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# Detection of Malaria Parasites using Deep Learning

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**Abstract - As technology has evolved it has become more and more efficient to diagnose, and treat multiple diseases. Malaria is one of the deadliest diseases on this planet. Each year it estimated that 1 million people die as a result of this disease. Furthermore 3.4 billion people are in danger of contracting malaria. With advances in the field of medicine it is now entirely possible to not only treat but also prevent malaria. The way in which people are diagnosed for malaria today is through blood samples. The techniques used currently are accurate however they are time consuming. This has necessitated doctors to start the treatment for malaria before the blood work is finished, since in its later stage's malaria can be very difficult to cure. The system that is discussed aims to cut this time requirement by at least half and increase the accuracy of the tests. An automated system that gathers the image data and analyses the images for malarial parasites is described. A system for collection of data and analysis is described. By implementing this system, the time needed for the diagnosis of malaria will be cut down. This will save lives and the medical resources that are used while waiting for the results of the tests from the old system.**

**Keywords—Deep Learning, Malaria, Parasite**

## I. INTRODUCTION

Malaria is a parasitic disease spread by the bite from a female Anopheles mosquito. People with malaria experience a flu-like illness that, if untreated, can cause severe complications and even death[1]. Symptoms of malaria include high fevers, shaking chills, headache, muscle aches, nausea, fatigue, and other flu-like symptoms. Additionally, patients can have anemia and jaundice due to loss of red blood cells. Symptoms usually appear 10 to 15 days after the mosquito bite[11]. If

untreated, severe infection can cause kidney failure, seizures, coma, and death. With timely diagnosis and treatment routine it is now possible to cure patients of this disease. However, the problem lies in the diagnosis phase. To diagnose malaria, your doctors will likely review the patient's medical history, conduct a physical exam and order blood tests. Blood tests are the only way to confirm a malaria diagnosis. There are a total of twenty two known parasites, out of which four cause the actual malaria infection. These include *P. falciparum*, *P. vivax*, *P. ovale*, and *P. malariae* [12]

The test is said to be positive when one of these five parasites are found in the blood cell. Due to the deadly nature of this disease doctors recommend starting treatment for malaria even before the blood tests results are in. One reason is that blood tests a long time and starting the treatment late might result in complications. The disease is typically found in regions of the world with tropical and subtropical climates. This includes regions of South Asia, Central Africa and Northern parts of Latin America. These regions tend to be developing or underdeveloped nations, making the population highly susceptible to this disease. Recent WHO reports paint a troubling picture According to the World Malaria Report the death rate of malaria cases has increased from 18% in 2017 to 28% in 2018. Even with all the progress in medical science, malaria continues to be a problem [11].

## II. EXISTING METHODOLOGY

Malaria must be recognized promptly in order to treat the patient in time and to prevent further spread of infection in the community via local mosquitoes[2].

Malaria should be considered a potential medical emergency and should be treated accordingly. Delay in diagnosis and treatment is a leading cause of death in malaria patients all over the world. Malaria can be suspected based on the patient's travel history, symptoms, and the physical findings at examination. However, for a definitive diagnosis to be made, laboratory tests must demonstrate the malaria parasites or their components. Malaria parasites can be identified by examining under the microscope a drop of the patient's blood, spread out as a "blood smear" on a microscope slide. Prior to examination, the specimen is stained to give the parasites a

distinctive appearance. This technique remains the gold standard for laboratory confirmation of malaria.

However, it depends on the quality of the reagents, of the microscope, and on the experience of the laboratorian. The technique used is as follows: A blood specimen collected from the patient is spread as a thick or thin blood smear, stained with a Romanovsky stain, and examined with a 100X oil immersion objective. Visual criteria are used to detect malaria parasites and to differentiate (when possible) the various species. Wright’s stain, which is commonly used in hospital laboratories for examining blood (called a CBC with manual differential), can be used if Giemsa stain is not available. However, species determination might be more difficult.

Microscopy results are only as reliable as the laboratories performing the tests. In regions where the disease is not endemic, the average laboratorian does not perform this test regularly, and may not be maintaining optimal proficiency[8].

As discussed earlier the core of the project is the construction, training and evaluation of a model that can accurately indicate whether or not a cell is infected. With the advances in computer hardware and processing power of it is now feasible for us to train a neural network, over a gigantic dataset, that can be used to accurately indicate whether the blood cell is infected or uninfected. In addition to this the availability of user-friendly APIs for developing neural networks as well as evaluating them has made this task much less daunting[3].

TABLE 1: LITERATURE SURVEY

Sr. No	Literature Survey		
	Title of Paper	Core Idea	Usage
1	Detection of Malaria Parasites Using Digital Image Processing (IEEE, 2017)	Basic Flow of Detection System	Information about the malarial parasite and the flow of the system was studied and discussed using this paper
2	A Study of Image Segmentation Algorithms Combined with Different Image Preprocessing Methods (IEEE, 2015)	Methods to preprocess the images for analysis	Methods of preprocessing images was gathered using this paper
3	Comparative Study of feature extraction Algorithms (IEEE, 2014)	Comparison of multiple algorithms in the feature extraction	Algorithms for feature extraction were studied

Sr. No	Literature Survey		
	Title of Paper	Core Idea	Usage
4	Scale Invariant Feature Transform Based Image Matching(IEEE, 2014)	Image matching techniques and methods	Detect image features like contours, point and corners.
5	Simplified Histograms of Oriented Gradient Features Extraction Algorithm (Manipal University, 2015)	Comparison of multiple algorithms in the feature extraction	This paper was used to get a basic idea of HOG algorithm
6	Image Segmentation Algorithm Overview (IEEE, 2013)	Presents an overview of image segmentation algorithms	Algorithms and techniques used in image segmentation were studied
7	Medical Image Segmentation Methods, Algorithm and Applications (IETE technical, 2014)	Presents an overview of various algorithms used for image processing the medical field	This paper was used to study about k-means and thresholding algorithms in detail
8	Algorithm and technique on various edge detection: A survey An International Journal (SIPIJ, 2013)	Various algorithms used in image processing are discussed	This paper was used to study in detail about how edge detection is carried out in image segmentation.
9	A review on Region Based Segmentation (IEEE, 2013)	Algorithms used in region-based segmentation	This paper was used to study in detail about how region-based segmentation is carried out.

### III. IMPLEMENTED METHODOLOGY

We have used a convolutional neural network as a model. The training dataset was available from [http://www.cdc.gov/malaria/about/biology/parasites.html]. In all, there are over twenty six thousand images that show infected and uninfected images. Figure 3.1 shows the sample image from the dataset by which the model was trained.

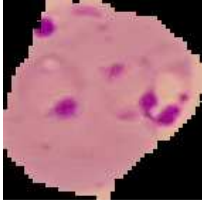


Fig. 3.1. Sample of the image used for training.

The basic model constructed is described below. Step 1 -This is done by adding pairs of convolution layers and pooling layer. Tentatively the system consists of used Convolution2D and MaxPool2D objects of the eras library for the same. The programming language to be used for developing this system is Python 3. Specifically, the version 3.6 is used. This is because the Keras 1.0 module works well with this version. This module allows for the quick and easy construction of a neural network. A preliminary model has been constructed and trained using about 1200 images from the dataset. The layers in this model are as mentioned here- Multiple pairs of the convolution layer and the pooling layer are used to convulse the image and reduce the size of the image for processing. The activation function used here is "ReLU" and the pooling type is Max Pooling. The layer is implemented by using the Convolution2D and the MaxPool2D object of the Keras library. The next layer converts the image data into a single column vector. This allows for the data to be fed to the network. This layer is implemented by using the Flatten object of the Keras library. Multiple fully connected layers of nodes form the next layer of the network. These nodes are fully connected. The number of nodes in each of these dense layers is as follows: 1024, 512, 256, 128, 64, 32. Each of these nodes have "ReLU" as the activation function. This layer is implemented through the use of Dense object in the Keras library. The final layer is having a single node that predicts whether or not the cell image is infected. It uses the "sigmoid" activation function. This layer is implemented through the use of Dense object in the Keras library.

However, the 'output dimensionality' is set to one. Finally, this model uses the popular Adam optimizer with a learning rate of 0.001 and the binary cross entropy loss function. The neural network constructed in such a way has over a million trainable parameters. With this, preliminary training and testing of this model using just over a thousand images for training and about two hundred images for testing over five epochs, yields a steadily increasing validation accuracy from 0.9490 to 0.9551 and a steadily decreasing loss from 0.1563 to 0.0550.

The system has a basic architectural flow in which the image is taken from the user (the blood sample image which needs to be checked) The image is pre-processed and further

segmented. The results are predicted using the constructed model. Figure 3.2 shows the basic flow of the system

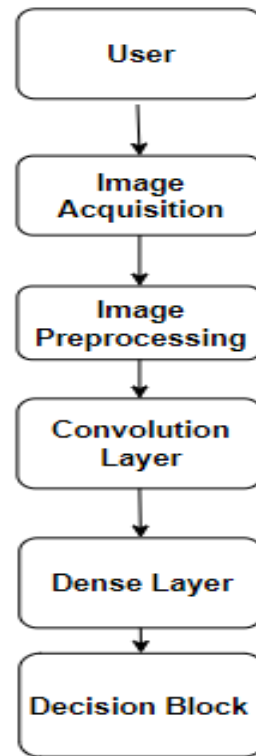


Fig. 3.2. Basic Flow of the system.

### IV. CONCLUSION

In this study, the basic idea of the malarial parasitic infection is given. The various species of parasites are also mentioned. The reason that malaria is such nuisance today is in no small part due to the time-consuming process of detection of the parasite in the blood cell. Due to this delay precious resources like manpower and medication are not used optimally. However by leveraging the high processing and storage capacities available today it is now possible to automate this process and increase the accuracy and cut down the time required to diagnose the patient. A system for the detection of malarial parasite in a blood cell is discussed. For this, the basic concept of convolutional neural network was studied. By effectively implementing such a model and a user-friendly interface to operate the system, it can be concluded that the time required to diagnose malaria will go down considerably and the accuracy with which it is detected can be increased. The study focuses on the model which is used for malaria parasite detection. The system is constructed by using python 3.7.

### V. FUTURE SCOPE

As per the discussed model the system is identifying whether the parasite is present or not. In future we are focussing on making the classification multiple. By saying multiple, we are focussing on classifying the parasite type which are mentioned above [6]. The system would be capable of detecting the

parasite name. This is not implemented in the system because while training and testing the model we found that the accuracy of predicting is 30%. Accuracy of 30% cannot be deployed for use as it is very minimal. Even though this is a limitation it is observed that multiple classification is not possible because of very minute differences between the parasites. Figure 1 describes the parasites and their species [5].

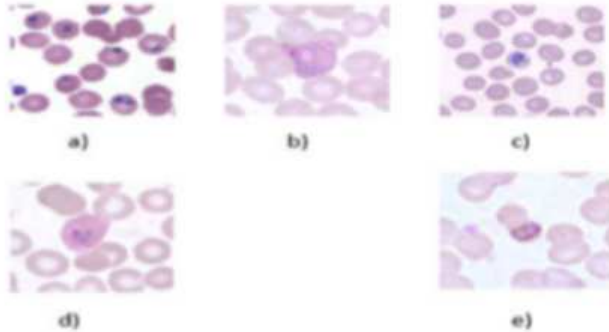


Fig. 5.1. Species of Malaria parasite, (a) Plasmodium Falciparum (b) P. Vivax (c) P. Knowleksi (d) P. Ovale (e) P. Malariae

The issue is occurred in identifying the multiple system is the parasite P. Knowleksi, P. Ovale and P. Malariae are very rare. The percentage of finding the parasite in the blood are minimal upto 0.001%. Since maximum parasite which is found in blood is vivax and falcipuram it is easy to classify them separately [7].

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