Malaria Detection Using Image Processing and Machine Learning

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Abstract- Malaria is mosquito-borne blood disease caused by parasites of the genus Plasmodium. Conventional diagnostic tool for malaria is the examination of stained blood cell of patient in microscope. The blood to be tested is placed in a slide and is observed under a microscope to count the number of infected RBC. An expert technician is involved in the examination of the slide with intense visual and mental concentration. This is tiresome and time consuming process. In this paper, we construct a new image processing system for detection and quantification of plasmodium parasites in blood smear slide, later we develop Machine Learning algorithm to learn, detect and determine the types of infected cells according to its features.

Index Terms- Malaria, Plasmodium, Edge Mask, RBC, Watershed Segmentation, Support Vector Machines

I. INTRODUCTION

Malaria is a mosquito-borne life threatening disease caused by Plasmodium parasite. Globally, an estimated 3.2 billion people are at high risk (>1 in 1000 chance of getting malaria in a year). According to the report, there were 212 million new cases of malaria worldwide in 2015 (range 148–304 million). The WHO African Region accounted for most global cases of malaria (90%), followed by the South-East Asia Region (7%) and the Eastern Mediterranean Region (2%). [1]. Visual detection and recognition of Plasmodium in RBC is possible via chemical process [2]. The staining process somewhat colorizes the RBCs but highlight Plasmodium, WBCs and platelets. The detection of Plasmodium requires detection of the stained objects. However, we need to analyzed stained objects further to determine if they are parasites or not to prevent false diagnosis. Several methods exist for malaria detection.

Malaria parasite (MP) in blood sample can be identified by using image segmentation and feature extraction using minimum distance classifier [3]. Based on Image Acquisition, Image Preprocessing, Image Smoothing, Thresholding and Dilation image segmentation is done. Feature extraction uses two phases in architectural model: 1) Training Phase and 2) Recognition Phase which helps to recognize the MP.

In this work, we focus 1) automated detection and quantification of malaria detection, 2) strategy to determine infected image using machine learning 3) discuss to improve the predictive value for detection of infected cells.

II. RELATED WORK

Traditional method of detecting malaria disease is using microscope which is time consuming and is difficult, which needs considerable expertise of laboratory technician. People who are bitten by female anopheles mosquito infected with P. falciparum are most at risk of dying from malaria. Most of the research has found that a person with little or no immunity to malaria such as young children, pregnant women, or travelers coming from areas with no malaria is most likely to become sick or die. Poor people living in rural areas who lack access to health care are at greater risk for the disease [7].

Most of the methodologies for detecting malaria disease are based on two criteria: (i) images acquired under well controlled conditions; (ii) the need of proper microscope equipment. Both criteria are different to accomplish in endemic area of malaria, where this type of equipment is scare or non-existent in health care facilities. So, L. Rosadoa and his team proposed different methodology approach for image processing of malaria-infected thick blood smears by using images exclusively acquired with low cost and accessible tools such as Smartphone. The methodology was divided into three main block; Optical Circle Detection, WBC Detection and Trophozoites Detection. It used two different Smart phones, HTC One S and LG Nexus 5, with image resolution ranging from 1456 × 2592 to 1944 × 2592 pixels. [8]L. Rosadoa and his team proposed the method that only represents a component of mobile-based framework for malaria parasite detection. They do not identify and count all possible species- stages combinations of MP that potentially infect humans.

N.A.Khan and his team proposed a computer vision based approach to identify the MP from light microscopy images. The research deals with the challenges involved in the automatic detection of malaria parasite tissues. It is based on pixel based approach. They used K-means clustering (unsupervised approach) for the segmentation to identify malaria parasite tissue [9]. The purpose of K-means clustering is that the clusters of items with the same target category are identified. The predictions for new data items are made by assuming that they are of the same type and nearest to the cluster center. They used chemical process that includes permeabilization, fixation, mounting and staining which is a little more difficult to do in rural areas because of insufficient materials and expertise [9].
III. METHODOLOGY

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 datasets. There are couple of approaches we can take we can try an 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.

B. 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 is shown in Figure A.

1) RBC’s Image Database:

Image acquisition is the first process in all the image processing steps. So, we will have RBC’s image database where malaria infected RBC’s and non-infected RBC’s will be placed. Some of the images that are tested for MP are shown below.

![Figure 1: Input Image](image1.png)

![Figure 2: Input Image](image2.png)

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

Instead of finding how many cells are 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 show the architecture we used for this research.

Fig. 1 b): Machine Learning algorithm to learn, detect and determine the types of infected cells according to its features.

1) RBC’s Image Dataset:

Create Visual BAG of Features

Visual or Feature Vectors

Train Category classifier

Predict class membership

Evaluate classifier

Plasmodium Image

Plasmodium and non-plasmodium image

Represent Bag of Features

Find the closest matches

Display the string label for image
Images that are taken first goes towards chemical process where pH will be maintain so that the MP will be visible clearly. Figure 1 is the input image which has two Malaria Parasite and some impurities. Figure 2 is the input image which does have Malaria Parasite but contains impurities. Figure 3 has one MP and shallow purple colored impurities. Figure 4 is the input image which contains one MP and impurities.

2) Global Thresholding
Segmentation is the process of separating an image into regions with respect to objects. We try to segment regions by identifying common properties. The simplest property that pixels in a region can share is intensity. So, a natural way to segment such regions is through thresholding, the separation of light and dark regions. Thresholding creates binary images from grey-level ones by turning all pixels below some threshold (T) to zero and all pixels above that threshold to one.

Let us suppose a point (x,y) for which f(x,y) > T is called an object point, otherwise the point is called background point. Mathematically, the operation can be expressed as,

\[ g(x,y) = \begin{cases} 
1 & \text{if } f(x,y) > T \\
0 & \text{if } f(x,y) < T 
\end{cases} \]

where the pixels labeled 1 denote object and the pixels labeled 0 denotes background.

3) Enhancement
Image enhancement is the process of adjusting digital image so that the result is more suitable than the original one and will be helpful for further processing. During the research, input image will be enhanced after we threshold the image. After we threshold the Figure-5 we found the following result.

From the result, we can see that the background and RBCs with parasite has been separated into white and black. For the better segmentation we will be doing complement of the above result.

4) Morphological Operations
Morphology is a tool for extracting image components that are useful in representation and description of region, shape. Morphological operations apply a structuring element to an input image, creating an output image of the same size. The value of each pixel in the output image is based on a comparison of the corresponding pixel in the input image with its neighbors.

Erosion and Dilation are fundamental steps for morphological processing. Dilation adds pixels to the boundaries of objects in an image, while erosion removes pixels on object boundaries. From Figure 7 it is noted that the pixels around the boundaries has been removed. Removing the pixel boundaries, noise can be reduced. Form Figure 6 it is noted that the pixels around the boundaries as been added. So, dilation helps in detecting the object clearly.

5) Segmentation
Segmentation subdivides an image into its constituent regions or objects. The level of detail to which the subdivision is carried depends on the problem being solved. Segmentation accuracy determines the eventual success or failure of computerized analysis procedures. For this reason, considerable care should be taken to improve the probability of accurate segmentation. Most of the segmentation algorithm is based on the basic properties of intensity values: discontinuity and similarity.[12] During the research, it is found that two types of segmentation have to be implemented to get the result. Watershed segmentation and Color-based segmentation are used in the research.

a) Watershed Segmentation
Watershed segmentation is relatively a recent approach which tends to separate touching objects. This research applied Watershed segmentation process so that the overlapped RBCs will be separated and will be helpful for counting RBCs.

In watershed segmentation, we assume 2D, grayscale image as a topological in which the location is given by the x,y image coordinates and the height at that location corresponds to the image intensity or grayscale value. A catchment basin defines that connected region for which any rainfall drains to the same

![Figure 5: After thresholding](image)

![Figure 6: Dilation](image)

![Figure 7: Erosion](image)
low point or minimum. In terms of digital image, catchment basins consist of a group of connected pixels. Line which divides one catchment basin from another is called watershed ridges, watershed lines or simply watersheds. [13] Rain which falls on the landscape will naturally drain downwards, under the action of gravity, to its nearest minimum point. We imagine the landscape being gradually flooded from below with the water entering through the local minima. As the water level increases, we construct dams which prevent the water from the catchment basins spreading into adjacent catchment basins. The construction process stops when the water level reaches the height of the highest peak. The dams built in this way are the watersheds which partition the landscape into distinct regions containing catchment basin. [13] Figure-8 represents watersheds and catchment basins.

![Fig. 8: Watersheds and Catchment Basin](image)

We can use original input image for the segmentation but for the suitable segmentation, gradient image is used because gradient magnitude is usually high along object edges and low elsewhere. So, the watershed ridges lie along the object edges. After the morphological operation, distance transform image is used. Distance transform is an operator that transforms the values of pixels in an image according to their distance from the boundary of the object. Farther the pixel from the boundary, higher the value is returned. This will result in transformed image where the area near and within the boundary will be dark whereas the area near the center of the image will be white. Here the distance is calculated as Euclidean distance. Figure-9 shows the distance transform image after morphological operations.

![Figure 9: Distance Transform](image)  ![Figure 10: Distance Transform after Negate](image)

Euclidean distance i.e. the distance from the every pixel to the nearest nonzero is calculated and Figure-9 shows the distance transformed image of Figure-6. Since the catchment basin in it is not shown properly, the distance transforms of the complement of Figure-6 and negate the distance is done and shown in Figure-10. Then after, watershed segmentation is done which is shown in the Figure-11. Noise and small-scale structures within the objects generally result in many local, small catchment basins. These spoil things and produce over-segmentation. [13] To overcome this, minima that are too shallow are removed and do watershed in the result. Final watershed segmentation is show in Figure-12.

![Figure 11: 1st Watershed transformed](image)  ![Figure 12: 2nd Watershed transformed](image)

b) Color based segmentation

Color based segmentation is an approach to separate the defined color from other colored object. Blood samples are gone through the chemical process, and mostly the MP will be in the form of purple color. So, we segment the image with respect to RBCs cells in Figure-13.

![Figure 13: Color based segmentation](image)

The CIE has defined a system that classifies color according to the HVS (the human visual system). Using this system we can specify any color in terms of its CIE coordinates and hence be confident that a CIE defined color will match another with the same CIE definition. The CIE has measured the sensitivities of the three broad bands in the eye by matching spectral colors to specific mixtures of three colored lights. The spectral power distribution (SPD) of a color is cascaded with these sensitivity functions to produce three tri-stimulus values. These tri-stimulus values uniquely represent a color, however since the illuminant and lighting and viewing geometry will affect the measurements these are all carefully defined. The three CIE tri-stimulus values are the building blocks from which many color specifications are made. CIELab has no associated two dimensional chromaticity diagram and no correlate of saturation. CIELhs can therefore not
be defined. [14]

CIE L*a*b* is an attempt to linearize the perceptibility of unit vector color differences. It is non-linear, and the conversions are still reversible. Coloring information is referred to the color of the white point of the system, subscript n. The non-linear relationships for L* a* and b* are the same as for CIE L*a*b* and are intended to mimic the logarithmic response of the eye.

\[
L* = \begin{cases} 
1.16 \times (Y/Yn)^{3/16} - 16 & \text{if } Y/Yn > 0.008856 \\
903.3 \times Y/Yn & \text{if } Y/Yn \leq 0.008856 
\end{cases}
\]

\[
a^* = 500 \times \left( f(X/Xn) - f(Y/Yn) \right)
\]

\[
b^* = 200 \times \left( f(Y/Yn) - f(Z/Zn) \right)
\]

where, \( f(t) = \begin{cases} 
t^6 & \text{if } t > 0.008856 \\
7.787 \times t + 16/116 & \text{if } t \leq 0.008856 
\end{cases} \)

Hue is an angle in four quadrants, and there is no saturation term in this system.

When determining CIEL*a*b* values for CRT displayed colors it is usual to used the CRT’s white point as the reference white. [14]

6) Calculate and find perimeter of parasite and mean perimeter of RBC cells.

After we finished the most important section of our process, we now have to find the mean perimeter of the RBCs. From the research it is found that most of the parasites are larger than the mean perimeter of RBCs cells. With the help of matlab function regionprops we can easily detect the perimeter of object in the image. Regionprops helps to measure properties of image regions. The syntax can be written as

\[
\text{Stats} = \text{regionprops}(L, \text{properties});
\]

\[
\text{Stats} = \text{regionprops}(L, \text{properties}) \text{ measures a set of properties for each labeled region in the label matrix } L. \text{ Positive integer elements of } L \text{ correspond to different regions. The return value, } \text{STATS, is a structure array of length max(L(:)). The fields of the structure array denote different measurements for each region, as specified by properties. We have used ‘Area’ and ‘Perimeter’ properties in our algorithm. ‘Area’ is scalar it returns the actual number of pixels in the regions. ‘Perimeter’ returns a scalar that specifies the distance around the boundary of the region. Regionprops computes the perimeter by calculating the distance between each adjoining pair of pixels around the border of the region. }[15]
\]

After finding the mean perimeter of RBCs cells, we will find the perimeter of each MP.

Basically, malaria is transmitted by female mosquitoes of the genus Anopheles. This mosquito is itself a parasite, the females visiting humans for occasional meals of blood. During feeding, infected mosquitoes pass on the malaria parasite from their salivary glands. The mosquito is described as vector. An immature form of plasmodium is injected into the blood of humans by the mosquito. This form disappears from the bloodstream as it enters various cells of the body, particularly the liver. Here it multiplies to produce large numbers of a form which can infect other liver cells. Each parasite in a red blood cell undergoes further division. The red blood cell bursts and released parasite can enter other red blood cells. As a result of this extensive division, millions of these parasites can be present in the blood. Some of the parasite transforms into male and female forms of the parasite.[10] The image of malaria infecting human blood cell is shown in Figure-14:

![Figure 14: Malaria Transmission Cycle](image)

**Figure 14:** Malaria Transmission Cycle[11]

So, the RBC’s are in the form of circular shape. When the RBC’s are infected by MP, the shape of RBC’s will be bursts and the shape of RBC’s will be changed.

7) Compare whether the parasite is greater than mean value of RBC cells

This process comes under the feature extraction process. To detect infected and non-infected cell, we will compare the parasite’s parameter with mean parameter of RBCs. If the perimeter of parasite in greater than the mean perimeter of RBCs cell, we will make a circle around the parasite. If the perimeter of the parasite is equal or less than the mean perimeter of RBCs cells we will do nothing.

8) Plot circle around infected RBC and calculate the infected cells.

Parasite perimeter greater than the mean perimeter of the RBCs cells are plotted with red circle as shown in Figure-15. And then the number of infected RBCs will be count.

![Figure 15: Final output](image)
If the proposed methodology will able to find at least one RBC infected by the parasite then the research will be successful because the person is considered to be malaria infected if at least one out of multiple parasite can be detected. With the help of doctor and lab technician we can validate whether the red marked circle are infected RBCs or not.

IV. RESULTS & DISCUSSION

During the research, more than 40 images have been tested and some of the testes images are listed below.

We have tested for malaria tested non-infected RBCs cells in Figure 16. Figure 17 is the binarize output image after threshold.

Figure 18 shows the segmented RBCs after watershed segmentation. Figure 19 shows the color based segmentation for parasite’s perimeter.

The mean perimeter of RBCs cells calculated is 318.0261 and the perimeter of parasite greater than mean perimeter of RBC is not found. So, the number of infected cells found is 0.

We have tested for malaria tested non-infected RBCs cells in Figure 21. Figure 22 is the binarize output image after threshold.

In the Figure 21, there are artifacts which have not been detected in final output Figure 25 which are true. Number of infected parasite is 1 which is not true because there is a MP adjacent to the red circle in Figure 25 which is not detected. Mean perimeter is 121.041. Greater than the mean perimeter of RBCs is detected parasite and mark circle around it.
As in input image 1, input image 4 Figure 31 has been tested. Mean perimeter of RBCs is 118.0082. Parasite greater than mean value is traced as circle. And finally found the number of infected cells 1 which is true.

So, from the above result we have found that parasites present in the RBCs cells have been detected. Some errors are still found like not counting the entire infected parasite, impurities greater than mean will be counted as infected cells. Although there are errors, if we find at least one parasite in the RBCs than it is said that she or he is malaria infected.

Remaining works
Around 20/20 of the infected and non infected RBCs cells images have been tested till now. Validation and verification has to be done. Some errors have been found and need to detect in which stage MP has been detected and which stage of MP are not being detected. We have to find the error percentage.

V. CONCLUSION

We have presented an approach and developed an algorithm for detecting malaria, automated malaria detection and quantification of malaria infection. Also, we developed a strategy to train with machine learning, adaptable to detection of malaria with other types of parasite and also discuss to increase the predictive value with results.

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