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Computerized Analysis of Blood Cell Images for the Accurate Diagnosis of Malaria

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ABSTRACT: In this paper, we are presenting an approach for the analysis of blood cell images which is used for the detection of malaria making use of computer techniques. We have used S and V component images of HSV color model. Sequential edge linking algorithm, Euclidian distance based clustering. Zack's thresholding technique is used to segment these images, The proposed approach is implemented with Pathology and blood cell images.

Keywords: Image segmentation, image thresholding, clustering, parasites

I. INTRODUCTION

Blood is main cause many of the diseases due to the blood. One of those diseases is malaria. Accurate malaria diagnosis is a successful management key of the disease. Operative diagnostics increases the management of patients with malaria, helps in differential diagnosis concerning fever, and it is essential for reporting close observation malaria. In the process of detection of malaria, usually the blood samples are tested manually by using a microscope. Most of the researchers have given their best in this area regarding the analysis of blood cell images by using the various processing techniques of images. The approach for the detection of the parasites and RBC count in the available blood cell image for the evaluation of malaria disease is presented in this paper. Segmentation techniques of images are used for the analysis of the blood cell image.

II. RELATED WORK

Various approaches are reported for the analysis of microscopic medical image from disease detection point of view. In this section, some approaches are being summarized related to the medical image analysis. In general the images are the microscopic images. Makkapati and Rao [1] explained about HSV color space segmentation. The scheme which is presented in [1] relies on HSV color space which segments Red Blood Cells and parasites, detecting the dominant hue range and by finding thresholds of optimal saturation. The methods that are less computation-intensive than the existing approaches are presented to remove artifacts. The scheme is accessed using images that taken from Leishman-stained blood smears. Sensitivity of the scheme is to be 83%. The method operates in HSV space and is dynamic in the sense that appropriate thresholds are calculated from the statistics of the image given rather than keeping statistics of image fixed for all images. Schemes determine optimal saturation thresholds to segment RBCs and chromatin dots which are robust compared to the color variability encountered. The work in [1] shows how color image processing techniques are used. Raviraja and et al. [2] introduced processing for blood images to detect and classify malarial parasites in images of blood slides stained by Giemsa stained, in order to find the parasitamia of the blood. Statistical based approach is used to detect the red blood cells which are infected by malarial parasites. color, shape and size information are used to separate the parasites automatically from the rest of an infected blood image, and later these images are compared with images which are infected after transformation of image by scaling, shaping so as to reconstruct the image. The images returned are statistically analyzed and compared to give a mathematical base. The evaluation of the size and shape of the nuclei of the parasite are also important and must be considered.

Meyer and Beucher [3] have used marker constrained watershed algorithm for the segmentation of image which uses the binary images only and distance transform may give more segmentation. If the image objects are irregular in shape and there are overlapping and touching objects, can lead to under segmentation. Only the binary images can be used for this operation. Therefore to avoid under segmentation and over segmentation, Rao and Dempster [4] have suggested morphological area opening on distance transform for choosing markers so as to avoid over segmentation and under segmentation. This given technique is also suitable for grey images if large variations in pixels within the image component. Rao and Dempster [5] have given the improvement over the calculating granulometry directly. They have introduced the technique for estimating the patches in the image component. The presented technique [5] computes granulometry function by two-stage process and helps to find the size of patches and granulometry function for microscopic images of blood sample. Ruberto et al. [6] have used the morphological method to detect malaria parasites in Giemsa stained blood slide. The two facilities provided by [6] to detect parasites to select automatic thresholding which is based on morphological approach by using Granulometries, which evaluates the RBC size and the nuclei of parasite. The regional maxima mark the nuclei of the parasite. The method which is presented here automatically identifies the parasite using size and color information which extracted by using morphological approach. The filters component of saturation and hue are used after Granulometry analysis.

III. PROPOSED APPROACH

On the basis of review of literature for the blood cell images which are microscopic, it is found that different techniques of image segmentation are applied on color images, grey images and binary images. The different types of color models are also used like RGB, HSV and in that a B, H; G and S components are used respectively to find parasites and RBC by using concept of image processing. To find of correct number of parasite and RBC, proper segmentation technique is required. Most of the authors have applied it as a combined approach of various segmentation schemes with morphological processing in order to improve the results.

A. Proposed Scheme

To identify the parasites the following procedure is as follows:

1. The microscopic blood cell images in RGB color space or model are collected.
2. The RGB color space image is converted to HSV color space.
3. S component image is extracted from HSV color space image.
4. The histogram of the S component image is prepared .
5. The Zack's method on histogram is used to find threshold value.
6. Calculated threshold value is not used directly to get the binary image, but some offset value is added to this threshold. This offset value is identified through some experimentation, and later it is found that the desirable value of this offset is 0.25 which is used in this procedure to get the binary image.
7. Hole filling is done by using morphology and apply erosion with disk specification.
8. Euclidean distance is calculated and forms the clusters to get the contours boundary.
9. All contour shapes are filled with pseudo colors.
10. Finally count the total number of contour shapes with different pseudo colors which will provide the total count of the RBC cells.

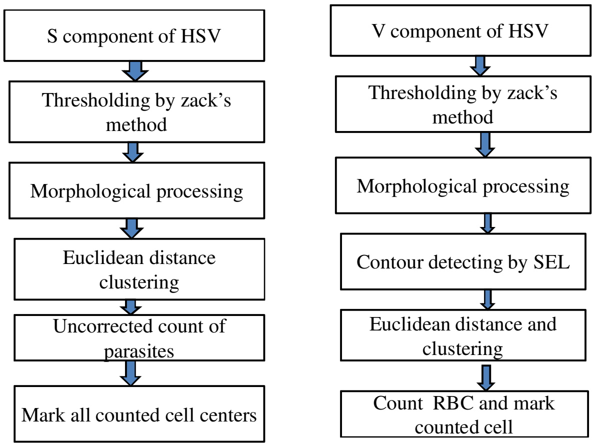

Fig. 1. Flow Schematic of Proposed Approach.

B. Thresholding and Contour Detection by SEL

The technique due to Zack is a graphical solution [8] and gives effective result because some the object pixels produce a weak peak in the histogram. This method also gives an optimal threshold for uni-modal distributions of the histogram. A line is constructed between the maximum of the histogram at intensity b_{max} and the lowest value b_{min} in the image. The distance d between the line and the histogram h[b] is computed for all values of b from $b = b_{min}$ to $b = b_{max}$. The brightness value b_o where the distance between $h[b_o]$ and the line is maximal is the threshold value, i.e. [illegible] $=b_o$.

By the combination of SEL (sequential edge linking) algorithm and thresholding [11] accuracy of segmentation will increase. In SEL [9], edge decisions are made by using global information derived from past decisions on the existence of an edge pixel.

A path will be defined as a set of connected nodes with the following property: for any subset of three nodes r_1, r_2, r_3 in the ordered set, the directions of r_1 r_2 and r_1 r_3 differ by /4 or less. The path may be modeled as a k^{th}- order Markov chain. SEL algorithm defines path metric to rank all the paths explored so far.

C. Euclidian Distance and Clustering

A cluster helps for the collection of objects which are "similar" between them. That is clustering refers to the classification of objects into groups according to certain properties of these objects. An important component of a clustering algorithm is the distance measure between data points. If the components of the data instance vectors are all in the same physical units then it is possible that the simple Euclidean distance metric is sufficient to successfully group similar data instances. Cluster analysis is used to identified the parasites exist [10]. It will focus on detecting the white pixel with a max grey level value with four basic cluster analysis steps:

1. Collection of data.
2. Finding of a similar type of gray level value from image.
3. Used of Euclidean Distance to make a decision about number of clusters.

The Euclidean Distance is used to measure the mathematical distance between pixels and these pixels are classified to their nearest cluster. For the validation of cluster solution calculate the mean value for each data set-

(a) Define the points of area with the same distance with the average value of data set.

(b) All of the points defined determine the line of discrimination that will separate between clusters.

IV. EXPERIMENTAL RESULTS

A. Image Database and Experimental Setup

The two types of malaria found in India one is vivax and other is falciparum but vivax is most common in many of the people. The scheme is evaluated using images taken from Leishman-stained blood smears. The images which are collected for the experiment from the Pathalogy Lab, market road, Gulbargr, Karnataka (India) by the Dr.DeepakY The size of collected images is 1280 × 960 resolution which increases the elapsed time computation time. The given images are infected by the malaria parasite which is having a type of vivax and faiciparum respectively. In total, the database contains 6 red blood samples infected by malaria parasites and original images are shown in Figure 3. The group contains mainly red blood cells which are infected by immature ring-form Schizont and Gametocyte of Plasmodium vivax, Plasmodium falciparum. The manual data with respect to total numbers of parasites, their types and total number of RBC count are observed in the laboratory. Implementation is carried out with Matlab 7.3 and 2 GB RAM. Implementation results are summarized in the Table 1.

Table 1: Summarization of results

Image	Manual count of parasites	Count of parasites by proposed approach
A	4	4
B	7	6
C	16	15
D	17	17
E	22	22

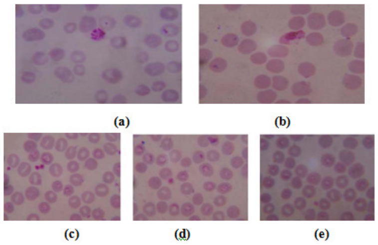

Fig. 2. Original Blood Sample Images from Pathology Lab.

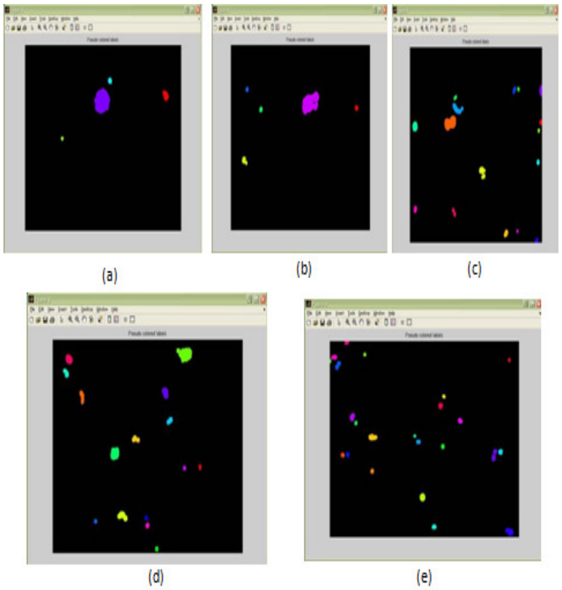

Fig. 3. Parasites Result of Image.

V. CONCLUSION

The detection of Malaria parasites is obtained by pathologists manually by using microscopes. Therefore ,the chances of false detection due to human error are very high, which results into fatal condition. This paper limits the human error while detecting the presence of malaria parasites in the blood sample by using image segmentation. After implementation of the proposed approach for the Lab sample images and for the available image database, it is found that parasites are near about matching with the manual count. In this proposed work, we are getting the accurate and required results in the short period of time The system in a robust manner is unaffected by the exceptional conditions and achieved high percentages of sensitivity, specificity, positive prediction and negative prediction values.

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