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Image processing Approach for Malarial Parasites Identification in Blood

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ABSTRACT

: Malaria is one of the serious infectious diseases which are because of mosquito bites. Diagnosis of malaria is done by microscopic examination of blood. But this diagnosis method is time consuming and requires pathologists. This paper aims to introducing fast and accurate method based on image processing for malaria parasite identification. The database was generated by taking the microscopic images of blood of 30 malarial patients. Based on morphological operations total number of cells are counted. Infected cells are analyzed based on intensity profiles within the cells. The result is validated by comparing with manual analysis. This approach can be used in rural areas where less experts are available and the delayed diagnosis may lead to complications in patient's health.

General Terms: Image processing

Keywords: *Malaria parasite, image, diagnosis, thinning algorithm, threasholding, labeling algorithm.*

1. Introduction:

Malaria is a life-threatening parasitic disease, caused by the protozoan parasites of the

Genus Plasmodium and is transmitted through the bite of a female Anopheles mosquito.

Inside the human body, the parasite undergoes a complex life cycle in which it grows and

Reproduces. During this process, the red blood cells (RBCs) are used as hosts and are Destroyed afterwards. Hence, the ratio of parasite-infected cells to the total number of red

Blood cells – called parasitaemia – can be used as a measure of infection severity and is an

Important determinant in selecting the appropriate treatment and drug dose [1].

Malaria is a mosquito borne disease caused by the parasites of genus plasmodium. The person gets affected by malaria when malaria parasites are introduced into the circulatory system by infected female anopheles mosquito bites. According to World Health Organization (WHO) it causes one million deaths per year and nearly 250 million people are affected by malaria [1]. Hence for the prevention and control of vector borne diseases i.e. Malaria, Dengue, Kala-azar, Japanese Encephalitis and Chikungunya Government of India has started National Vector Borne Disease Control Programmed (NVBDCP) under Directorate General of Health Services [2].

2. HISTORY: Although the parasite responsible for P. falciparum malaria has been in existence for 50,000–100,000 years, the population size of the parasite did not increase until about 10,000 years ago, concurrently with advances in agriculture and the development of human settlements. Close relatives of the human malaria parasites remain common in chimpanzees. Some evidence suggests that the P. falciparum malaria may have originated in gorillas. In 2006, the Malaria Vaccine Advisory Committee to the WHO outlined a "Malaria Vaccine Technology Roadmap" that has as one of its landmark objectives to "develop and license a first-generation malaria vaccine that has a protective

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efficacy of more than 50% against severe disease and death and lasts longer than one year" by 2015. In December 2013 a new diagnosis method was promoted as faster, precise, inexpensive and operable by non-medical personal. Human trials have not yet been done [3].

3. METHODOLOGY: The image processing based approach is developed on MATLAB version 7.12. The steps included are 1) pre-processing, 2) morphological operations, 3) RBC count, 4) contour formation, 5) parasite counting.

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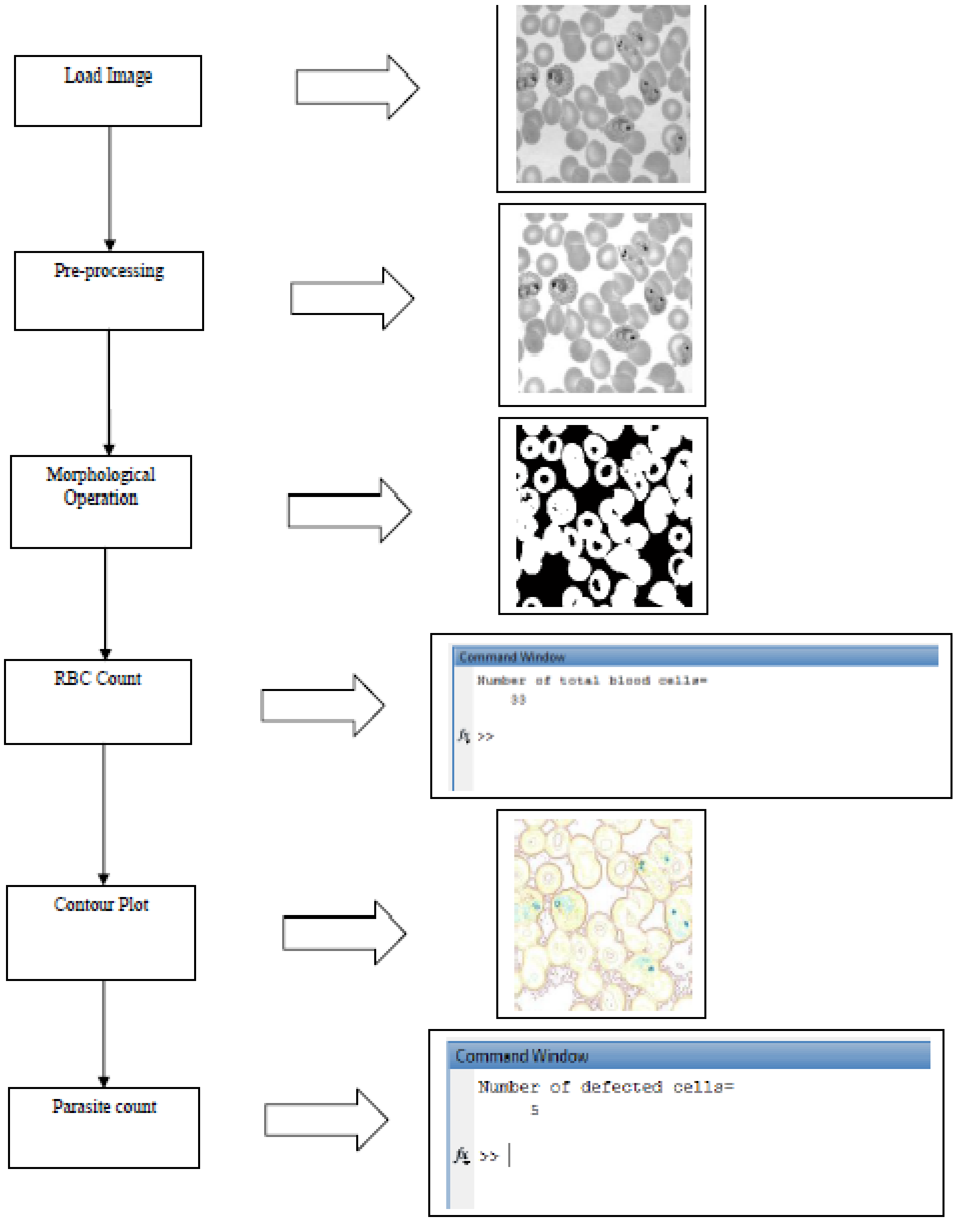

Fig 1: Flowchart and result images describing the steps of the proposed algorithm [4]

4. System Architecture:

Method-1

System architecture used for Malaria parasite detection involves following steps: Threasholding, gray scale image conversion, binary image, edge detection algorithm, thinning of binary image, labeling algorithm

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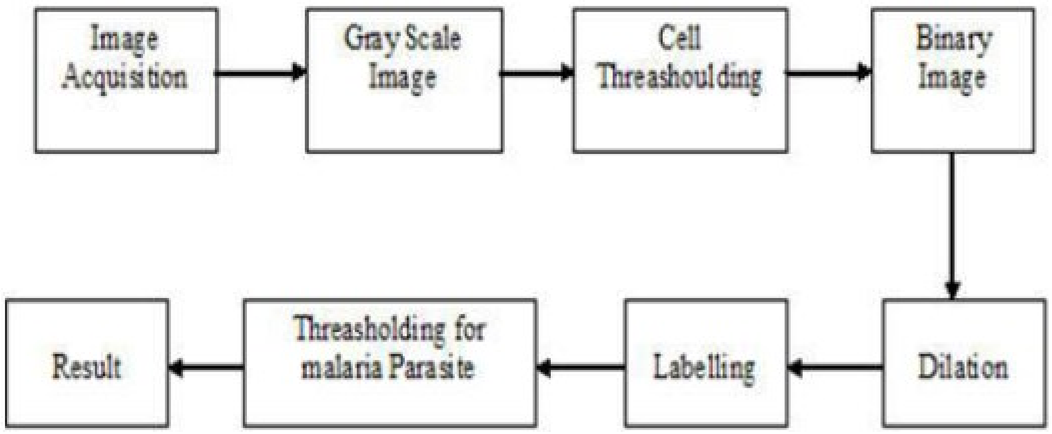

1 Image Acquisition

The input images of Giemsa stained blood smears are selected from the database Library. Images are of different shape and sizes. Images show high variations in intensity, contrast color tone, etc.

2 Image Preprocessing

The pre-processing block is designed, to remove unwanted effects from the image and to adjust the image as necessary for further processing The microscopic input image is converted from RGB to gray scale to reduce the processing time. RGB to gray conversion is done by averaging all the three components i.e. R, G and B which results in gray scale.

3 Image Smoothing

Smoothing is often used to reduce noise within an image or to produce a less pixilated image.

Most smoothing methods are based on low pass filters. Smoothing is also usually based on a single value representing the image, such as the average value of the image or the middle (median) value. The simplest approach is neighbor-hood averaging, where each pixel is replaced the average of the by value pixels contained in some neighborhood about it. The simplest case is probably to consider the group of pixels centered on the given pixel, and to replace the central pixel value by the un-weighted average of these (nine, in case of 3*3 neighborhood) pixels.

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4 Thresholding

Thresholding is the simplest method of image segmentation. From a grayscale image, thresholding can be used to create binary images.

Image Segmentation

1) The purpose of image segmentation is to partition an im-age into meaningful regions with respect to a particular application.

2) The segmentation is based on measurements taken from the image and might be Gray-level, color, texture, depth or motion.

5 Dilation

Dilation is one of the two basic operators in the area of mathematical morphology, the other being erosion. It is typically applied to binary images, but there are versions that work on grayscale images. The basic effect of the operator on a binary image is to gradually enlarge the boundaries of regions of foreground pixels. Thus areas of foreground pix-els grow in size while holes within those regions become smaller.

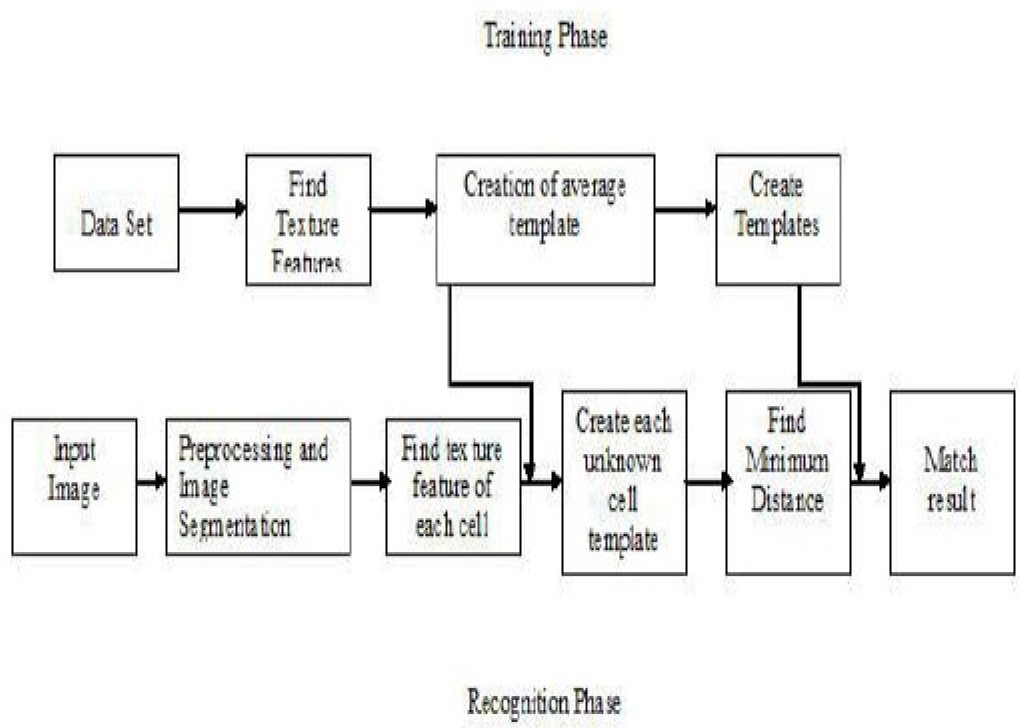
Method-2

There are two phases in this architectural model:

1. Training Phase and 2. Recognition Phase

1.Training Phase: In this phase we find out texture features from the data set and create average template, which will mapped with each cell template in recognition phase.

2. Recognition phase: This is second phase in this module, in which we find texture feature of input image and create template. Compare result with average template from training phase and find the minimum distance and display the final result.



5. Result Analysis

: In order to test and compare the performance of the two methods which we have used in our system design can be explained with the help of some parameters such as, Accuracy-cy, Sensitivity and PPV (Positive Predictive Value). Formulae for the same are given below,

Accuracy= (TP+TN) / (TP+TN+FP+FN)

Sensitivity= (TP) / (TP+FN) PPV= (TP) / (TP+FP)

Where, TP: True positive, TN: True negative, FP: False positive, FN: False negative [5] [6].

Confusion Matrix for Model I

		Yes	No	
Model-I	Yes	35	5	Positive predicate value: 87.50%
	No	8	32	Negative predicate value: 80.00%
		Sensitivity: 81.39%	**Specificity: 86.49%**	**Accuracy: 83.75%**

Table: Confusion Matrix for ModelI

Confusion Matrix for Model II

		Yes	No	
Model-II	Yes	31	9	Positive predicate value: 77.50%
	No	12	28	Negative predicate value: 70.00%
		Sensitivity: 72.93%	**Specificity: 75.76%**	**Accuracy: 73.75%**

Table: Confusion Matrix for Model II [7]

6. Conclusion:

The detection of Malaria parasites is done by pathologists manually using microscopes. So, the chances of false detection due to human error are high, which in turn can result into fatal condition. This paper curbs the human error while detecting the presence of malaria parasites in the blood sample by using image segmentation and feature extraction using minimum distance classifier. It shows the comparative study between two methods as mentioned above. In image segmentation we are getting the accurate and required results in the short period of time whereas in case of feature extraction more time is required i.e more CPU utilization is there.. The system in a robust manner so that it is unaffected by the exceptional conditions and achieved high percentages of sensitivity, specificity, positive prediction and negative prediction values. And the extraction of red blood cells achieves a reliable performance and the actual classification of infected cells.

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