

AN AUTOMATIC SYSTEM TO DETECT AND COUNTING THE MALARIA PARASITE CELLS USING MATLAB

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Abstract — In this work a picture handling framework was created to recognize jungle fever parasites in thin blood spreads and to arrange them into one of the four unique types of intestinal sickness. Numerous methods were actualized in the preprocessing stage to improve the pictures. In the initial segment of the framework morphological preparing is connected to remove the Red Blood Cells (RBC) from blood pictures. The created calculation picks the suspicious districts and recognizes the parasites in the pictures including the covered cells. As needs be, the RBCs are ordered into tainted and non-contaminated cells and the quantity of RBCs in each picture is computed. The second piece of the framework utilizes the Normalized Cross-Correlation capacity to group the parasite into one of the four animal categories in particular, *Plasmodium Falciparum*(P.F), *Plasmodium Vivax*(P.V), *Plasmodium Oval*(P.O), and *Plasmodium malariae*(P.M). Contrasted with manual outcomes, the framework accomplished 95 % exactness for location and checking of RBCs and 100% for discovery and grouping the parasite into one of its four sorts.

Keywords—Image processing, Malaria parasite detection, Normalized Cross-Correlation. Malaria diagnosis

I. INTRODUCTION

Malaria is a fatal parasitic disease found all around the world particularly in tropical and subtropical countries [1]. The parasite undergoes a complex life cycle inside the human body, using the red blood cells (RBCs) as hosts [2]. The infections of malaria are diagnosed manually by pathologists who observe the microscopic images of strained blood files on glass slides and count the infected blood cells. If sample size of patient is large, there is always a chance to detect inaccurately. There is human error possibility, hence computer based classification using digital image processing techniques gives better results than the manual diagnoses of Malaria [3]. The aim of this work is to develop a detection and classification system to accurately detected malaria parasites present in images of thin blood smears, and to differentiate the parasite species. In the pre-processing stages digital image processing techniques are used to obtain high-quality medical images.

II. LITERATURE SURVEY

Various techniques for the preprocessing stage are proposed in literature. Deepa. A. Kurer et al. [4], proposed a new approach for low-level image processing—SUSAN (Smallest Unvalued segment assimilating nucleus) Principle, which performs Edge and Corner detection. Image features based on color, texture and the geometry of the cells and parasites are generated, as well as features that make use of a priori knowledge of the classification problem and mimic features used by human technicians. A two-stage tree classifier distinguishes between true and false positives, and then diagnoses the four types of the infection. The algorithm detects the species of parasite with a sensitivity of 99% and a positive predictive value of 90-92%.

Daniel Maitethia Memeu et al. [5] proposed a method for detection of plasmodium parasites from images of thin blood smears. The method is based on Artificial Neural Net-work (ANN) for testing the presence of plasmodium parasites in thin blood smear images. Pre-processing, features extraction are implemented and eventually diagnosis was made based on the features extracted from the images. Classification accuracy of 95.0% in detection of infected erythrocyte was achieved with respect to results obtained by expert microscopes.

S. Kareem et al. [6] proposed a novel idea to identify the total number of red blood cells (RBCs) as well as their location in a Giemsa stained thin blood film images. The method utilizes basic knowledge on cell structure and brightness of the components due to Giemsa staining of the sample and detects and locates the RBCs in the image. For detection of Malaria, this study presented a simple approach based on the shape and size of each RBC by calculating its roundness using an appropriate threshold. The classification of malaria parasite is implemented using NCC does not require training like the ANN.

III. IMPLEMENTATION

System architecture used for Malaria parasite detection involves the following main steps: image acquisition, preprocessing, morphological processing, Malaria detection, and Malaria classification. The block diagram shown in Fig 1

illustrates all system steps. Matlab is used in all system implementation steps.

A. Image Acquisition

A total of 160 images of thin blood smears stained with Giemsa were collected from the Center for Disease Control and Prevention (CDC) [7]. All images were prepared using oil immersion views (10x1000) of blood films stained with Giemsa captured using a binocular microscope mounted with a digital camera. Mat lab is used to read each of the images. These images have different characteristics in magnifications and sizes. In this experiment, the images were selected accurately (180 × 240).

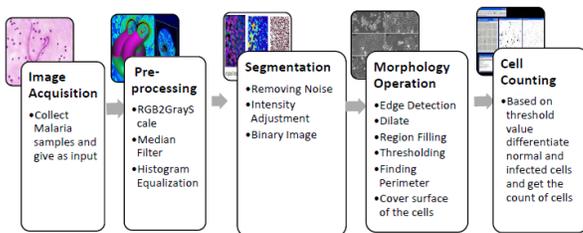


Fig. 2: System block architecture

B. Pre-processing

The goal of preprocessing is to eliminate unwanted objects and image noise to facilitate the segmentation of the image into significant regions. The Mat Mat functions are used to implement the following steps: conversion of color images to grayscale presentation, background estimation using the morphological aperture technique, subtracting the background image from the original image, improving the image contrast and conversion of grayscale images into binary presentation. By means of thresholding techniques, converting images into their negative presentation. The resulting negative presentation images will be used to obtain the RBCs in white and that makes it easier to detect their state and texture content, and segment the images into significant regions.

The objective of this step was to make the acquired images more suitable for subsequent processes, mainly the segmentation of images and the extraction of characteristics. Basically, there are three main objectives for image preprocessing. One of them is to change the size of the image in order to increase the image by digital zoom or reduce the size of the image to accelerate the processing. The second objective of image preprocessing is to reduce or eliminate the noise of the acquired image. The third is to improve the contrast of the image for visual evaluation. In this case, digital zoom and contrast enhancement were not necessary since the task of image classification and

recognition had to be done by a computer and not by a human operator. However, the size reduction was necessary so that all images with a uniform size went to the next stage. The CDC images had a different spatial resolution, with 300 by 300 pixels of square images, being the smallest of all. The KEMRI images had their size normalized to 300 by 300 square pixels by the software of the microscope.

C. Segmentation

Segmentation divides the image into its constituent regions or objects. The goal of segmentation is to simplify and / or change the representation of an image into something that is more meaningful and easier to analyze. Image segmentation is generally used to locate objects and boundaries in images. In our study, we first eliminate noise, adjust the intensity of the image, perform a gray threshold and convert the image to a binary form.

D. Morphology Operation

Morphological operations are image processing operations that process images based on shapes. Applies a structuring element of specific shape and size in the input image. The output image is created by comparing the value of each pixel with its neighbors. These operations are sensitive to the form of structuring. Additional operations are carried out such as filling holes, overlapping, which helps the detection of infected cells.

E. Cell Counting

By comparing the superposition of the original image and the masked image and depending on the intensity profile, the differentiation between normal and infected cells is carried out. Finally, using mathematical operations, the count of the number of such cells is determined and displayed.

IV. ORESULTS AND DISCUSSION

A. Experimental Results

After preprocessing and contrast enhancement, we obtain a noise-free image and clearly distinguishable components. Then, morphological operations are performed. The edges are detected by sliding a core over the image pixel by pixel. The edges are amplified with this filter according to the distribution of the values in the matrix or kernel. There are 2 methods for edge extraction, namely Sobel and Canny. We use Canny in which a partial derivative is made in each pixel because it is more accurate. Next, the region fill slides a disk over the image to fill the unwanted voids so that it is easier to detect the circular regions. In the third step, it is used to detect RBC cells using a circular Hough transform. In the

evaluation step of the color channel, we extract the green channel. We can also extract the blue channel, but not the red one because the malignant cells are reddish in color. The image is segmented by threshold and green channel extraction. The final step shows the centers of the red blood cells and surrounds the malignant cells with a bounding box.

B. Performance Analysis

The proposed automated method of cell segmentation and classification is simple. An approach is proposed to detect red blood cells with consecutive classification in normal cells and infected parasites for the estimation of parasitaemia. The extraction of red blood cells achieves reliable performance and the actual classification of infected cells. The sensitivity of the system is 93.12% and the specificity is 93.17%. Totally 5 samples are taken from different blood samples. The images were used as raw data for malaria parasite count. The result of some sample images is reported in Table1.

TABLE 1 Table 1 Result Analysis

Image No.	Manual RBC count	Proposed System RBC Count	Manual count of malaria parasite	Proposed system count of malaria parasite	Difference in algorithmic count and manual count (%)
Image 1	60	56	14	10	0.5
Image 2	120	17	35	5	2.54
Image 3	62	21	15	8	5.08
Image 4	286	36	41	12	1.03
Image 5	803	39	139	13	0.24

The counting values by the proposed method differ slightly from the counting values obtained manually. Increasing the database by collecting images from various sources can make the algorithm used in the software more robust.

V. CONCLUSION

An efficient method for counting red blood cells has been used in this document. To improve accuracy, red blood cells differ from white blood cells, noise and the background of the image. The preprocessing process helps to achieve clarity of the image. This further helps in the segmentation and discarding of white blood cells and platelets is performed depending on the number of responsibilities and the size of the cells, respectively. Most of the previous available methods that were used to classify red blood cells are slow and expensive. The skill of the pathologist plays an important role in the accuracy of the results. Despite all these facts, the various outcomes excluded sometimes do not have coordination between them. It can be for the same sample, two pathologists can give different opinions on the classification of the cells.

In the method used, we carry out morphological operations that have a good efficiency because they consider the cells at the limit of the image and the superposition of the cells. In comparison with previous work in this field, people were required to learn the system, but in this work we have introduced a new method that eliminates this need. The blood cell count is only limited to red blood cells, but white blood cells and platelets are equally important. We have used the integrated functions of the system to increase the accuracy. The use of integrated functions makes our system faster and more optimized. The red blood cell count may differ sometimes, but the malignant cells are detected accurately.

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