AUTOMATED DIAGNOSIS AND IDENTIFICATION OF MALARIAL PARASITE IN BLOOD IMAGES

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ABSTRACT: *Malaria is a mosquito borne infectious disease of humans and other animals caused by unicellular parasitic micro-organism of plasmodium genus under protozoa. This disease is transmitted through the bite from an infected female Anopheles mosquito. The organism is introduced from its saliva into the host circulatory system. Within the blood stream the parasite travels to the liver where they mature and reproduce. Malaria is a serious global health problem and nearly one million deaths is reported each year. Malaria causes symptoms that typically include high fever and headache that under severe infection can progress to coma or death. The disease is prevalent in tropical and subtropical regions around the equator region, including much of sub- Saharan Africa, Asia, and America. Accurate diagnosis is important to control the disease. There are several diagnostic tools available but microscopic analysis is the gold standard. An image processing method to automate the diagnosis of malaria in blood smear images is proposed in this paper using image segmentation approach for detection of malaria parasite.*

KEYWORDS: Malaria, Erythrocyte, Schizont, Plasmodium, Segmentation.

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. Within the human host, the parasite multiplies asexually through exoerythrocytic cycle in liver cells and erythrocytic schizogony in blood. The liver cell suffer damage as the unicellular organisms called merozoites are released in the blood stream. The merozoites enter the Red Blood Cells (RBC), infect them, and multiply within them and finally the cells rapture to release multiple schizonts for further infection. This ratio of parasite-infected cells to the total number RBC is an important in determining and selecting the treatment and drug dose.

Malaria is a serious global disease and a leading cause of mortality in tropical and sub-tropical countries. It affects between 350 and 500 million people and results in more than a million deaths every year. Most of the malaria infections are curable. Rapid and accurate diagnosis enables prompt treatment is an essential requirement to control the disease spread. It is caused by a type of parasitic unicellular microorganism protozoa of the genus Plasmodium. The parasites is transmitted between hosts through the bites of infected female Anopheles mosquitoes. They are called "malaria vectors" and the most effective bite during dusk and dawn when the parasites migrate to the vector's salivary glands. Female Anopheles injects the parasites from its saliva into the host circulatory system. The cycle is re-initiated when the mosquito feeds on contaminated human blood with mature parasites. The intensity of transmission depends on factors availability of abundant vector, the human host, and favourable environment.

There are five species of Plasmodium that can infect or be propagated by human as host. The severe infections and deaths are caused by P.falcipraum and P.vivax. The species of P.ovale, and P.malariae are less severe and very few mortality reported. The species P.knowlesi is prevalent in Southeast Asia on macaques monkeys but it is also known to cause infections in humans. Malaria is widespread across the tropical and subtropical regions where there is abundant rainfall and warm temperatures with stagnant waters provide

ideal propagation for mosquito larvae. Control of mosquito propagation, prevention of bites by mosquito nets and insect repellents, or extensive mosquito-control measures such as spraying insecticides and proper drainage facility can control malaria infection.
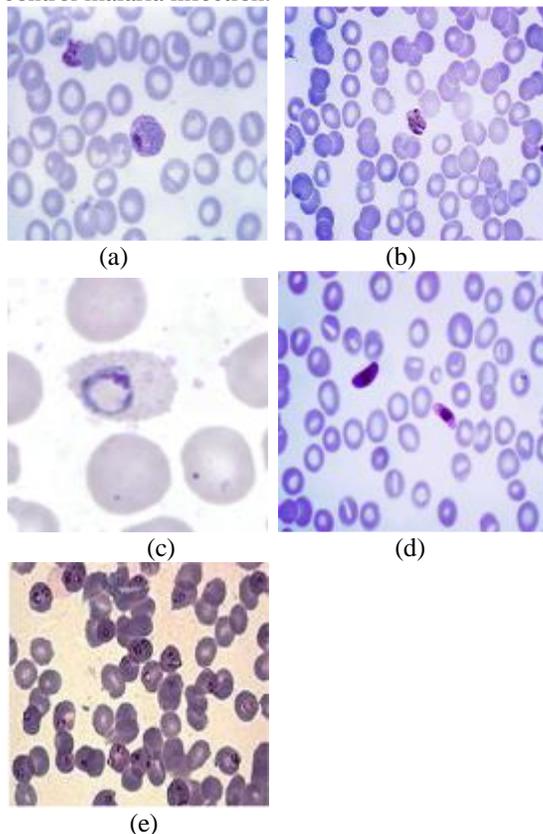

Fig 1 Images of the malarial species

Fig.1 (a),(b),(c),(d) and (e) shows Plasmodium Vivax, Plasmodium Malariae, Plasmodium Ovale, Plasmodium Falciparum,Plasmodium knowlesi.

Current pathological diagnosis involves taking a blood sample from patient. This blood sample is smeared onto a slide and stained in order to colour cell nuclei and microscopic examination is carried out. Next stage involves manual counting by a laboratory technician who can differentiate staining artefacts from actual nuclei and white blood cells. Although manual counting is relatively inexpensive to implement, accuracy of diagnosis is difficult to achieve because of technical limitations and human inconsistency. To overcome this problem many researchers are concentrating on digital image processing algorithms for automatic malaria detection. The only drawback of such systems that focuses on detection of parasites from thin blood films is that the existence of parasites may remain undetected due to low parasite density or lower Parasitaemia.

2. LITERATURE SURVEY

The World Health Organization (WHO) in its World Malaria Report 2011, stated that "Malaria is a serious global health problem, causing widespread sufferings and deaths particularly in Africa and south Asia. According to the report in 2010, about 3.3 billion people which are half of the world populations are at risk of malaria. Additionally, this disease has caused the death of an estimation of 655,000 people in 2010, with 86% of the victims are children under five years of age" [1]. In the research citation of Cox-Singh et al, "Malaria is caused by a peripheral blood parasite of the genus Plasmodium. The genus Plasmodium has five species that can cause human infection namely P. falciparum, P. vivax, P. ovale, P. malariae and P. knowlesi" [2].

Moody, Purwar et al Makler et al reported that "prompt and accurate diagnoses of malaria infection are the main key to control and cure this disease effectively. Currently, the most economic and reliable diagnosis which is based on microscopic examination of blood slide, especially based on the thin blood smear, still remains the gold standard for laboratory diagnosis of malaria" [3]-[5]. In the research paper of Tek et al, the authors outline the fact that "general, detection of the presence of malaria parasites in the examined blood slide is one of the most important tasks in malaria diagnosis" [6]. Purwar et al Makler et al further reiterated the fact that the best possible solution is that "the procedure is performed manually by expert microbiologists by searching for the parasites in blood slide using a light microscope [4], [5]. The WHO, Basic Malaria Microscopy provides the guideline that "during malaria diagnosis, the presence of the parasites is recognizable by their physical features as well as the appearance of the red blood cells (RBCs) that they have infected" [7].

According the research citation by A. Moody, in the year 2012, among "62 countries of 103 that had ongoing malaria transmission in 2000, reporting was considered to be sufficiently consistent to make a reliable judgment about malaria trends for 2000–2012. In the 41 remaining countries, which account for 80% of estimated cases, it is not possible to reliably assess malaria trends using the data submitted to WHO (World Health Organization). Information systems are weakest, and the challenges for strengthening systems are greatest, where the malaria burden is greatest" [3].

In order to identify the malaria parasites autonomously, the primary tasks required through image processing technique is the segmentation of malaria image. Before the parasite can be identified segmentation of infected cell from the cellular background is necessary. Several contemporary research work is concentrated towards developing better approaches in segmentation of smear slide image by using various image processing techniques such as thresholding [8]-[10], watershed [11]-[13], morphological [14], normalized cut [15] and fuzzy divergence [16].

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Mandal et al. [15] have proposed a segmentation method based on optimized normalized cut (NCut) algorithm for segmenting the RBCs that have been infected with malaria parasites in peripheral blood smears. The "NCut algorithm" is based on a global criterion and it maximizes both the total dissimilarity between the different groups and the total similarity within the groups. Here, the "NCut" has been applied in four colour models which are RGB, HSV, YCbCr and NTSC. By using this method, the segmented trophozoite and schizont have been obtained. The results indicate that the performance of the "NCut algorithm" is best in HSV colour model. The drawback of this algorithm is that the artefacts still appeared on the segmented image. Since this algorithm is based on global criterion, any unintended noises can significantly reduce the segmentation accuracy.

Anggraini et al. in their research citation[9] have proposed a histogram-based thresholding method to identify the presence of malaria parasites in thin blood smears of P. falciparum species. The grayscale malaria images have been segmented using global thresholding to obtain the RBCs and other blood cells components in each image. The parasite and infected cell components are obtained by applying multiple thresholds on the segmented image. This step is based on the knowledge that cytoplasm of the parasite infected cell appears lighter, while the parasite appears darker compared to the cytoplasm of the RBC. The drawback of the algorithm proposed is that even the threshold values have been selected automatically, the image quality may affect the results and the methods fails to identify when the histogram does not have distinct valleys.

To overcome the limitations observed among several algorithms discussed a new method has been proposed.

3. PROPOSED METHOD

For the study of microscopic blood cell images are captured using digital microscope interface and from thin smear slide after proper staining. It is observed that different image segmentation algorithms can be applied on the obtained colour images, grey images obtained after grayscale conversion and binary images obtained after image binarization. The images can be transformed into different colour models like RGB, HSV and in that an R, G and B; S components are used respectively for the identification of parasites and RBC by using image processing concept. The proposed method is based on two parameters i.e. number of parasite identified within the image and RBC count of the respective image block. The proposed scheme is divided into two distinct phases whereas in the first phase, the number of isolated chromatin dots corresponding to an infected cellis detected and in the second phase the total numbers of RBC are enumerated for that image frame.

System architecture used for Malaria parasite detection involves following steps:
1. Image Acquisition

2. Pre-Processing
3. Image Segmentation
4. Morphological operation
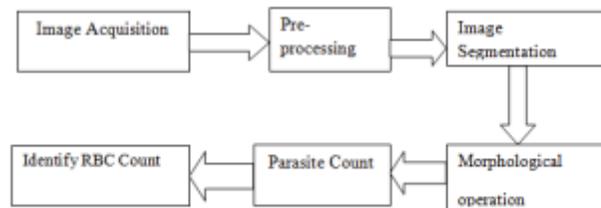5. Parasite Count
6. Identify RBC count

Fig 2: System Block Architecture

The steps followed for the identification of the parasites is as follows:
• Collection of the thin blood smear digitized microscopic blood cell images in RGB colour model.
• Conversion of the images from RGB colour space to HSV colour space.
• Extraction of S component of the image from HSV colour space image.
• Obtaining the histogram of the S component of the image from HSV colour space.

• Calculation of standard deviation of the image S value and storing the value in TS.
• Calculating the threshold value as a product of standard deviation with a predefined constant H. Threshold intensity value T= TS*H.
• Threshold intensity value T= TS*H.
• The obtained threshold value is added with an offset value obtained through rigorous experimentation and fixed to a value of 0.25. The sum of this value with obtained dynamic thresholding value is used in this procedure to get the binary image.
• The segmentation cells with holes at the centre is filled with hole filling using morphology and application of erosion with disk specification.
• The segmentation cells with infections are identified and isolated using the obtained thresholding intensity value.
• The Euclidean distance is calculated that form the clusters to get the contours boundary.
• All the obtained contour shapes are filled with pseudo colours.
• Finally counting of the total number of contour shapes with filled pseudo colours will provide the infected cell count of the RBC cells.

Procedure to identify the RBC count is as follows:
• Collection of the thin blood smear digitized microscopic blood cell images in RGB colour model.
• Conversion of the images from RGB colour space to HSV colour space.

• Extraction of V component of the image from HSV colour space image.
• Obtaining the histogram of the V component of the image from HSV colour space.
• Use the same methods on histogram to obtain the threshold value and finally obtain the binary image.
• This is followed by the hole filling using morphology and applies erosion with disk specification.
• Removal of small area contours using some particular threshold (it can be measured in terms of the total pixels covered by the contour shape), here the value of this threshold is 2000 and 100 for lab data and available data respectively.
• The Euclidean distance is calculated that form the clusters to get the contours boundary.
• Finally counting of the total number of contour shapes with filled pseudo colours will provide the total count of the RBC cells.
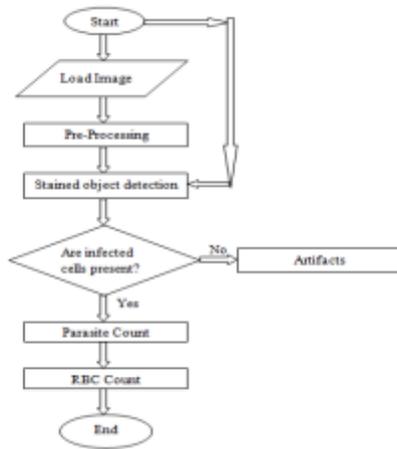

Fig 3:Flowchart

4. RESULTS

The two types of malarial species generally found in India one is vivax and other is falciparum but mostly the vivax is common in most of the people. Most images used in our experiment primarily contains above said species. Here we use microscopic blood sample images collected from clinical laboratory. The size of the images are 500×500, we also used set of images from internet. The proposed work is implemented in MATLAB R2014b running on Windows 10 with Intel core i3 processor and 4GB RAM, also this work is implemented in SCILAB. Graphical User Interface(GUI) has been created in order to make easier using the program. The input images are shown in Fig 4.
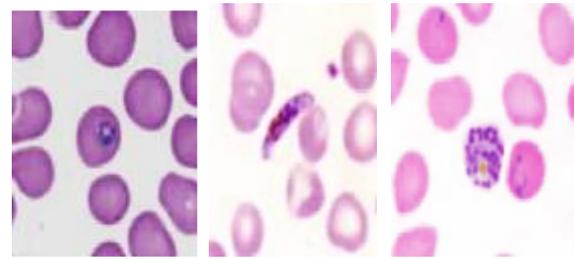

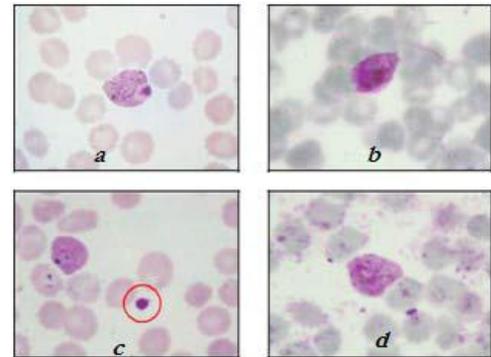Fig 4: Original Image Samples

Fig 5 Samples of the captured malaria images

Fig.5(a) and (b) show the sample images of the digitized malaria slide images with uniform distribution of RBCs and stacking RBCs, respectively. Meanwhile, Fig.5(c) and (d) show the samples of the digitized slide image showing the presence of platelet (red circle) and artefacts, respectively. Based on presence of malaria parasite in the images, it can be seen that the colour of the parasites and normal RBCs regions varies in each slide due to the non-standard preparation of the blood slides.

(a) *(b)*

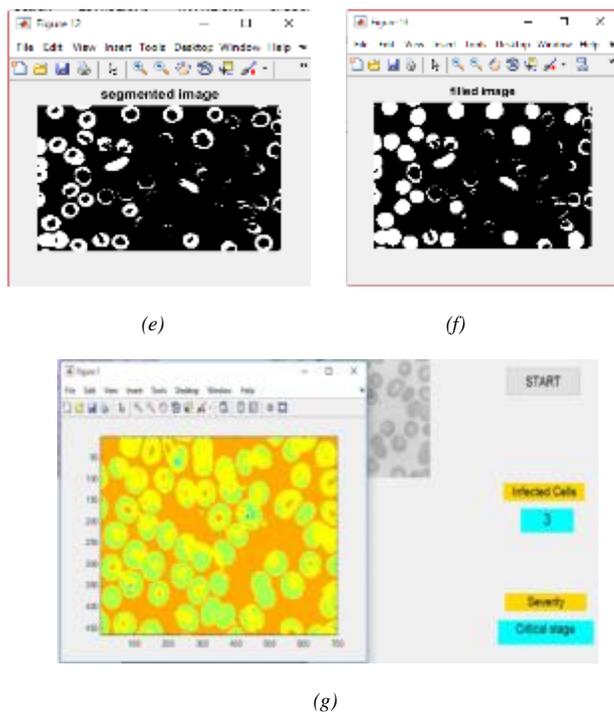*(c)* *(d)*

(e)   *(f)*

(g)
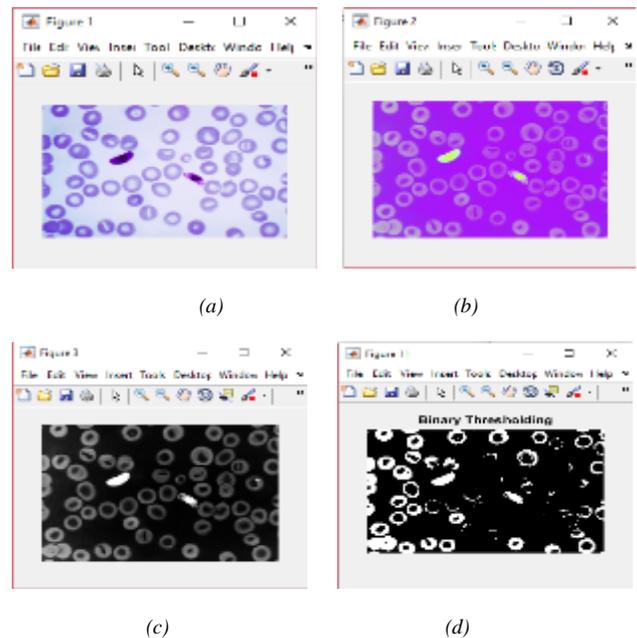
Fig 6 Resulting images with various stages

Fig.6(a) shows the microscopic blood sample image in RGB. Fig.6(b) shows the conversion of RGB image to HSV color model. Fig.6(c) and (d) shows the extraction of S component and binary image. Fig.6(e) and (f) shows the segmented image and image after hole filling. Finally, Fig.6(g) shows the parasite count with GUI representation.

5. CONCLUSIONS

Malaria is a life-threatening parasitic disease that affect tropical countries like India and its prevalence due to lack of maintenance of proper sanitation, health and hygiene. Difficulty in eradicating mosquito has worsen the situation by creating a pan-endemic infection in very little time. Application of digital image processing techniques can assist the pathologists by reducing the number slides that they need to investigate. Absence of sufficient manpower and technicians can be overcome by introduction of CAD systems that can segregate normal slides from infected slides thus reducing the burden. The system proposed shows promising results. It is found that for obtained images, though with low quality due to absence of high resolution cameras, the proposed methodology can work around the problem algorithmically by intelligent combination of colour and light based operations.

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