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Vellore Institute of Technology

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REVIEW-3

DETECTION OF MALARIAL PARASITES

IMAGE PROCESSING – J COMPONENT

CSE 4019

SLOT : G1+TG1

handled by

Dr. SANTHI V

Submitted by

Mayukh Ghosh – 18BCE0417

Abhimanyu Atri – 18BCE2192

S. Aditya Reddy – 18BCE2272

Shreyas Sahu – 18BIS0044

ABSTRACT

This project uses image analysis studies aiming at automated diagnosis or screening of malaria infection in microscope images of thin blood film smears. Malaria is a mosquito-borne infectious disease of humans and other animals caused by parasites (a type of microorganism) of the genus *Plasmodium*. Infection is initiated by a bite from an infected female mosquito, which introduces the parasites via its saliva into the circulatory system, and ultimately to the liver where they mature and reproduce. The disease causes symptoms that typically include fever and headache, which in severe cases can progress to coma or death. Malaria is widespread in tropical and subtropical regions in a broad band around the equator, including much of Sub-Saharan Africa, Asia, and the Americas

INTRODUCTION

Malaria is a mosquito borne disease caused by parasites of genus *plasmodium*. The person gets affected by malaria when malaria parasites are introduced into circulatory system by infected female anopheles mosquito bites. Approximately, 40% of the world's population, mostly those living in the world's poorest countries, is at risk of malaria. A child dies of malaria every 30 seconds. Every year, more than 500 million people become severely ill. With malaria. Between 300 million and 500 million people in Africa, India, Southeast Asia, the Middle East, the South Pacific, and Central and South America have the disease.

GOAL

The biggest detraction of microscopy, namely its dependence on the skill, experience and motivation of a human technician, is to be removed. 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. 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.

Input: Digitalised malaria blood smear image

Output: The count of total RBC and parasites infected cells.

OVERVIEW

Loading the image is the first phase, later the image is being pre-processed to remove unwanted noise and brightness. Feature extraction and successive segmentation techniques are then applied on the image to focus on important parts of the image. Finally, Morphological operations are carried out to differentiate parasite cells from the RBC cells and their respective count is determined.

ALGORITHM AND SYSTEM ARCHITECTURE

The architectural steps and details for the proposed project are as follows:

- 1.) Pre-processing
- 2.) Segmentation
- 3.) Morphology Operations
- 4.) Cell Counting

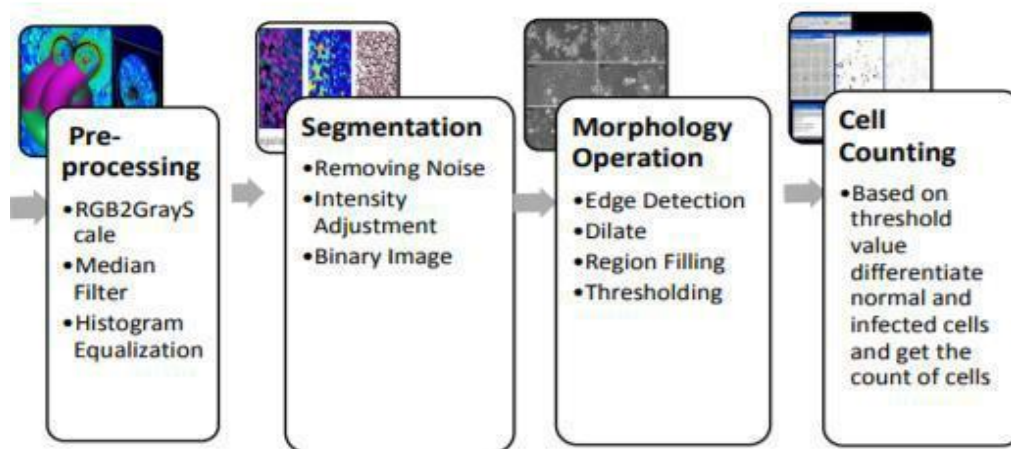
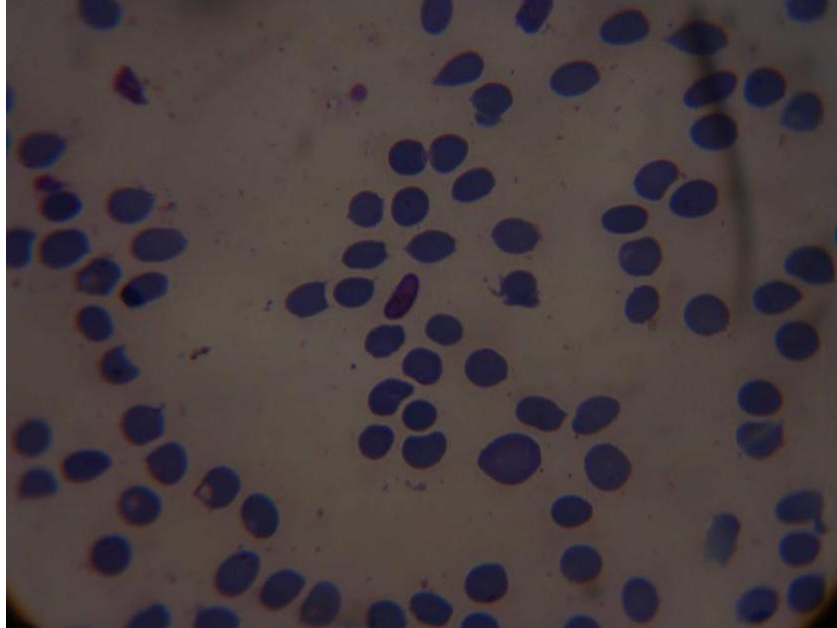


Figure1: System block architecture

SYSTEM RUN ON AN INSTANCE

LOADING

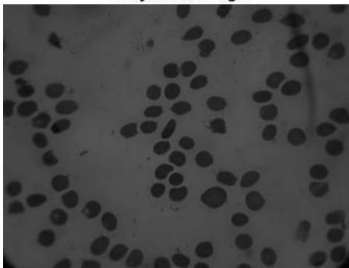
Microscope images of thin blood film smears are loaded in.



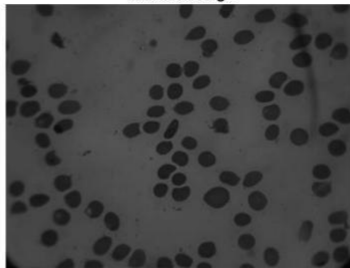
PRE-PROCESSING

Real-world images are highly susceptible to noisy, missing, and inconsistent data. The input image may have low brightness and contrast. Also, Low-quality data will lead to low-quality results. Hence it is essential to pre-process the data. There are a number of pre-processing techniques. In our project, we mainly aim at conversion to Grayscale, median filter and histogram equalization.

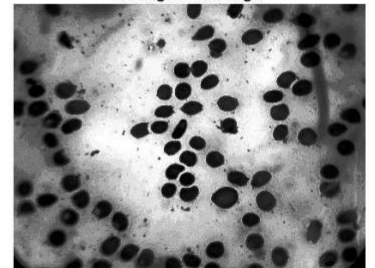
Grayscaled Image



Filtered Image



Histogrammed Image

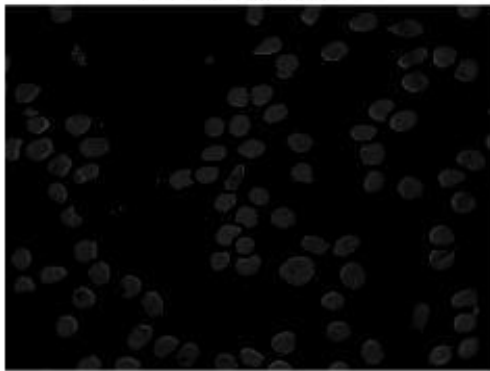


SEGMENTATION:

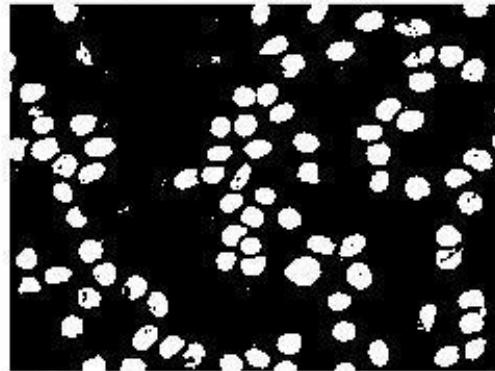
Segmentation divides the image into its constituent regions or objects. The goal of segmentation is to simplify and/or change the representation of an image into something that is more meaningful and easier to analyse. Image segmentation is typically used to locate objects and boundaries in images. In our project, we first extract the RBC and the infected cells by using the blue plane thresholding. Then we remove noise, adjust intensity of the image, perform gray threshold and convert the image to binary form.

STEP1 - Separation of blue plane and the RBC and Infected cells extraction.

Seperation

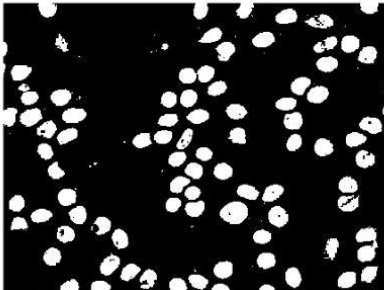


RBC and Infected Cells

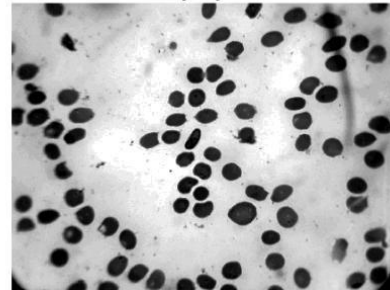


STEP2 - Removal of noise, intensity adjustment of the image, perform gray threshold and convert the image to binary form

Noise Removal



Intensity Adjustment

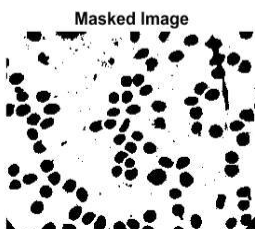
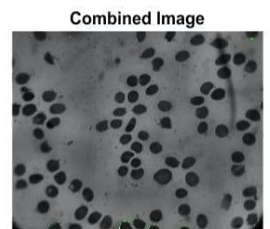
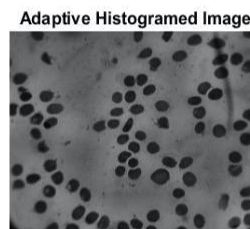
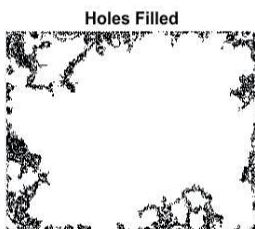
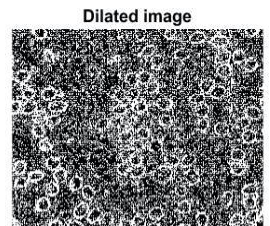
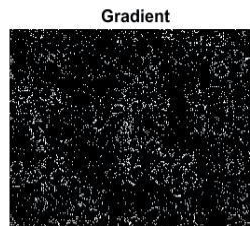
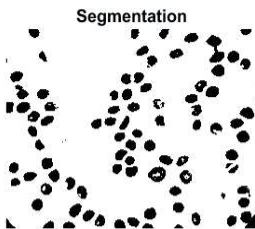


Binary Image



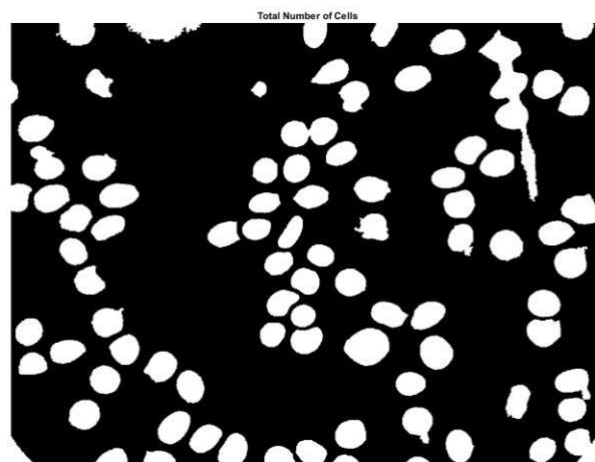
MORPHOLOGICAL OPERATIONS

Morphological operations are image processing operations which processes images based on shapes. It applies a structuring element of specific shape and size on input image. The output image is created by comparing the value of each pixel with its neighbours. These operations are sensitive to the shape of the structuring. Further operations such as holes filling, overlaying is carried out which helps in detection of infected cells.



CELL COUNTING

By taking the complement of the masked image formed in the morphological process, we now can label each individual connected component of image which are in fact our total RBCs. By comparing the overlay of original image and masked image and based on the intensity profile, differentiation between the normal and infected cells is carried out.



CODE

```
[filename pathname]=uigetfile({'*.jpg'; '*.bmp'; '*.png'}, 'File Selector')
imname=strcat(pathname,filename)
```

```
%% Step 1
% Loading
I=imread(imname);
figure(1);
imshow(I);
title('Input Image');
```

```
%% Step 2
% Preprocessing
figure(2);
I2=rgb2gray(I);
subplot(1,3,1);
imshow(I2);
title('Grayscaled Image');
```

```
I3=medfilt2(I2,[3 3]);
subplot(1,3,2);
imshow(I3);
title('Filtered Image');
```

```
I31=histeq(I3);
subplot(1,3,3);
imshow(I31);
title('Histogrammed Image');
```

```
%% Step 3
% Seperating Out the Infected Cells(Blue Plane)
```

```
figure(3);
bluecells = I(:,:,3) - 0.5*(I(:,:,1)) - 0.5*(I(:,:,2));
subplot(1,2,1);
[m,n] = size(bluecells);
```

```
temp = zeros(m,n);
for i=1:m
    for j=1:n
        if (bluecells(i,j) > 0)
            temp(i,j) = 1;
        end
    end
end
```

```
imshow(bluecells);
title('Seperation');
```

```
Blue = bluecells > 10;
subplot(1,2,2);
imshow(Blue);
```

```

title('RBC and Infected Cells');

%% Step 4
% Noise Removal

figure(4);
NRem = bwareaopen(Blue, 10);
subplot(2,2,1)
imshow(NRem);
title('Noise Removal');

I5=imadjust(I3);
subplot(2,2,2);
imshow(I5);
title('Intensity Adjustment');

f=graythresh(I2);

I6=im2bw(I5,f);
subplot(2,2,3);
imshow(I6);
title('Binary Image');

%% Step 5
% Morphology

figure(5);
I7=bwareaopen(I6,20);
subplot(3,3,1);
imshow(I7);
title('Segmentation');

[~, thd] = edge(I2, 'sobel');
ha = 0.5;
seg = edge(I2, 'sobel', thd * ha);
subplot(3,3,2);
imshow(seg);
title('Gradient');

linepp = strel('line', 3, 90);
linepl = strel('line', 3, 0);

segdil = imdilate(seg, [linepp linepl]);
subplot(3,3,3);
imshow(segdil);
title('Dilated image');

segf = imfill(segdil, 'holes');
subplot(3,3,4);
imshow(segf);
title('Holes Filled');

I2=rgb2gray(I);
Iadeq = adapthisteq(I2);
subplot(3,3,5);

```



```

imshow(Iadeq);
title('Adaptive Histogrammed Image');

ad = im2bw(Iadeq, graythresh(Iadeq));
adp = imfill(ad, 'holes');
adpt = imopen(adp, ones(5,5));

adptv = bwareaopen(adpt, 5);
adper = bwperim(adptv);
comb = imoverlay(Iadeq, adper, [.3 1 .3]);
subplot(3,3,6);
imshow(comb);
title('Combined Image');

mimg = imextendedmax(Iadeq, 80);
subplot(3,3,7);
imshow(mimg);
title('Masked Image');

%%title('MASKED IMAGE');
mimg = imclose(mimg, ones(5,5));

%% Step 6
% RBC Count

mimg5 = imcomplement(mimg);
mimg5 = bwareaopen(mimg5, 2500);

I9=bwlabel(mimg5);

rbc=max(max((I9)));
RBC = rbc

figure(6);
imshow(I9);
title('Total Number of Cells')

I8=imfill(I7, 'holes');

L=bwlabel(I8);
%% Step 7
% Infected Cells Count

infcells=max(max(L));
Infected_Cells = infcells

Ratio = infcells/rbc

% The End

```

COMMAND WINDOW OUTPUT

```
Command Window
>> process

filename =

    'Img1.JPG'

pathname =

    'F:\DETECTION OF MALARIAL PARASITE\images2\'

imname =

    'F:\DETECTION OF MALARIAL PARASITE\images2\Img1.JPG'

RBC =

    88

Infected_Cells =

    2

Ratio =

    0.0227

fx >>
```

CONCLUSIONS

The detecSon of malaria parasites is done by pathologists manually using microscopes. so, the chances of false detecSon due to human error are high, which in turn can result into fatal condiSon. this project eliminates the possibility of human error while detecSng the presence of malaria parasites in the blood sample by using image processing and automaSon. we achieved this goal using image segmentaSon smoothing processing techniques to detect malaria parasites in images. the system in a robust manner so that it is unaffected by the excepSonal condiSons and achieved high percentages of sensiSvity, specificity, posiSve predicSon and negaSve predicSon values. and the extracSon of red blood cells achieves a reliable performance and the actual classificaSon of infected cells.

FUTURE SCOPES

1. Support Vector Machine (SVM) techniques can be used to analyze and classify the parasite species.
2. The system which is at present developed using MATLAB software can further be implemented in android platform.

REFERENCES

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