Detection of Malarial Parasites in Blood using Image Processing

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***Abstract*— One of the most infectious and a highly transmissible disease caused by a blood parasite which belongs to genre of Plasmodium is Malaria. Considering the traditional and the general microscopy method, which is "The Gold Standard" for malaria detection has been proven to be inconsistent, because the process requires significant amount of time and the results are difficult to reproduce as and when required. Malaria is causing a serious global health issues, and the appraised process is of high significance. The system developed here represents a model that uses image processing techniques and algorithms that are, definite, rapid and cost-effective detection of malaria by training and testing over the acquired stained thin blood smear images. Datasets consisting of images of affected and non-affected erythrocytes are collected, preprocessed, closely connected features are extracted from the acquired images and finally, it is confirmed whether the sample image is infected or not based on the features that are extracted from them. A set of characteristics depending on the features are suggested, and the performance from the created database of the features on the erythrocytes samples is classified using a SVM and MSVM classifier**.

Keywords— Plasmodium, Image Processing, SVM, MSVM, Erythrocytes

I. INTRODUCTION

The protozoan parasites called plasmodium is responsible for the transmission and infection of the disease Malaria. There are around 400 different species of anopheles mosquitoes and out of this 30 are malarial vectors. These bite during dusk and dawn. The range of injection depends on the surrounding and the environment where the person lives. The surrounding must be well maintained with proper coverage of sewage passage and cleanliness. Some of them are Plasmodium Falciparum, Plasmodium Malariae, Plasmodium vivax, and Plasmodium Ovale. Anopheles mosquitoes carry these plasmodium parasites to human body. These parasites affect the RBC and complete its life cycle with the help of hosting in RBC then rupture the RBC [9]. The rupturing of RBC increases the severity of infection. According to the WHO statistics in 2000- 262 million cases of this deadly disease lead to an approximately 839,000 deaths. In 2015- 214 million cases where found and death rate decreased to 438,000. The method suggested by the WHO during the year 2010, for the diagnosis of malaria was the light microscopy or the rapid diagnostic test (RDT) [18][19].
The remote places where microscope or skilled microscopist is not available RDT is used; the two hosts namely the insect host and the vertebrate host is infected in its life cycle by the plasmodium,so the density of the parasite cannot be determined but this method gives instant results. This paper develops an automatic system for image classification that will identify the malaria parasites present in the blood smears positively. The common technique to diagnose malaria is Visual Examination of microscopic image. This is carried out by the microscopist. This technique is time consuming because of the number of steps required to manually validate and assessment . This technique is also inconsistent because inexperienced microscopist may confuse platelets with malaria parasites. This inconsistency caused because the ruptured RBC looks similar to parasites. And the microscopist may assume the parasites as the platelets. This result in the wrong diagnosis of problem. Some deaths are because of incorrect diagnosis method and time consuming problem. The standard procedure involves testing the red blood cells through microscope. This method requires high skilled professional who must have proper knowledge about the protozoans and pathology [17]. The professionals should be highly paid for their work hence it is very expensive. Moreover, the accuracy level also matters along with the time required to detect the malaria disease. The normal microscopic test does not give the level of blood infection degree, instead it just gives the result as positive or negative case of malaria. Hence this method is inadequate because of its complexity, labor intensive, expensive and long duration. Therefore, due to modern technology, with the help of image processing one can easily
determine the extent of malarial infection. The process involves testing the disease using the microscopic images obtained from laboratories. It does not require a skilled pathologist to test the disease, instead a person with average knowledge of computer can easily detect the infection
degree [1].

II. RELATED WORK

According to[2], Main objective here is to build an computerized system ,and by using image analyzation approaches ,thus eliminating manual approaches for the identification and analyzing of the species of the parasite on thick blood films .

In [3], Methods such as automation and image processing are implemented this helps in supervising and checking the mistakes or errors made by an individual during the

identification of parasites of malaria in the blood samples . Here ,In Giemsa stained peripheral blood samples the recognition of the affected and normal images in the set is the target to be achieved here also the methods like edge detection,image-segmentation is implemented .

With reference to [4], A simple categorization algorithm is suggested that classifies the point by allocating close to the 2 parallel planes and Otsu's threshold which helps in obtaining binary images of the cells, segregation of cells which overlap and lastly, discovery of infected and non-infected images with the study of SVMnetworks.

Here in [7], Techniques used are diafeature extraction, classification, ANN algorithm. Segmentation and enhancement of image was developed before it. Here in this paper the main focus is on increasing the accuracy of the result obtained, helping the microscopists by assisting them to make their job easy by developing an computerized system.

According to [12], The primary concept here is, initially conversion of the input color blood image to grayscale , and then calculating the range of y^{th} order of a grayscale image.Here in this paper an Effective algorithm, with the gamma equilization(GE) method is implemented whose main motive is to protect the fundamental structures of the acquired blood images which is infected by malaria .

III. METHODOLOGY

The two main phases of the system architecture that is the training and the testing phases is shown in figure 1.
Training phase starts with taking the images from the dataset. Multiple images are given to the training phase so that the images are well processed and enhanced so that the amount of data to be handled gets reduced. As the number of images to be trained increases the performance of the system also increases. The segmentation technique removes the noise and other disturbances present in the images . The segmented image is further enhanced by extracting only the necessary features and are classified by using a classifier [6].
In the testing phase, a test image is subjected to all the above mentioned stages and then identifies the test image as an infected or a healthy sample.

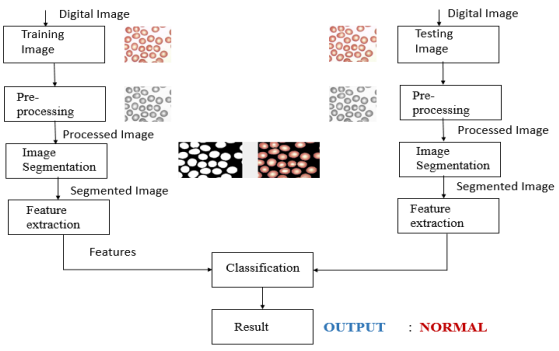


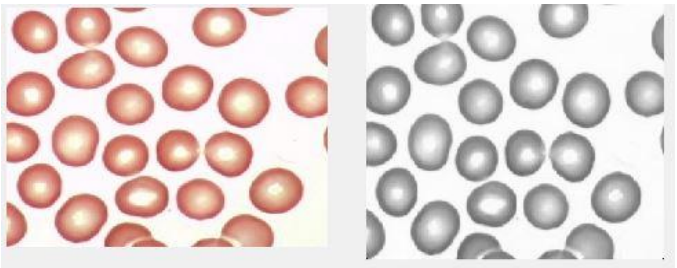
Figure 1. System architecture

A. Pre-Processing

There are a number of pre-processing techniques used in image processing for the enhancement of the images. Grey scale conversion, resizing of the image, increase the brightness of the images and other pre-processing techniques are applied to change the image into desired format for the next segment [5]. Pre-defined and in-built filtering techniques are applied for the better contrast on an image and also other techniques for multiple dimension for images are applied [20]. The main objective of pre-processing are :

- Resizing the image.
- Reduce or eliminate noise
- Enhancing the image contrast for visual evaluation.

The preprocessed image is shown in Figure 2.

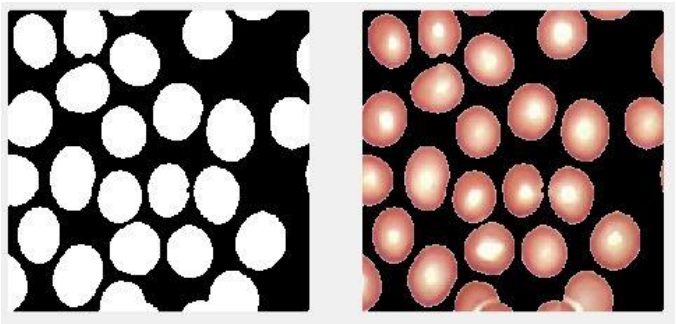


(a) (b)

Figure 2. (a) Original image (b) Pre-processed image

B. Segmentation

The process is used to divide image into objects and region. Representing an image into a much simpler and more understandable, which can be easy to analyse in the next process segmentation is used. This helps to analyse the code simpler [10]. It segments the image pixels based on region of homogeneity by extracting certain features which are in common. It also removes the noise present in the images. The ultimate goal is to differentiate between the blood cells and background. The image obtained by segmentation as shown in figure 3 are passed on to the next process. The cells that have been identified as possibly infected are then extracted from the image and passed to the next stage of the algorithm for feature extraction [15][16].



(a) (b)

Figure 3. (a) Segmented Binary Image (b) Segmented RGB image

C. Feature Extraction

Feature extraction is the next step in the process where the segmented image from the previous step is provided as an input. This technique reduces the amount of data to be loaded by extracting only the features those are required. The features include contrast, correlation, homogeneity, energy, entropy, Kurtosis, color histogram, color moments and so on. As the number of features increase the level of accuracy also increases [8].

1)Contrast

It is the difference in the luminance or color which makes the images distinguishable. It is obtained by the change in brightness of the image or object from one pixel to another.

2)Correlation

It is an operation which is used to extract information from images. The two key features: shift-invariant and linear. Shift invariant performs the same operation at every point on the image and linear replaces every pixel of the image with that of its neighbours .

3) Homogeneity

An image that is uniform in composition or character refers to homogeneity in images. It is calculated as follows

homogeneity = graycoprops(graycomatrix(img), 'Homogeneity')

Where *graycoprops* calculates the parameters based on GLCM

4) Energy

Energy determines the intensity of the pixels. The maximum energy of a pixel is obtained by

maxGrayLevel = max(grayImage(:))

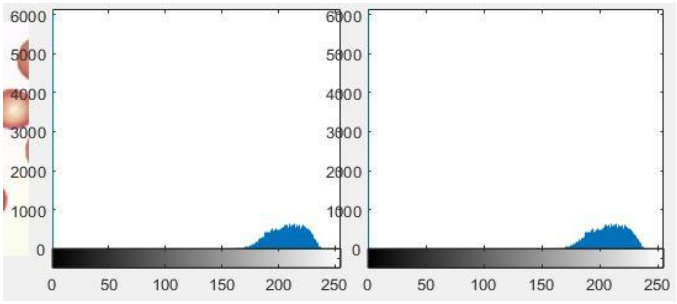
5) Kurtosis

Kurtosis is a proportion of whether the information are crested or level in respect to an ordinary circulation. Datasets that have high kurtosis will in general have a particular crest close to the mean, refuse rather quickly, and have substantial tails.

6) Color Histograms

It represents the distribution of colors in an image. For digital images, it represents the number of pixels that have colors in each of fixed ranges of colors .

Figure 4 shows the histogram representation of the features extracted from the images.



(a) (b)

Figure 4. (a) Color moments SVM (b) Color moments of MSVM

D. Classification

The classification technique is done by using multi-class support vector machines (msvm). It is a technique where in instances are classified into one or more classes based on their similar properties. It classifies using one-against-one approach. SVM technique is also implemented and used for the classification of the trained images so as to compare and see the results obtained through both SVM and the MSVM classifiers [13][14].

IV. RESULTS

The proposed system successfully detects the malarial parasites in blood. The performance is measured using precision and recall graph. It calculates the accuracy of the system which is given by the formula

*accuracy = 100*sum(diag(cmat))./sum(cmat(:));*

where cmat is the confusion matrix which holds the values of image pixels and diag(cmat) gives the diagonal elements of the confusion matrix. The receiver operating characteristics(ROC) graphs and confusion matrices of SVM and MSVM are shown below in figures 5,6 and 7.

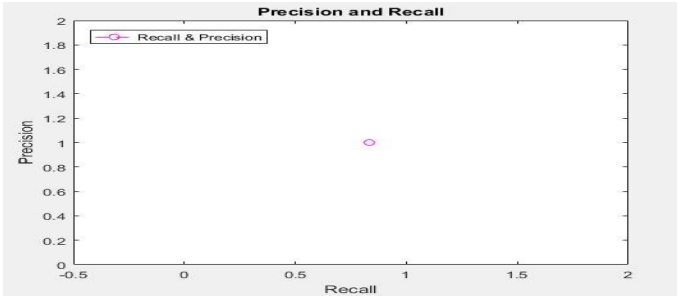


Figure 5. ROC plot

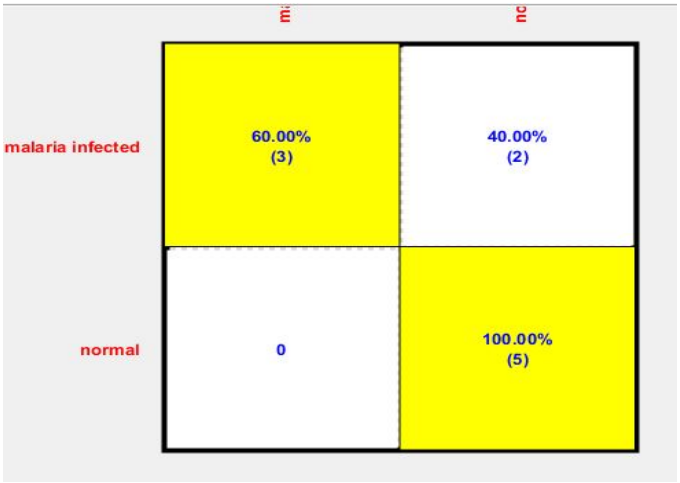


Figure 6. Confusion matrix plot of SVM classifier

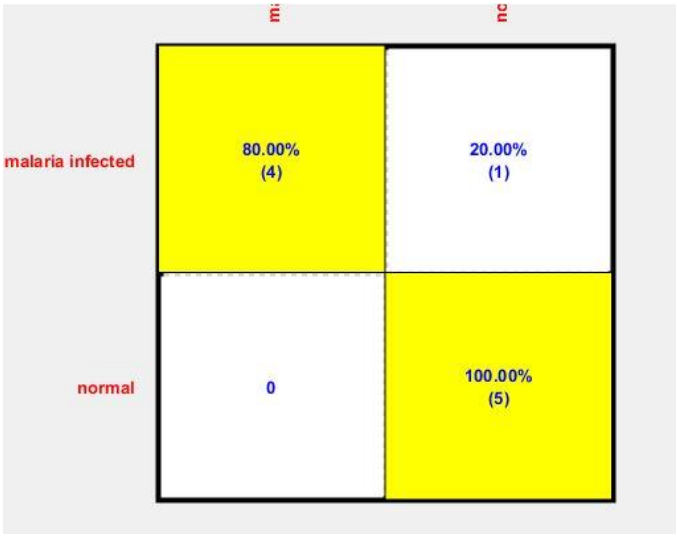


Figure 7. Confusion matrix plot of MSVM

V. CONCLUSION

The purpose of this paper is to develop an accurate, rapid and affordable system for the identification of parasites of malaria in thin images of blood using ImageProcessing. Here, microscopic bloodImages of normal, malaria infected are acquired, which is preprocessed and segmented.Certain features are extracted from the segmented image inorder to reduce the amount of data to be held for analysis. Thereafter svm and msvm classifiers are used to detect whether the microscopic image of the blood cells is malaria infected or not as the final result.

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