of this disease will be very valuable for patients, as traditional methods require tedious work for its detection. Recently, some automated methods have been proposed that exploit hand-crafted feature extraction techniques however, their accuracies are not reliable. Deep learning approaches modernize the world with their superior performance. Convolutional Neural Networks (CNN) are vastly scalable for image classification tasks that extract features through hidden layers of the model without any handcrafting. The detection of malaria-infected red blood cells from segmented microscopic blood images using convolutional neural networks can assist in quick diagnosis, and this will be useful for regions with fewer healthcare experts. The contributions of this paper are two-fold. First, we evaluate the performance of different existing deep learning models for efficient malaria detection. Second, we propose a customized CNN model that outperforms all observed deep learning models. It exploits the bilateral filtering and image augmentation techniques for highlighting features of red blood cells before training the model. Due to image augmentation techniques, the customized CNN model is generalized and avoids over-fitting. All experimental evaluations are performed on the benchmark NIH Malaria Dataset, and the results reveal that the proposed algorithm is 96.82% accurate in detecting malaria from the microscopic blood smears

II Literature Survey

PROBLEM STATEMENT

Traditional approaches for malaria detection are very time-consuming, may produce inaccurate reports due to human errors, and are laborious for extensive diagnoses. This motivates us to propose an automatic detection of malaria applying deep learning techniques and using a mobile application that leads to early diagnosis which is fast, easy, and effective.

MOTIVATION

Malaria is a deadly, infectious mosquito-borne disease caused by Plasmodium parasites. These parasites are transmitted by the bites of infected female Anopheles mosquitoes. While we won't get into details about the disease.

THE NEED FOR AN AUTOMATED MALARIA DIAGNOSIS PROCESS

The issues associated with manual diagnosis present the case for automation of the malaria diagnosis process. The automation of the diagnosis process will ensure accurate diagnosis of the disease and hence holds the promise of delivering reliable health-care to resource-scarce areas. Hence, rural areas suffering from lack of specialized infrastructure and trained manpower can benefit greatly from automated diagnosis. Automating the diagnosis of malaria involves adapting the methods, expertise, practices, and knowledge of conventional microscopy to a computerized system structure [3]. Early detection of malaria is essential for ensuring proper diagnosis and increasing chances of cure. In consideration of the severity and the number of fatalities claimed by this disease, it is rational to accept potential small implementation errors introduced by an automated system. An automated system consists of streamlined image processing techniques for initial filtering and segmentation and suite of pattern recognition and/or machine learning algorithms directed toward robustly recognizing infected cells in a light or whole slide microscopic image [4]. Previous studies have shown that the degree of agreement between clinicians on the severity of the disease in a given patent's sample is very low. Hence, a computer-assisted system as a decision support system can be paramount to faster and reliable diagnosis. It can help provide a benchmark and standardized way of measuring the degree of infection of the disease [5].

EXISTING SYSTEM

Traditional methods of automating the malaria detection process involve complex image-processing techniques with hand-engineered features e.g., shape, color, intensity, size, and texture [5–7]. In these methods, the red blood cells are detected from microscopic images by using different segmentation techniques. After the selection of appropriate features for red blood cells, a computed set of features is used in the classification of segmented images into infected and uninfected classes.

In the literature, various methods are adopted for the segmentation, feature extraction, and classification of malaria diagnosis [8]. After analyzing conventional and recent malaria detection methods, it is observed that there is a tradeoff between accuracy and the computational complexity of models, that is, when the accuracy of a model increases, its computational complexity also increase [9].

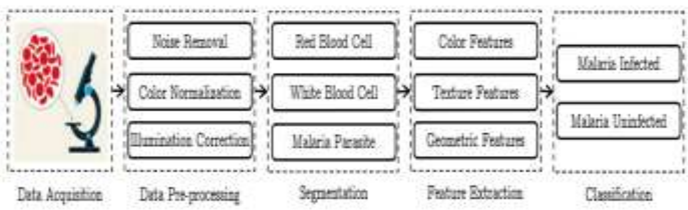


Figure 1. Traditional automated malaria detection pipeline.

PROPOSED SYSTEM

The proposed system for detection of malaria using slides of red blood cell images consists of various steps which are shown in figure 2. Initially the red blood cell images are pre-processed and then the splitting of samples into training and testing is done. Then training of CCN classifier is done using the training samples. Once the CNN classifier is trained, the trained CNN classifier gets the input of testing samples to detect malaria. Evaluation parameters are then applied to the system to evaluate the accuracy, sensitivity, and specificity and classification error. Convolutional Neural Networks (CNN), a category obtained from deep learning (DL) models is used to obtain superior end results with feature extraction and categorization. CNN based DL models are a characteristic extractors towards classifying the blood cells. CNN is a promising device for feature extraction. Automated malaria screening using DL techniques, consequently, function an effective diagnostic aid.

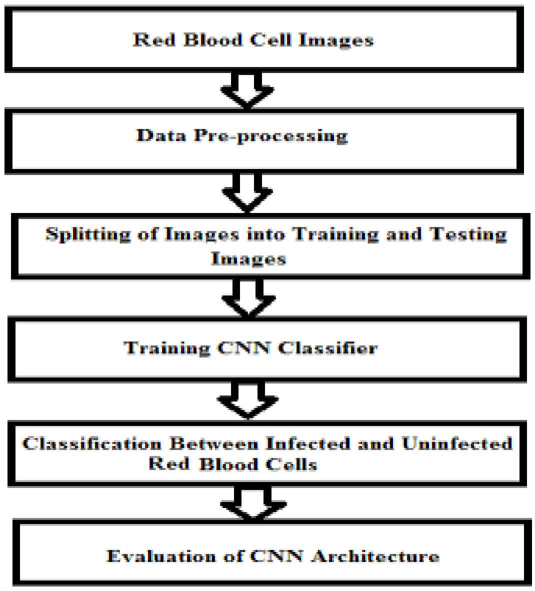
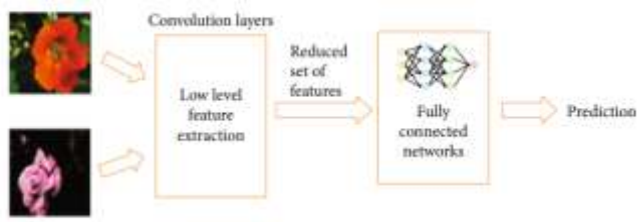


Fig 2 Block Diagram for Malaria Detection

PROPOSED METHOD

Deep Learning for Malaria Detection. Deep learning techniques are now widely used for image classification, video recognition, and medical image analysis. A convolutional neural network (CNN), a type of deep neural networks, is mainly considered for research in computer vision field. The deep architecture of CNN is its main power. The convolutional layer in the CNN works as an automatic feature extractor that extracts hidden and important features. Extracted features are passed to a fully connected neural network which performs classification images by maximizing the probability scores. A general CNN model is shown in Figure 3.



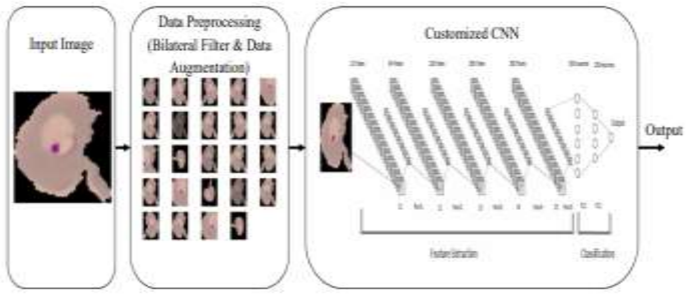


Figure 3. Block diagram of the proposed malaria detector.

PROPOSED ALOGORITHM

Deep learning (DL) techniques are exploited for automated malaria diagnosis with appreciable detection rates. Deep learning models eliminate the computation of hand-crafted features, as the hidden layers of deep models extract features automatically by analyzing the data. Deep learning models require large datasets for training neural networks and to improve the accuracy of the model. However, in medical applications like malaria diagnosis, relatively small datasets are available. This is because building an annotated dataset requires input from pathologists that is not readily available. To overcome the paucity of the dataset, recently introduced image augmentation techniques in deep learning models provide better generalization and reduce the over-fitting. Image augmentation increases the dataset by taking the original image and transforming it into multiple images by using transformation techniques such as rotation, shear and translation, thus enabling the model to achieve higher accuracy. A convolutional neural network (CNN) is widely used for classification tasks and it is computationally efficient too [10]. In this paper, we evaluate the effectiveness of various existing deep learning models for malaria detection from microscopic blood images, and also propose an efficient DL method for the classification of infected and uninfected malaria cells. The proposed customized CNN-based algorithm outperforms all observed deep learning models. The proposed method uses bilateral filtering for improving image quality and image augmentation techniques for better generalization of the model. Our model has a simple CNN architecture containing 5 convolutional and pooling layers. The performance of the proposed method is evaluated on a benchmark malaria dataset, and the results are compared with other existing, similar techniques. The results show that our method achieves excellent performance and outperforms the compared techniques.

PROPOSED ARCHITECTURE

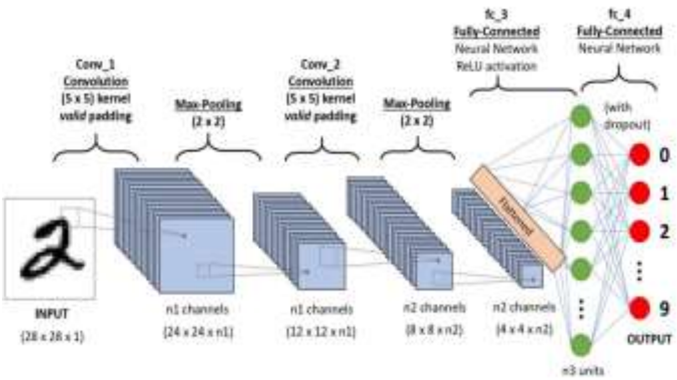


Fig 4 CNN Architecture

Fig 4 shows A convolutional neural network (CNN) is a specific type of artificial neural network that uses perceptron, a machine learning unit algorithm, for supervised learning, to analyze data. CNNs apply to image processing, natural language processing and other kinds of cognitive tasks. This study proposes a new and robust machine learning model based on a convolutional neural network (**CNN**) to automatically classify single cells in thin blood smears on standard microscope slides as either infected or uninfected.

EXPERIMENTAL SETUP

These experiments are conducted on a device with Windows system with Intel Core(TM) i3 CPU @2.40GHz processor,1TB HDD, 64 GB RAM, Python 3.7.And CNN model is trained and evaluated using Google Colab [45] which is a cloud-based Jupyter notebook environment available for free access. Colab provides a preconfigured system for training and evaluating deep learning applications and offers access to high-performance graphical processing units (GPUs) without any cost.

DATASET

This study is implemented on the Giemsa-stained thin blood (red blood cell) images from the dataset created by National Institute of Health (NIH) [19]. These images were collected from 50 healthy patients and 150 patients infected with Plasmodium falciparum. The dataset contains a total of 27,558 red blood cell images; 13,779 infected and 13,779 uninfected. An expert slider reader pathologist manually annotated the images. Some sample images from this dataset are demonstrated in Figure 5. The differences in colors are owing to the different stains during image acquisition. Malaria infected images have numerous forms of parasites.

III RESULT AND ANALYSIS

The dataset was divided into training (60%), validation (20%), and test (20%) sets; therefore, 16,534 images were stored for training, 5,512 images for validation, and 5,512 images for testing purposes. For dataset training and testing, the five-fold cross-validation procedure was used. Five independent iterations were performed. One of the folds was used as the test set, and the remaining were used as the training set. This process was repeated until each unique fold had been used as the test set.

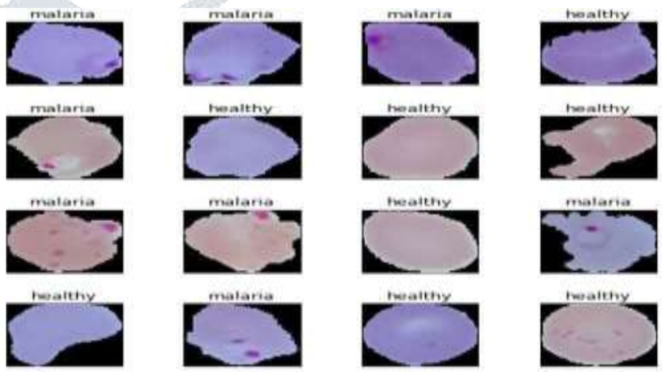


Fig 5 Proposed system input images

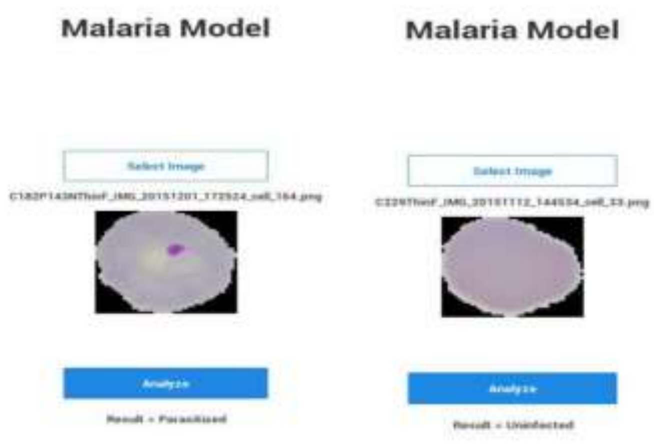


Fig 6 Malaria Model

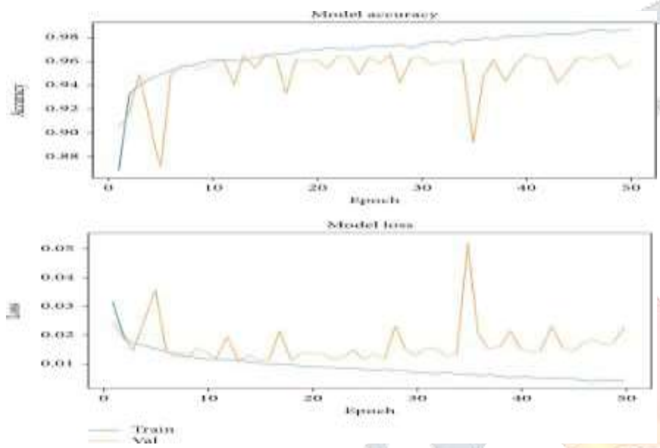


Fig 7 Graph Analysis

CONCLUSION

CNN-based end-to-end deep learning model to improve malaria detection on thin blood smear images. In this work, experiments are performed in series which are then concluded on the basis of end to end deep learning to advance the classification of malaria which is done from red blood cell images. Different preprocessing techniques such as standardization and normalization were used in the model. Data augmentation procedures are done on training set of images that gives the encouraging results. In addition, CNN network model designed are trained with training dataset and features from a convolutional network (CNN) were extracted. From the proposed models, an accuracy of 97.9% and sensitivity of 95.1 is achieved which outperforms all the other models.

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