Malarial Parasites Detection in RBC using Image Processing

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Abstract— The gold standard for the diagnosis of malaria is microscopy in which the blood slide is examined under a micro scope, but the reliability, accuracy and timely diagnosis of the results are highly based on the proficiency of the technician examining the slide. False Detection can occur in the case of poorly skilled technician. In this research work we have proposed a system for automating the manual work done by a technician in order to cut down the human error and increasing the accuracy of the malaria diagnosis. The System is tested for a dataset of80images of a thin blood smear. The infected cells are extracted using HSV segmentation. This approach will be beneficial for the rural areas, with a scarcity of experts.

Keywords: Image Processing, Malarial Parasite Detection, Pre-Processing, Feature Extraction, Segmentation, Morphological Operations, RBC Counting, Plasmodium Detection

I. INTRODUCTION

Malaria, being a mosquito borne disease, is caused by parasites of genus plasmodium. An infected female anopheles mosquito is mainly responsible for the infection. The bite introduces malarial parasites into the circulatory system. The parasite, just like other life forms, possesses a complex life cycle through which it ages and reproduces and to complete this life cycle the parasite uses RBCs as hosts which are then destroyed after the cycle completes. The statistics of World Health Organization (WHO) say that malaria leads to one million deaths per year and people infected by malaria sum up to nearly 250 million. The number of cases concerning malaria has been increasing worldwide mainly due to the decrease of malaria control in some areas causing quick transmission of the infection.

Diagnosis of malaria involves manual study of the patient's strained blood files and identification of malarial parasites present in it through a microscope. Chances of inaccuracy may arise if the patient's sample size is large. Untrained technicians may fail to distinguish the infected cells from the healthy ones while examining the blood smears since the various types of cells in the blood have to be differentiated which could be strenuous. Hence it is required to have experienced and well trained technicians for this job to avoid false negative and false positive detections. In some underdeveloped countries, the lack of resources could pose as a major barrier in accurate and timely diagnosis. Due to any of the above mentioned reasons there is a considerable probability of human error which makes the medical experts realize that machine identification would provide more reliable results.

1) Abstract
2) Introduction
3) Research Elaborations
4) Results or Finding
5) Conclusions

II. IDENTIFY, RESEARCH AND COLLECT IDEA

Asian Journal of Applied Science and Technology (AJAST) Volume 1, Issue 2, Pages 211-213, March 2017 © 2018 AJAST All rights reserved. www.ajast.net Page | 211 Detection of Malarial Parasite in Blood Using Image Processing S.Punitha1 , P.Logeshwari2 , S.Priyanka3 and P.Sivaranjani4 1Assistant Professor, Department of ECE, SVS College of Engineering, Coimbatore, India. Email: spunitha86@gmail.com 2UG Student, Department of ECE, SVS College of Engineering, Coimbatore, India. Email: logeshwariece1196@gmail.com 3UG Student, Department of ECE, SVS College of Engineering, Coimbatore, India. Email: priyankakavi27496@gmail.com 4UG Student, Department of ECE, SVS College of Engineering, Coimbatore, India. Email: sivaranjani.14.ece@gmail.com Article Received: 11 March 2018 Article Accepted: 20 March 2017 Article Published: 22 March 2017

A. 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. Malaria is a serious global disease and a leading cause of morbidity and mortality in tropical and sub-tropical countries. It affects between 350 and 500 million people and causes more than 1 million deaths every year. There were an estimated 190311 million clinical episodes of malaria. It becomes the 5th cause of death from infectious diseases worldwide in low income countries. Yet, malaria is both preventable and curable. Rapid and accurate diagnosis which enables prompt treatment is an essential requirement to control the disease. Currently, clinical diagnosis primarily utilizes microscopy to study the prepared blood smears. However, evaluation of smears is arduous and time consuming, especially in situations where large numbers of samples require reliable analysis. Hence, it is important to develop an automated image analysis that is able to identify the uninfected and infected RBCs in a blood smear image

III. GOAL OF THIS RESEARCH WORK

The biggest detraction of microscopy, namely its dependence on the skill, experience and motivation of a human technician, is to be removed. Used with an automated digital microscope, which would allow entire slides to be examined, it would allow the system to make diagnoses with a high degree of certainty. It would also

constitute a diagnostic aid for the increasing number of cases of imported malaria in traditionally malaria-free areas, where practitioners lack experience of the disease.

IV. FOREMOST OBJECTIVES

The objective of the project is to develop a fully automated image classification system to positively identify malaria parasites present in thin blood smears, and differentiate the species. The algorithm generated will be helpful in the area where the expert in microscopic analysis may not be available. The effort of the algorithm is to detect presence of parasite at any stage. One of the parasites grows in body for 7 to 8 days without any Symptoms. So if this algorithm is incorporated in routine tests, the presence of malarial parasite can be detected Automatic parasite detection has based on color histograms.

V. TEST ALGORITHM & SYSTEM ARCHITECTURE

The design is essentially an image classification problem, and thus takes the form of a standard pattern recognition and classification system. It consists of five stages:

1) Image Acquisition
2) RBC Extraction
3) Edge Detection
4) Binary

VI. WRITE DOWN YOUR STUDIES AND FINDINGS

1) The work presented in the paper processes a blood image in order to detect and classify parasite in blood
2) A statistical based approach is used in order to detect infected RBCs. Color, shape, and information of the size are used to separate the parasites. The images obtained finally are analyzed statistically in order to form a mathematical base. The shape and size of the nuclei is considered as well. The Automated system based on image analysis "Malaria count" for parasite determination is presented in this paper is based on edge detection that represents cells and boundaries of parasites
3) The system is based on the techniques including pre-processing, edge detection, linking of edge, clump splitting and detection of parasites. The methods start from pre-processing, that involves contrast enhancement followed by detection of edges. The system requirements are well separated and well stained cells for efficient results. A framework for the WBCs segmentation by digital image processing is presented in Sadeghianetal
4) The process is divided into two parts. First the morphological analysis based nucleus segmentation and then pixel intensity based cytoplasm segmentation.
5) A segmentation framework is presented which is an integration of several segmentation approaches. The dataset consists of 20 thin blood smear images. The accuracy of the nucleus
6) And the cytoplasmic segmentation were 92 & 78 respectively.
7) The presented framework has the ability to extract the nucleus and cytoplasmic regions in a WBC sample image.
8) A morphological approach to cell segmentation is introduced by Ruberto et althat is accurate than watershed based algorithm. Non-flat disk shaped structuring elements proved to improve the normal watershed based algorithm whereas flat disk shaped structuring element separated
9) The overlapping cells.
10) The applied method is better than existing watershed segmentation. The work presented by Diaz et al. contributes to detecting the parasites of malaria by the support vector machineand artificial neural network.

VII. PLASMODIUM DETECTION

Plasmodium is a genus of unicellular eukaryotes that are obligate parasites of vertebrates and insects. The life cycles of Plasmodium species involve development in a blood-feeding insect host which then injects parasites into a vertebrate host during a blood meal. Parasites grow within a vertebrate body tissue (often the liver) before entering the bloodstream to infect red blood cells. The ensuing destruction of host red blood cells can result in disease, called malaria. During this infection, some parasites are picked up by a blood-feeding insect, continuing the life cycle.[1]

Plasmodium is a member of the phylum Apicomplexa, a large group of parasitic eukaryotes. Within Apicomplexa, Plasmodium is in the order Haemosporida and family Plasmodiidae. Over 200 species of Plasmodium have been described, many of which have been subdivided into 14 subgenera based on parasite morphology and host range. Evolutionary relationships among different Plasmodium species do not always follow taxonomic boundaries; some species that are morphologically similar or infect the same host turn out to be distantly related.

Species of Plasmodium are distributed globally wherever suitable hosts are found. Insect hosts are most frequently mosquitoes of the genera Culex and Anopheles. Vertebrate hosts include reptiles, birds, and mammals. Plasmodium parasites were first identified in the late 19th century by Charles Laveran. Over the course of the 20th century, many other species were discovered in various hosts and classified, including five species that regularly infect humans: P. vivax, P. falciparum, P. malariae, P. ovale, and P. knowlesi. P. falciparum is by far the most lethal in humans, resulting in hundreds of thousands of deaths per year. A number of drugs have been developed to treat Plasmodium infection; however, the parasites have evolved resistance to each drug developed.

[6]. The plan assesses a segmentation based on color to separate the pixels into 3 classes, parasite, RBCs and the background based on standard classification algorithms. KNN, Naïve Byes, SVM and ANN are four different techniques which are evaluated on different color spaces RGB, HSV, YCbCr the complex mix of colors that are presented in parasite makes the discrimination of pixels difficult. The digital image of oil immersion view from

microscopic slides captured through a capture card is done by Premaratnea.

The images were segmented and very converted into gray scale in order to minimize their dimensionality and then are fed into a fed forward back propagation neural network in order to train them as seen in work by K. Edwards .and later the filtered image is enhanced by histogram equalization G. Theo et al [9]. The output is a pre-processed grayscale image.

S. Raviraja, in his research, presents a statistical model to detect the malarial parasites infecting the red cells from a blood image to evaluate the number of parasitaemia in the sample. Then the image is compared to an infected image as it is reconstructed and transformed by scaling, after which a mathematical base is generated. Area-normalized central moments are computed to detect the nuclei of the parasites. The proposed method works on separating the parasites from the rest of the image on the basis of color, shape and size of the infected cells.

Heechang Kim has presented an algorithm of image analysis for high content screening (HCS) of drugs against malaria that quantitatively detects and classifies the stages in the lifecycle of a Plasmodium. The algorithm is capable of discriminating between living and dead parasitaemia. There exist five Plasmodium species that are known to cause malaria in humans and P.falciparum is considered to be the most virulent amongst them all. The newly introduced algorithm estimates the number of isolated or clustered red blood cells and identifies parasitized erythrocytes in viable parasites. The performance of the algorithm was validated by taking count of the infee order mentioned.

Our data consists of heterogeneous datasets, we have lot of variability in the images. So it might be easy to develop an algorithm that works for particular image but it is much different challenge to find an algorithm that works across the board of heterogeneous data sets. There are couple of approaches we can take we cantryan algorithm that is robust to the heterogeneity or we can cached the data into more homogeneity state.

A. Data Collection

Digital image are the main data sources for this research. The images used in this research are taken from Vector-Borne Disease Research and Training Center (VBDRTC), Hetauda, Epidemiology and Disease Control Division, Teku, Kathmandu, Nepal. These images are of highly defined and magnified. Image of RBC's that are taken in thin smear are further processed and analyzed for the MP detection.

Purposed Architecture Using malaria infected images which is of less noisy and devoid of artifact [4] [5] [6], this research can be done. The method used for the counting malaria infected RBCs.

Fig. 1 a): Methodology of Image Processing system for detection and quantification of plasmodium parasites.

Instead of finding how many cell sare infected we will find what types of infection it is using machine learning. A machine learning algorithm takes examples of inputs and outputs associated with a task and produces a program that can automatically differentiate them. In this research we are not going to discuss about machine learning but we will the architecture we used for this research.

Fig. 1 b): Machine Learning algorithm to learn, detect and Bits and Pieces together

In this approach combine all your researched information in form of a journal or research paper. In this researcher can take the reference of already accomplished work as a starting building block of its paper.

B. Use of Simulation software

The abbreviation of MATLAB Matrix Laboratory is a programming environment for algorithm development, data analysis, visualization, and numerical computation, developed by Math Works. MATLAB is widely used matrix-based computation designed for scientific and engineering use. It is also good for many forms of numeric computation and visualization. MATLAB can be used in wide range of applications, including signal and image processing, communications, control design, test and measurement, financial modeling and analysis, computational biology etc.

VIII. GET PEER REVIEWED

We aim at "Automated malaria parasite detection based on image processing", to introduce fast and accurate method for malaria parasite detection. A single blood smear image can be processed multiple times for various detection of blood components unlike or original blood sample using both thick and thin films, The objective are to differentiate RBC and the infected cells which are present in blood smear side, mitigate problems posed by different conditions such as noisy and degrading to set on efficient and awareness result. Better image enhancement algorithm and Morphological operation are proposed to get the count of RBC and parasite in order to speed up the diagnosis process. Input: Digitalized malaria blood smear image Output: Differentiate normal and infected cell and give the count of total RBC and parasites infected cells.

IX. IMPROVEMENT AS PER REVIEWER COMMENTS

Analyze and understand all the provided review comments thoroughly. As mentioned above, traditional malaria diagnostic methods remain problematic. New laboratory diagnostic techniques that display high sensitivity and high specificity, without subjective variation, are urgently needed in various laboratories.

Recent developments in molecular biological technologies, e.g. PCR, loop-mediated isothermal amplification (LAMP), microarray, mass spectrometry (MS), and flow cyto metric (FCM) assay techniques, have permitted extensive characterization of the malaria parasite and are generating new strategies for malaria diagnosis.

This completes the entire process required for widespread of research work on open front. Generally all International Journals are governed by an Intellectual body and they select the most suitable paper for publishing after a thorough analysis of submitted paper. Selected paper get published (online and printed) in their periodicals and get indexed by number of sources.

X. CONCLUSION

The proposed automated parasite detection algorithm avoids the problems associated with rapid methods, such as being species-specific and having high per-test costs, while retaining many of the traditional advantages of microscopy, viz. species differentiation, determination of parasite density, explicit diagnosis and low per-test costs. On the basis of these results we can differentiate the simple RBC and parasite affected blood cells and also differentiate the species of malaria parasites. The proposed algorithm is optimized to overcome limitations of image processing algorithms used in the past. Among the tested test algorithms, 'SUSAN edge detection technique' gave good localization of edges but formed a thick border making cell separation difficult. If the staining of RBC is not properly done even than the edge of parasite affected RBC can be easily detected by the help of SUSAN algorithm, this is the important property of SUSAN algorithm. 'Otsu's algorithm' gave accurate separation of RBCs where as local and global thresholding segmented the parasites. Granulometry provides the size distribution of object in image. The first order features provide the mathematical ranges for simple RBC and parasite affected RBC these values are different for different malarial parasites. Results prove that the algorithm developed in this project has best sensitivity than F.Borey Tek and best positive predictive value than Selena W.S. Sio and F. Borey Tek, and is applicable to many other blood cell abnormalities other than malaria in contrast to the algorithm developed by Jean Phillipe. This is because the percentage of pathological differences in various diseases has very less effect on this robust algorithm. The algorithm detects the species of parasite.

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After successful implementation of the algorithm it can be modified for additional facilities in routine blood check –up like differential white blood cell count, presence of any other parasite causing measure disease, etc.

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