Image Processing

CSE4019

School of Computer Science and Engineering

VIT Vellore

Title

Detection of malarial parasite in blood using image processing Based on color based discrimination and morphological operations

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Abstract:

Malaria has been a severe fatal disease for a long period of time. The mostly used method to diagnosis malaria is manual method which is a time consuming process and this method also involves chances of error in obtained result due to particular assessment of the sample. Here, an innovative and reliable method of detection of malaria parasite in blood is introduced which involves techniques based on image processing. This project reviews the image analysis studies aiming an automated diagnosis of malarial infection in microscope images of thin blood film smears. Some algorithm has been proposed like consisting of color based pixel discrimination technique and morphological operation to identify malaria parasites in thick smear images. Morphology is a broad set of image processing operations that process the images which are based on their shapes. Morphological operations apply structuring element to given image or input image, forming an output image of the same size. In morphological operations the value of the pixel in the output image is based on the comparison of the corresponding pixel in the input image with its neighbors. By choosing the size and shape of the neighborhood, we can construct a morphological operation that is sensitive to specific shapes in the input image. This algorithm will be helpful in the area where the expert in microscopic investigation may not be available. Color based discrimination is finding out malaria cells using difference between each pixel's value and finding out the accuracy of the using mathematic classifier like SVM. This project provides restriction or control the human error while detecting the presence of malaria parasites in the thick blood sample using image processing. The methods on which image analysis of blood smears have been construct, especially fall into two types namely, analysis based on morphology and that based on color. Evaluation of the percentage and efficiency shows that which algorithm like color based pixel discrimination technique and morphological operation has higher baleful rate, which is comparative study or will give good output when tested on same input slide.

Keywords: **Color based pixel discrimination, Morphological operation, Dilation, Erosion, Gray Scale Image, thin blood film smears**

Introduction:

Malarial disease is one of the most and dynamically occurring challenging problem all over the world mainly in Asian and African continents. Presently, even 110 years after the Nobel Prize of Ronal Ross for his work on malaria, people in European region are also at risk from these diseases. And mostly 1 million of the people are being dead in Africa due to malaria (Breman, 2016). As it is all known to us that treatment of malarial is itself a challenging task its quick detection is also a problem with more obstacles. There are mainly four species of malaria parasites infecting human beings namely, plasmodium falciparum, plasmodium vivax, plasmodium ovale and plasmodium malaria (Kwenti, 2017). Plasmodium vivax, is found mainly in tropical and subtropical areas and has several clinical demonstrations. Rapid detection of presence of Malaria parasites in human blood and early institute of Antimalarial drugs are the backbone of management of the disease. WHO recommends that all cases of suspected malaria be confirmed using parasite-based diagnostic testing before managing treatment. In the malaria detection test, microscopy based diagnosis has the major importance for species differentiation, parasite quantification, management of serious or critical disease. Additionally, the method may be tractable to large section of the society because of its scalability and low running cost.

Mainly two types of blood smears are there as, thick and thin, are prepared from the blood of patients, those who are clinically reckon to be suffering from malaria. The thick smear blood is more useful for parasite detection whereas the thin smear is practically used for identification of malaria species. When the parasite load is low, malaria may be detected about 20 times more rapidly in thick smear then in thin smear. The methods on which image analysis of blood smears have been construct, especially fall into two types namely, analysis based on morphology and that based on color. Some of the reported methods use direct training sets and lack of availability of appropriate training sets may determine the scalability of such methods.

The following research papers were referenced for the preparation of this paper

Kazarine, Alexei et.al. suggested a approach called third harmonic generation image scanning cytometry combining with third-harmonic generation imaging, high-speed motorized scanning, and automated software processing. It is a non-linear process that uses the selectivity of this contrast mechanism to perform label-free image scanning cytometry of patient blood smears for automated malaria detection (Alexei and Baakdah, 2019) . Kishor Roy et.al. using colour and segmentation based algorithms i.e. HSV segmentation and watershed segmentation. On using 100 real samples and 200 internet samples, watershed segmentation detected 85 and 164 respectively whereas HSV segmentation detected 70 and 160 respectively but the detection increased when both segments were mapped (Roy, 2018). Sneha Narayan Chavan, using support vector machine and neural network algorithm malarial parasite was detected in which overall sensitivity to capture cases of malaria is 100% and specificity ranges from 50-88% for all species of malaria parasites (Chavan, 2016). Frean, build a morphologic based analysis system to count parasites from individual microscopic images. But there was some inconsistency of detecting the parasite which is in primary state (Frean, 2010). Pallavi T Suradhkar propose is effectively an image classification issue, and therefore the form of a standard classification and pattern recognition method. Thresholding, grey scale image conversion, thinning labeling algorithm involves in system design used for malaria parasite detection. Image segmentation techniques and color range are used by it to identify infectious cells present in images obtained from giemsa stained blood samples (Suradkar, 2017). Diaz in

his research determines a color segmentation method for division of pixels into three distinct classes: red blood cell, parasite and background, on the basis of standard supervised classification algorithms (Diaz, 2018). The paper by Silvia Halim, designed a system for estimating parasitemia. Template matching approach is used for RBCs detection. Detection of parasites are done by means of the variance based system from grayscale images and next approach is based on color co-occurrence matrix which is on the basis of the individual color index of pixel and color indices of its eight neighboring pixel (Halim, 2006). Deepa. A. Kurer et.al. designs a new approach for low-level image processing – SUSAN (Smallest Unvalued segment assimilating nucleus) Principle, that performs Edge and Corner detection. Image features depend on the geometry of the cells, texture and color and generation of parasites takes place, also features which uses a priori knowledge of the classification problem and mimic features used by human technicians (Kurer, 2018). Somasekar proposed a linear programming based Image segmentation and morphological operations for detection of malarial parasites. Two applications are presented: formulation of a linear programming based on the given data and solving given problem using graphical method approach for detecting parasites. But there was no complete system for detecting different parasites (Somasekar, 2018). Snehal Suryawanshi, Prof. V. V. Dixit et.al. proposed enhanced technique for Malaria Parasite Detection, in which cell segmentation process consists of various steps such as image binarization using Poisson's distribution based Minimum Error Thresholding, followed by Morphological Opening for the purpose of refinement. Results executes that SVM (Support Vector machines) gives better accuracy of 93.33% than that of Euclidean Distance Classifier which is 80% (Suryawanshi, 2018). In Paper of Edison, Maombi, Jeeva et.al. Blood samples of malaria patients selected based on the seriousness of parasitemia, were divided into low (LP), medium (MP) and high (HP) parasitemia, which represent increasing levels of the disease severity. By processing of erythrocytes images their contours were obtained and from these the shape parameters area, perimeter and form factor were gained. The gray level intensity was determined by scanning of the erythrocyte along its largest diameter. The gray level intensity decreases with the increase of seriousness of the disease. The changes in shape parameters directly and gray level intensity variation inversely are correlated with the increases in parasite density due to the disease (Edison, 2011). Ahmedelmubarak Bashir, Zeinab A.Mustafa et.al. made use of the intensity features of Plasmodium parasites and erythrocytes. Images of infected and non-infected erythrocytes were acquired, pre-processed, relevant features extracted from them and eventually diagnosis was made based on the features extracted from the images A set of features that are established on intensity have been planned, and the performance of those features on the RBC samples from the created database have been tested by using an artificial neural network (ANN) classifier. The results have shown that these features could be successfully used for malaria detection (Bashir, 2017). Satishkumar L. Varma Satishkumar S. Chavan et.al. used Local binary pattern(LBP) to classify blood smear into thin and thick blood smears. The experiments thus performed over are standard datasets using segmentation and morphological operations for thick and thin blood smear images. The results are then compared using sensitivity and specificity (Varma, 2019)

RESEARCH FRAMEWORK

RESEARCH ARCHITECTURE

Architecture Diagram is a graphical representation of the concepts, their principles, elements and components which are the part of an architecture. For system developers, system architecture diagrams are needed to understand, clarify, and communicate ideas about the system structure and the user requirements that the system must support. It's a basic framework which can be used at the system planning phase helping partners understand the architecture, discuss changes, and communicate intentions clearly.

The general diagram of the system has been shown in fig 1.1

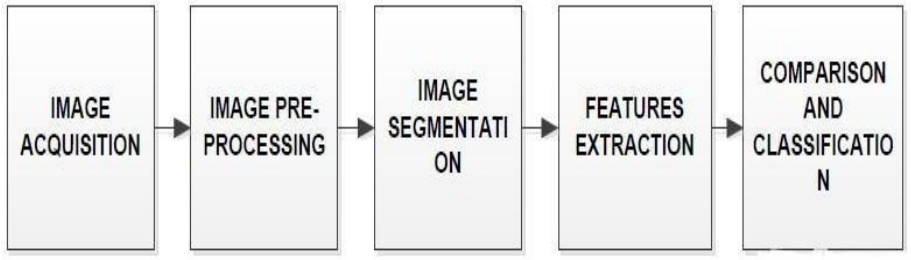
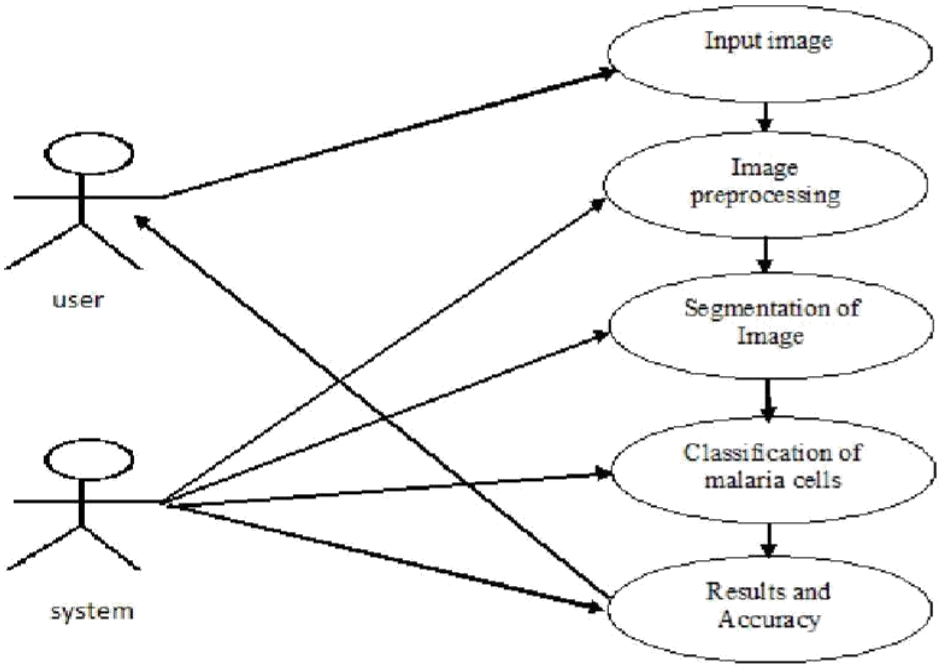


Fig: System Architecture

As it can be seen that image followed by user is processed and followed by segmentation and features extraction and at last comparison has also been done.

USE CASE DIAGRAM

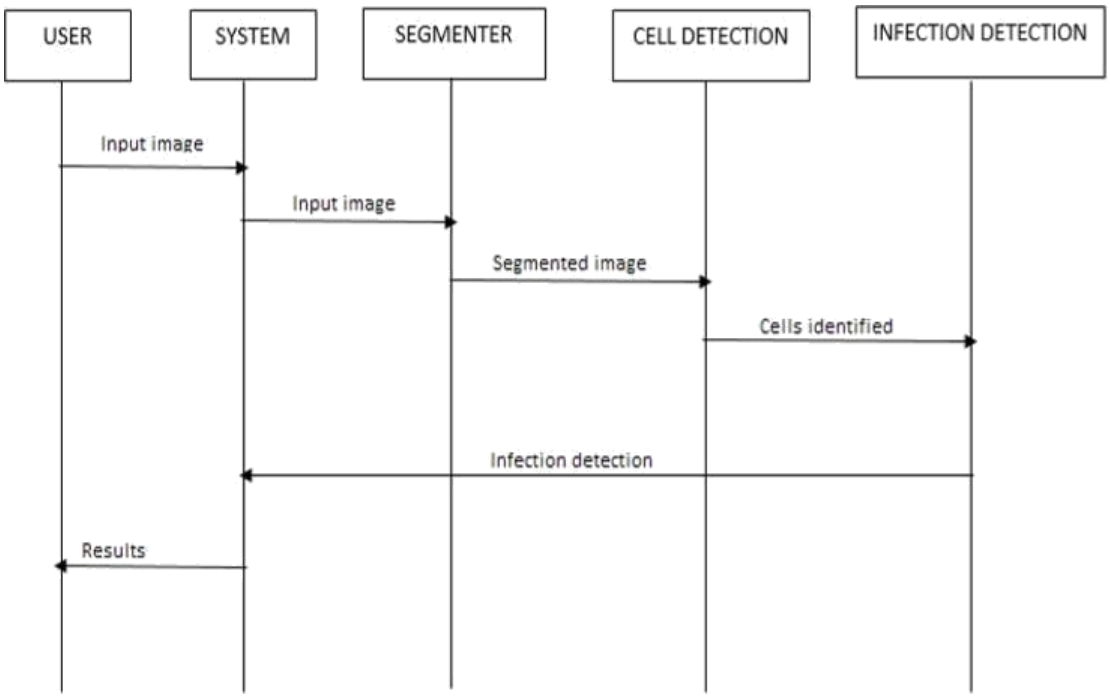
A use case diagram is a graphical representation of a user's interaction with the system and depicting the specifications of a use case and the relationship between the user and the different use cases in which the user is involved. A use case diagram can portray the different types of users of a system and the various ways that they interact with the system. This type of diagram is typically used in conjunction with the textual use case and will often be accompanied by other types of diagrams as well.



In this system, sequence diagram there are two actors i.e. the user and system where the image is accepted by the system and it is further preprocessed, segmented and classified to give the results.

SEQUENCE DIAGRAM

A sequence diagram is an interaction diagram that shows how processes operate with one another and in what order. It is a construct of a Message Sequence Chart. A sequence diagram shows object interactions arranged in time sequence. It depicts the objects and classes involved in the scenario and the sequence of messages exchanged between the objects needed to carry out the functionality of the scenario. Sequence diagrams are typically associated with use case realizations in the Logical View of the system under development. Sequence diagrams are sometimes called event diagrams, event scenarios. A sequence diagram shows, as parallel vertical lines (lifelines), different processes or objects that live simultaneously, and, as horizontal arrows, the messages exchanged between them, in the order in which they occur. This allows the specification of simple runtime scenarios in a graphical manner.



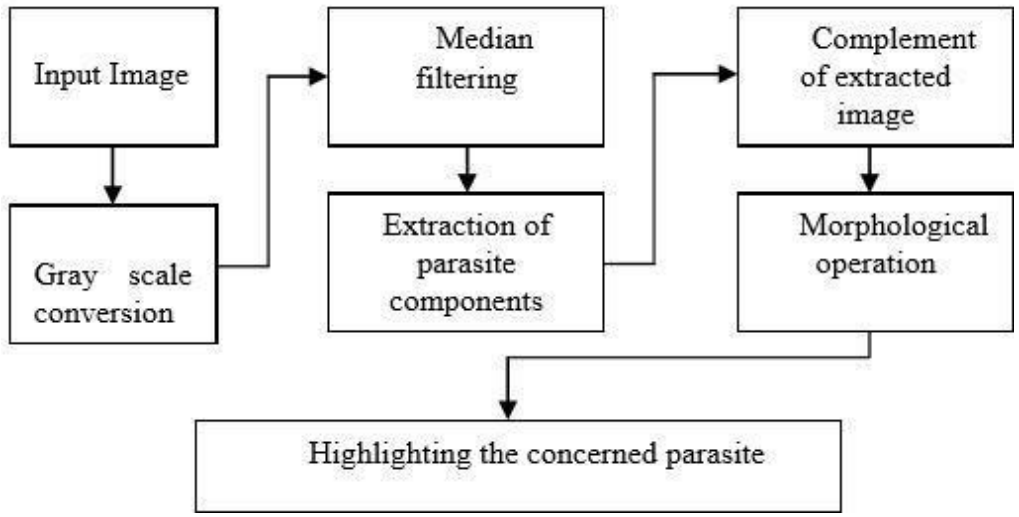
IMPLEMENTATION

Here the proposed system includes two algorithms

1. Morphological Operation.
2. Colour based discrimination.

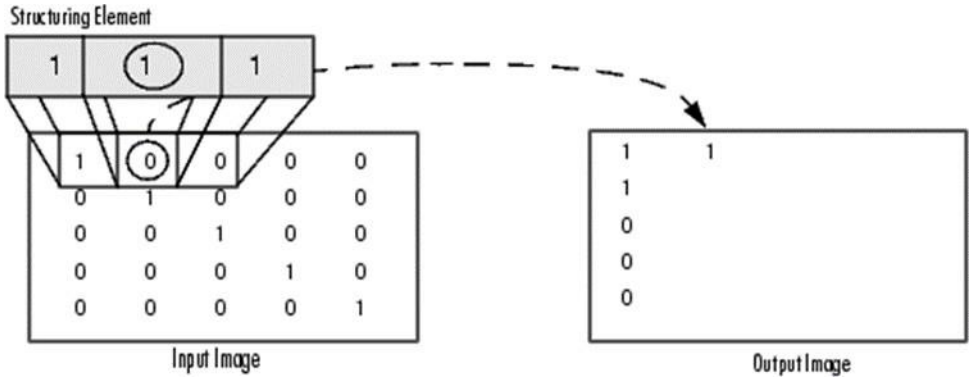
Algorithm 1: Detecting using Morphological Operations

MODULE:



Morphology is a broad set of image processing operations that process images based on shapes. Morphological operations apply a structuring element to an input image, creating an output image of the same size. In a morphological operation, 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. By choosing the size and shape of the neighborhood, you can construct a morphological operation that is sensitive to specific shapes in the input image.

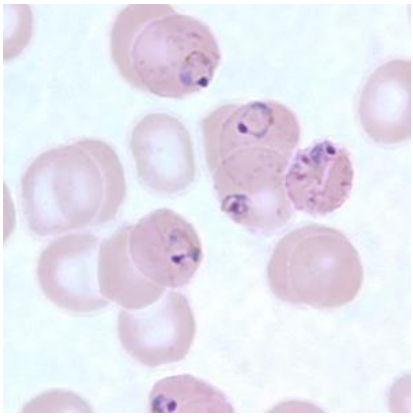
The most basic morphological operations are dilation and erosion. Dilation adds pixels to the boundaries of objects in an image, while erosion removes pixels on object boundaries. The number of pixels added or removed from the objects in an image depends on the size and shape of the structuring element used to process the image. In the morphological dilation and erosion operations, the state of any given pixel in the output image is determined by applying a rule to the corresponding pixel and its neighbors in the input image. The rule used to process the pixels defines the operation as a dilation or an erosion.

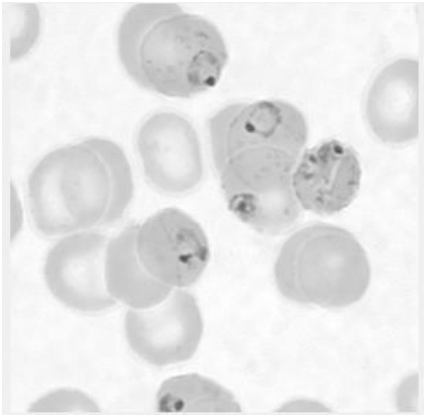


The above figure illustrates this processing for a grayscale image. The figure shows the processing of a particular pixel in the input image. Note how the function applies the rule to the input pixel's neighbourhood and uses the highest value of all the pixels in the neighbourhood as the value of the corresponding pixel in the output image.

1.1 Pre-Processing of image

Pre-processing of image consists of converting the original image into grayscale image that can be done by using an inbuilt function **rgb2gray().** RGB to gray conversion is done by averaging all the three components i.e. R, G and B which results in gray scale





RGB to grayscale conversion

After the conversion of grayscale image we apply inbuilt function **edge()** that detect edges using the Canny method. The Canny method finds edges by looking for local maxima of the gradient of I. The edge function calculates the gradient using the derivative of a Gaussian filter. This method uses two thresholds to detect strong and weak edges, including weak edges in the output if they are connected to strong edges. By using two thresholds, the Canny method is less likely than the other methods to be fooled by noise, and more likely to detect true weak edges.

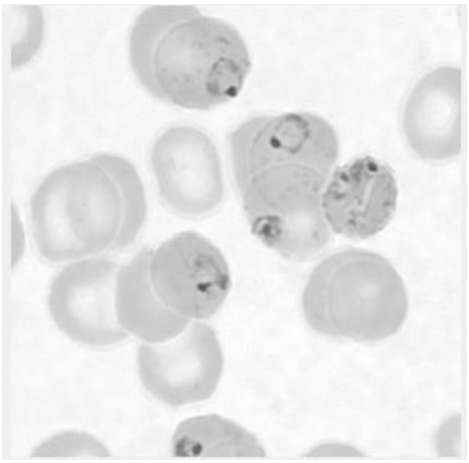
1.2 Segmentation

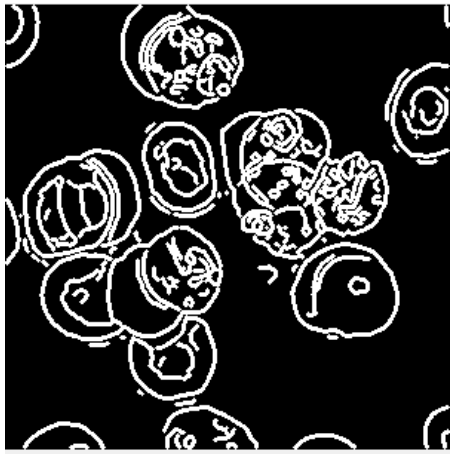
Segmentation process starts with the **strel()** function which takes the pre-processed image as an input. A strel object represents a flat morphological structuring element, which is an essential part of morphological dilation and erosion operations.

SE = strel('disk',R,N) creates a disk-shaped structuring element, where R specifies the radius. N specifies the number of line structuring elements used to approximate the disk shape. Morphological operations using disk approximations run much faster when the structuring element uses approximations.

After applying strel function, the output of this function is taken as input for **imdialte()** function.

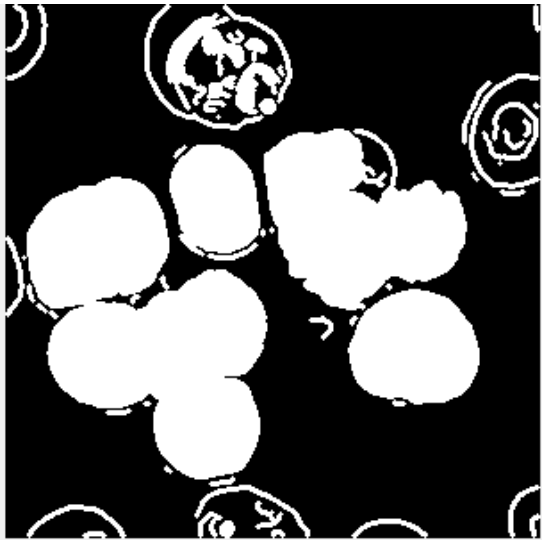
IM2 = imdilate(IM,SE) dilates the grayscale, binary, or packed binary image IM, returning the dilated image, IM2. The argument SE is a structuring element object, or array of structuring element objects, returned by the strel or offset strel function.





Conversion of grayscale to dilated image

Next, **BW2= imfill(BW,'holes')** fills holes in the input binary image BW using **imfill().** In this syntax, a hole is a set of background pixels that cannot be reached by filling in the background from the edge of the image.



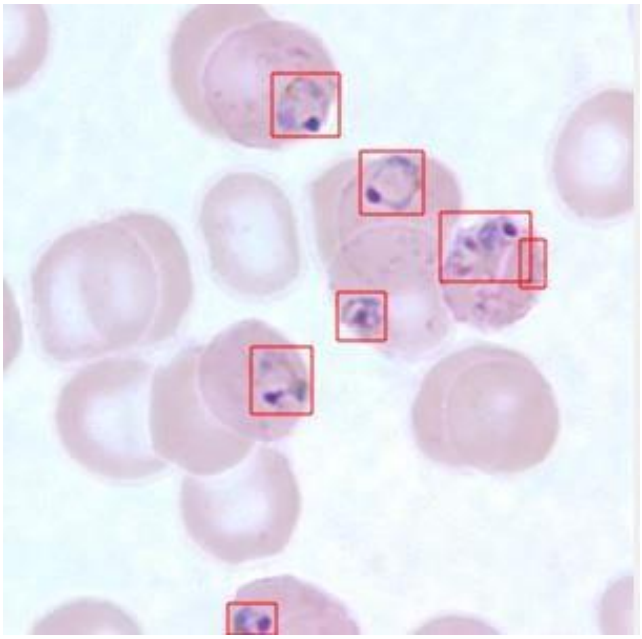
Filling the holes

Next, **BW2 = bwareaopen(BW,P)** removes all connected components (objects) that have fewer than P pixels from the binary image BW, producing another binary image, BW2. This operation is known as an area opening.

1.3 Classification

After applying bwareopen we apply regionprops, graycomatrix and graycoprops to measure properties of image regions and apply red rectangular box for each detected region using bounding box.

glcms = graycomatrix(I,Name,Value,...) returns one or more gray-level co-occurrence matrices, depending on the values of the optional name/value pairs. Parameter names can be abbreviated, and case does not matter. **stats = graycoprops(glcm,properties)** calculates the statistics specified in properties from the gray-level co-occurrence matrix glcm. glcm is an *m*-by-*n*-by-*p* array of valid gray-level co-occurrence matrices. If glcm is an array of GLCMs, stats is an array of statistics for each glcm.



Detection of malaria infected cells

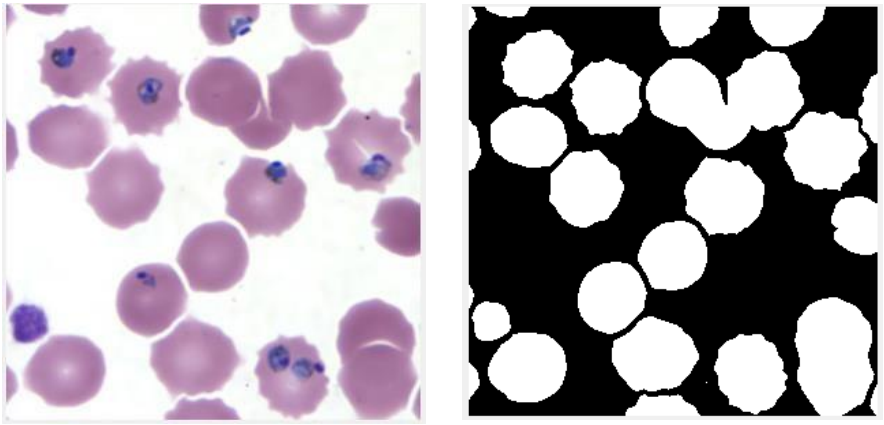
Algorithm2: colour based discrimination

Colour based discrimination is finding out malaria cells using difference between each pixels value and finding out the accuracy of the using mathematic classifier like SVM. This process can be explained by the series of process

- Segmentation.
- Water segmentation.
- Finding number of RCBs cells in a image.
- Intensity adjustment and identification of infected malarial cells

2.1 Segmentation

When we "segment" an image, we distinguish the regions of interest (ROIs) from the non-ROI portion, generally creating a binary mask of what we want to qualify, quantify, track, etc. This segmentation done by an app called image segmenter which is inbuilt in matlab and able to export code.



segmentation of cells from original image

You can improve the results by using in built function bwareaopen() on the segmentation image.

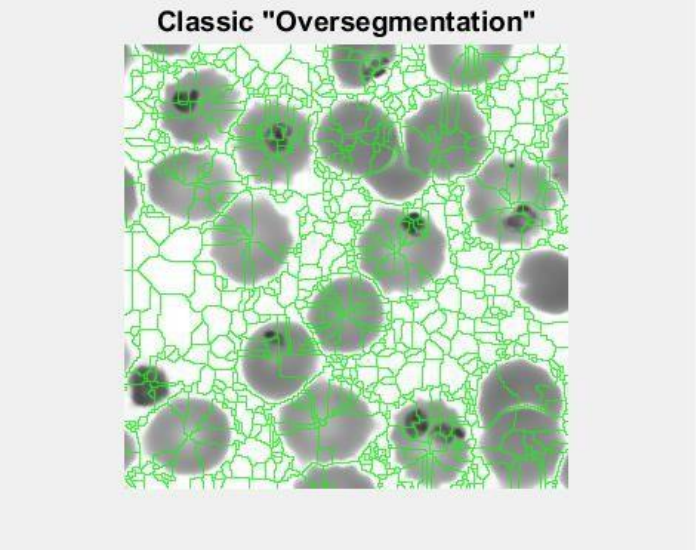
BW2 = bwareaopen(BW,P) removes all connected components (objects) that have fewer than P pixels from the binary image BW, producing another binary image, BW2. This operation is known as an area opening. But this results of segmentation is not enough so we go for water segmentation.

2.2 Water Segmentation

A watershed is a transformation defined on a grayscale image. The name refers metaphorically to a geological watershed, or drainage divide, which separates adjacent drainage basins. The watershed transformation treats the image it operates upon like a topographic map, with the brightness of each point representing its height, and finds the lines that run along the tops of ridges.

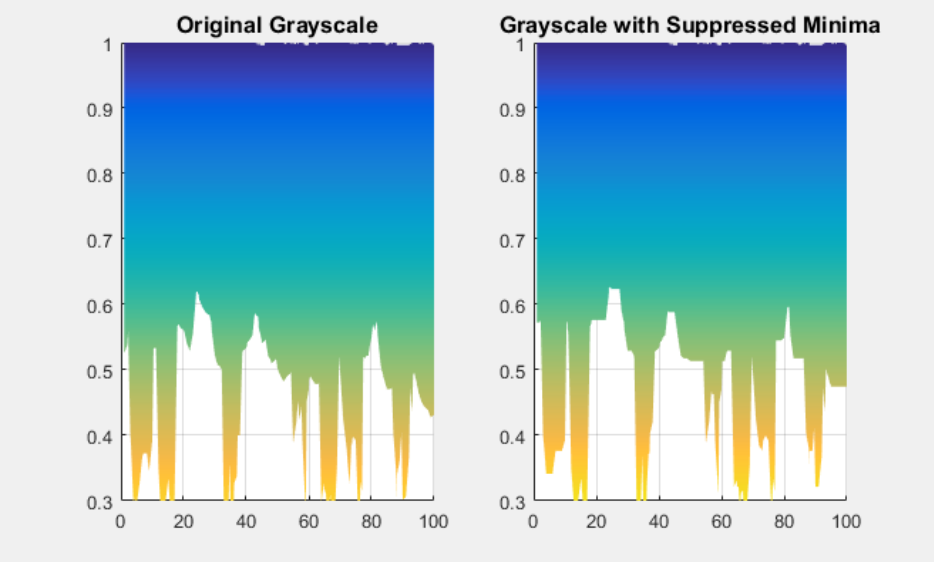
To apply water segmentation on a grayscale image, we use inbuilt function called **watershed() .**

By applying this function we get a results as fig 5.7, but this image has lots of watershed line which is over segmenting the cells. To get a watershed line in between the each cells for proper segmentation we need to further process it using IMHMIN.



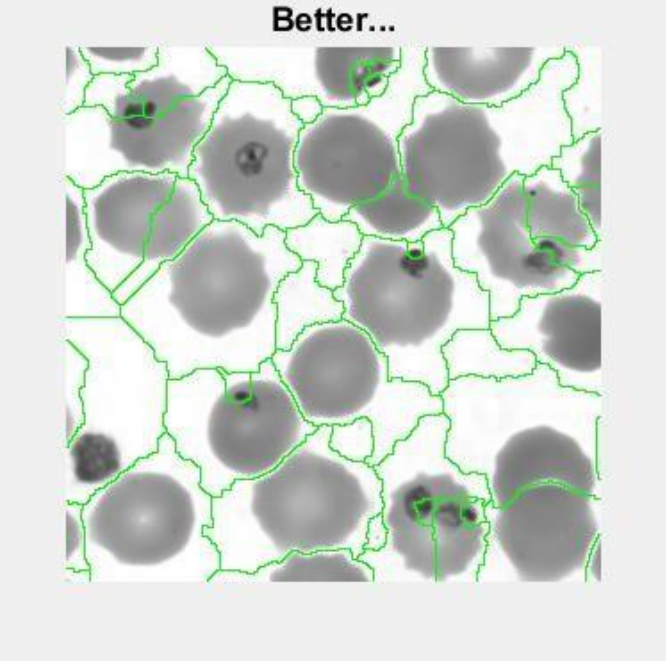
Over segmentation of watershed

Improving that result, **I2 = imhmin(I,h)** suppresses all minima in the intensity image I whose depth is less than h, where h is a scalar. Regional minima are connected components of pixels with a constant intensity value, t, whose external boundary pixels all have a value greater than t. After applying imhmin function we get a suppressed grayscale image.



Suppressed minima in the intensity of grayscale image.

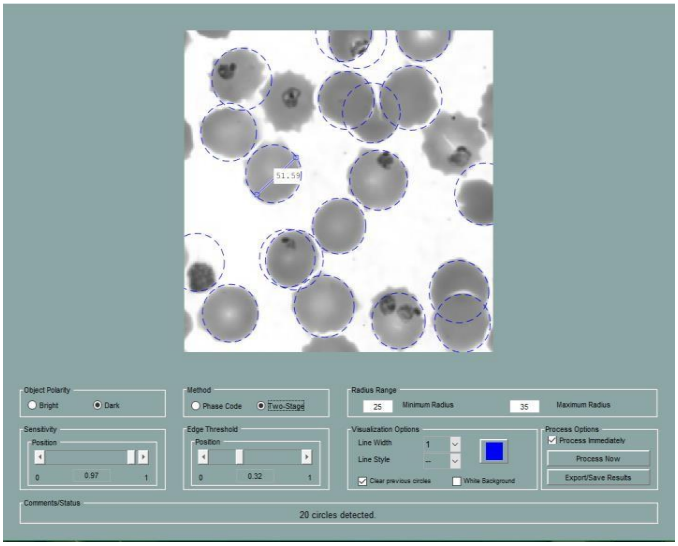
After applying suppressed minima on a grayscale image if we apply watershed we get a better segmentation of cells using water segmentation.



Better segmentation of wartershed.

2.3 Finding number of RBCs cells in a image

To find the RBC cells in a image we need to start with how questioning how many circles are there in a cells. So by finding out how many circles are there in a image we can determine the number of cells on a image. There are a lot of technique to find a circle like imfindcircles-Find circles using circular Hough transform inbuilt function. But in our project we are using an app called circleFinder.



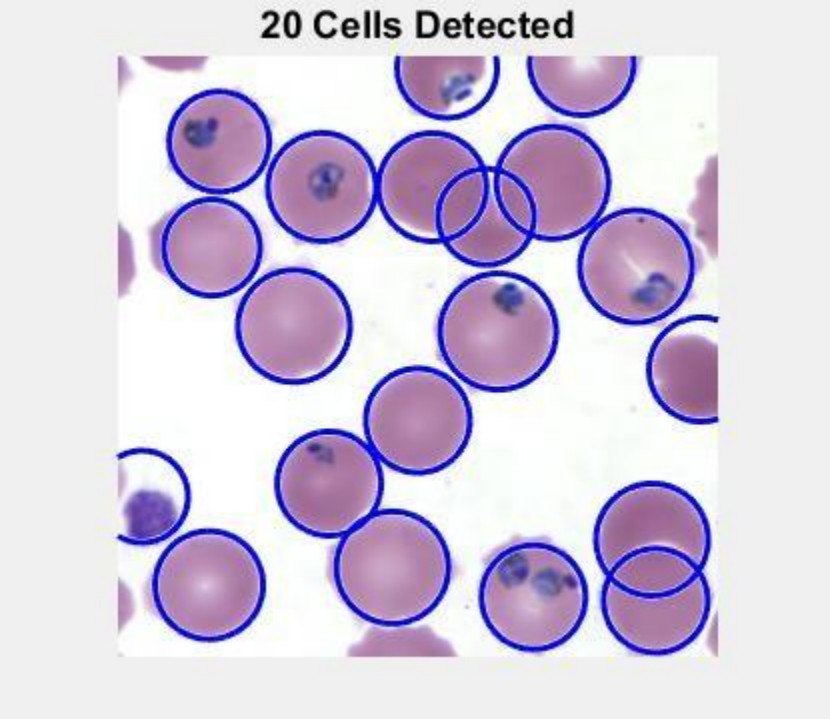
Which can be setup as

- Object polarity which in this case is a dark i.e. dark cells on bright background.
- Radius range by measuring
- Sensitivity and method to detect a cells on a image as shown above.

After exporting a results from a circleFinder app from single image you use the same results to find the cells on all the images.
The results generated by cirlceFinder app :

```
detectCircles = @(x) imfindcircles(x,[20 35], ...
     'Sensitivity',0.89, ...
     'EdgeThreshold',0.04, ...
     'Method','TwoStage', ...
     'ObjectPolarity','Dark');
[centers, radii, metric] = detectCircles(grayscale);
```

When we use the exported value from cirlceFinder app in our algorithm to find the cells in a image. We get



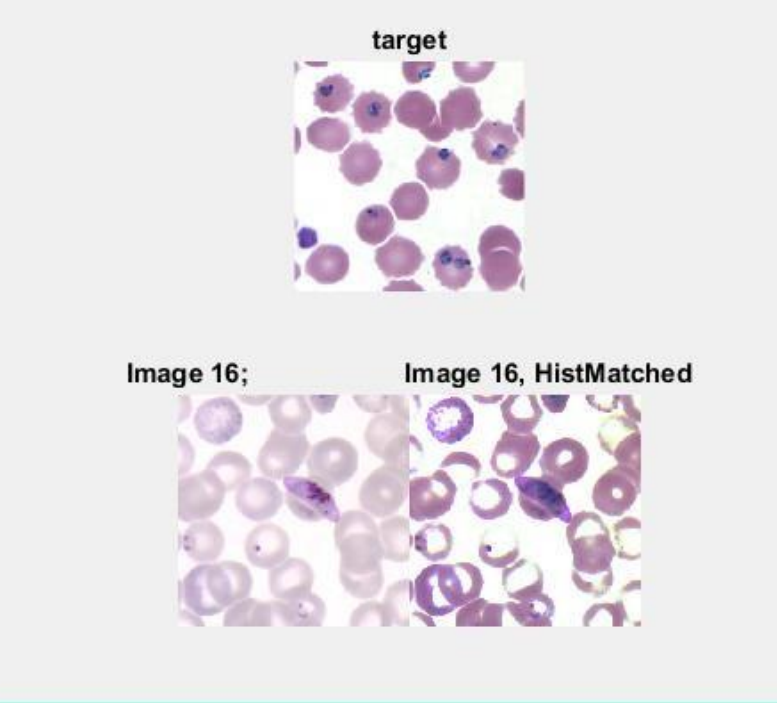
Cells detection.

2.4 Intensity adjustment and Identification of infected malarial cells

Before identification of infected cells on a image, we need to adjust the intensity of a image because there will be heterogeneous data that can have varying in intensity. Adjusting a image intensity helps in identifying a cells very fast and effective because lots of infected images will have darker regions which has high threshold value.

Adjusting a intensity is done by inbuilt function called imhistmatch-Adjust image to match its histogram to that of another image.

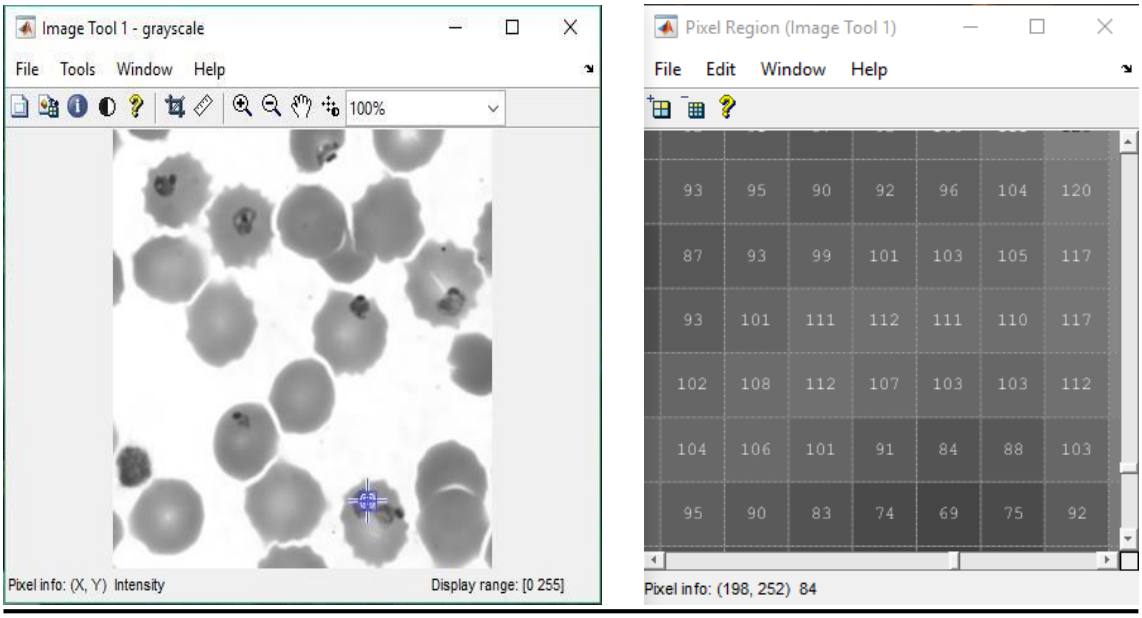
b = imhistmatch(A, REF) transforms the input grayscale or TrueColor image A so that the histogram of the output image B approximately matches the histogram of the reference image REF, when the same number of bins are used for both histograms. For TrueColor images, each color channel of A is matched independently to the corresponding color channel of REF.



Intensity adjustment

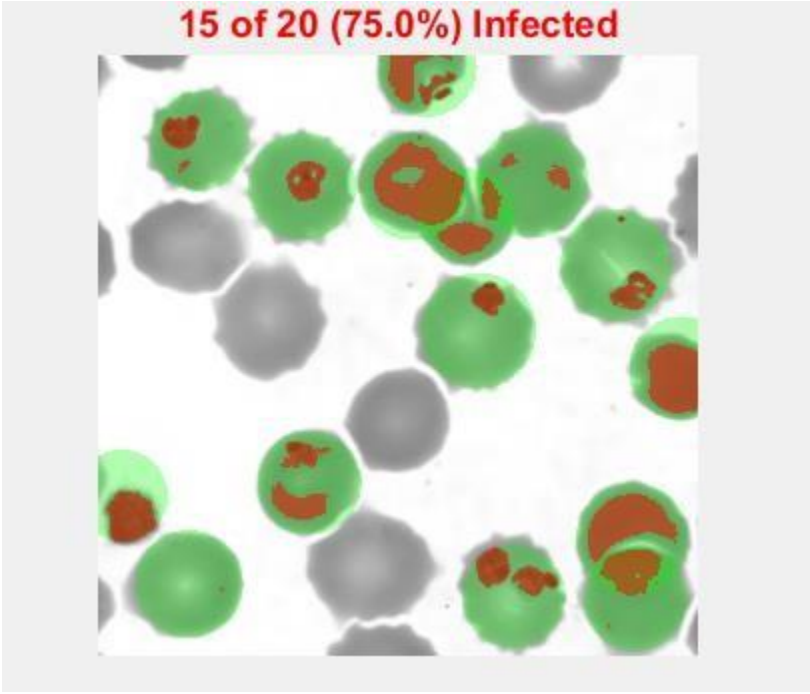
By adjusting intensity we can able to find the threshold value of infected cells by finding out the pixel value of the infected pixel cells. This is done by matlab app called imtool which helps in identifying each pixel value in the image.

Looking at the fig u can tell that the infected cells have higher pixel value and other region in which we have no interest has lower pixel value from that we decide the threshold for identification of infected cells in a image.



Threshold for infection using imtool

After applying every step explained as above we can able to identify a infected cell in a image using this algorithm.



Identification of infected cells

ACCURACY OF ALGORITHMS

In many areas of information science, finding predictive relationships from data is a very important task. Initial discovery of relationships is usually done with a training set while a test set and validation set are used for evaluating whether the discovered relationships hold. More formally, a training set is a set of data used to discover potentially predictive relationships. A test set is a set of data used to assess the strength and utility of a predictive relationship. Test and training sets are used in intelligent systems, machine learning, genetic programming and statistics "ground truth" refers to the accuracy of the training set's classification. By classifying this data sets we can able determine the Accuracy of classification applied on a algorithm.

Accuracy in morphological operation

Accuracy in morphological operation is obtained by applying k-nearest neighbour classification on train set and test set of sample.

Class = knnclassify(Sample, Training, Group) classifies the rows of the data matrix Sample into groups, based on the grouping of the rows of Training. Sample and Training must be matrices with the same number of columns. Group is a vector whose distinct values define the grouping of the rows in Training. Each row of Training belongs to the group whose value is the corresponding entry of Group. knnclassify assigns each row of Sample to the group for the closest row of Training. Group can be a numeric vector, a character vector, or a cell array of character vectors. Training and Group must have the same number of rows. knnclassify treats NaNs or empty character vectors in Group as missing values, and ignores the corresponding rows of Training. Class indicates which group each row of Sample has been assigned to, and is of the same type as Group.

```
ObtainedLables=knnclassify(TestFM,TrainFM,GT_Train);

temp1=length(find((ObtainedLables-GT_Test)==0));

Accuracy=(temp1/length(GT_Test))*100;
```

The obtained results of the morphological operation u sing knnclassifer is

```
Accuracy = 57.142857

Time taken to classify 28 samples is = 6.691605e-02
```

Accuracy in colour based discrimination

To find out accuracy in colour based discrimination, we use of Machine learning. Machine learning is a type of artificial intelligence (AI) that provides computers with the ability to learn without being explicitly programmed. Machine learning focuses on the development of computer programs that can change when exposed to new data.

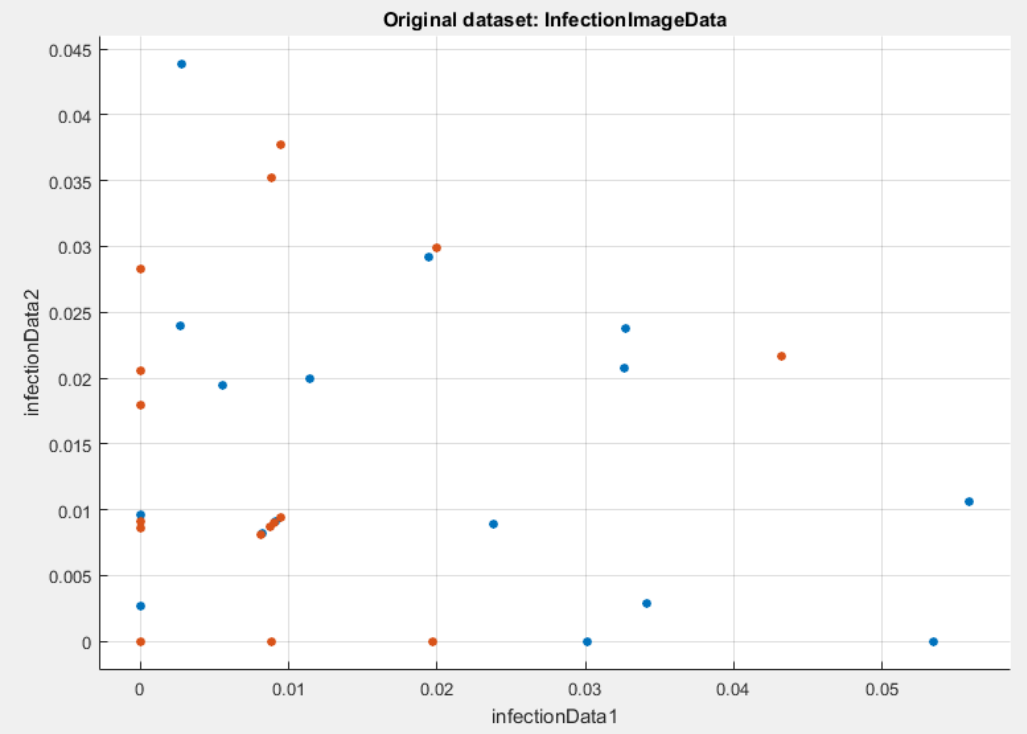
In machine learning and statistics, classification is the problem of identifying to which of a set of categories (sub-populations) a new observation belongs, on the basis of a training set of data containing observations (or instances) whose category membership is known.

In machine learning, support vector machines are supervised learning models with associated learning algorithms that analyse data used for classification and regression analysis. Given a set of training examples, each marked as belonging to one or the other of two categories, an SVM training algorithm builds a model that assigns new examples to one category or the other, making it a non-probabilistic binary linear classifier (although methods such as Platt scaling exist to use SVM in a probabilistic classification setting). An SVM model is a representation of the examples as points in space, mapped so that the examples of the separate categories are divided by a clear gap that is as wide as possible. New examples are then mapped into that same space and predicted to belong to a category based on which side of the gap they fall.

First we take trained data set and extract a features from which we can able to find a infection i.e. extraction of infected regions to check against test data set. This feature of extraction is called bag of feature.

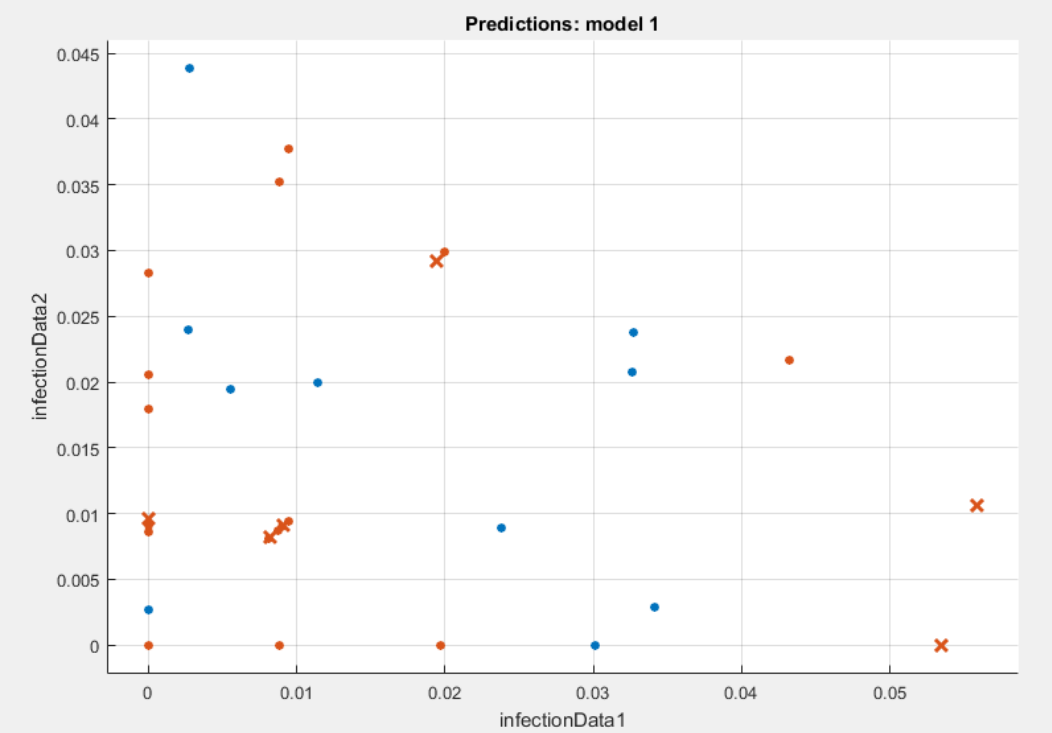
After specifying train set of images to our algorithm which contains both clean cells and infected cells, we can call classificationLearner app from which we can apply a classification technique like SVM and train the data set to obtain the accuracy of that classification.

Task Analysis Graph



Distribution of clean and infected images in x-y plane.

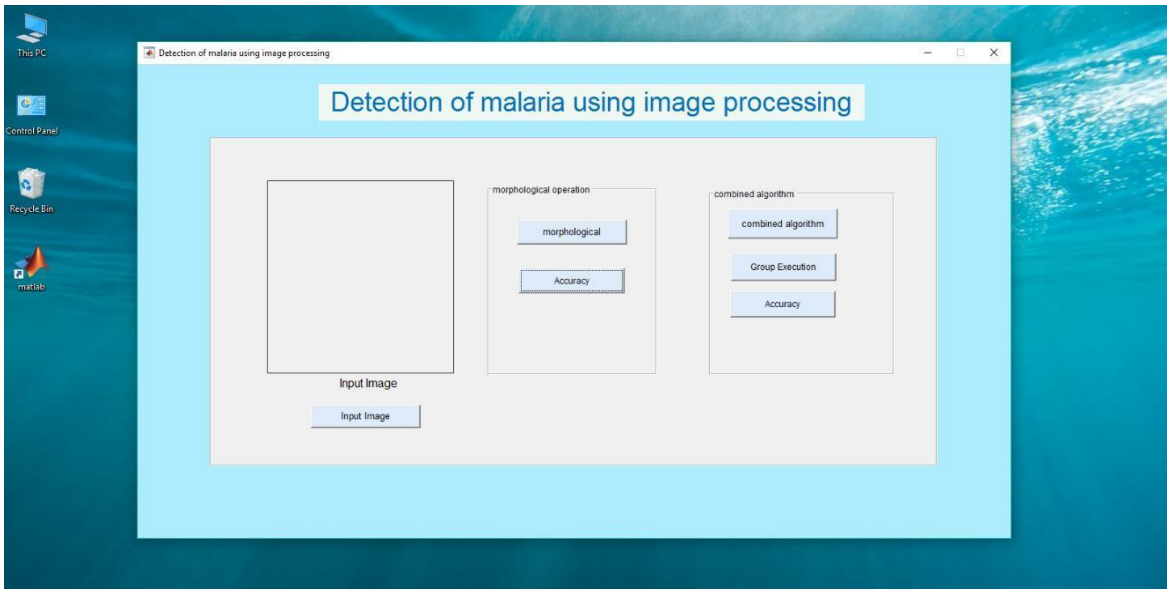
Blue dots in the plane tells about the infected cells and orange dots tells about the cleacells from original data set



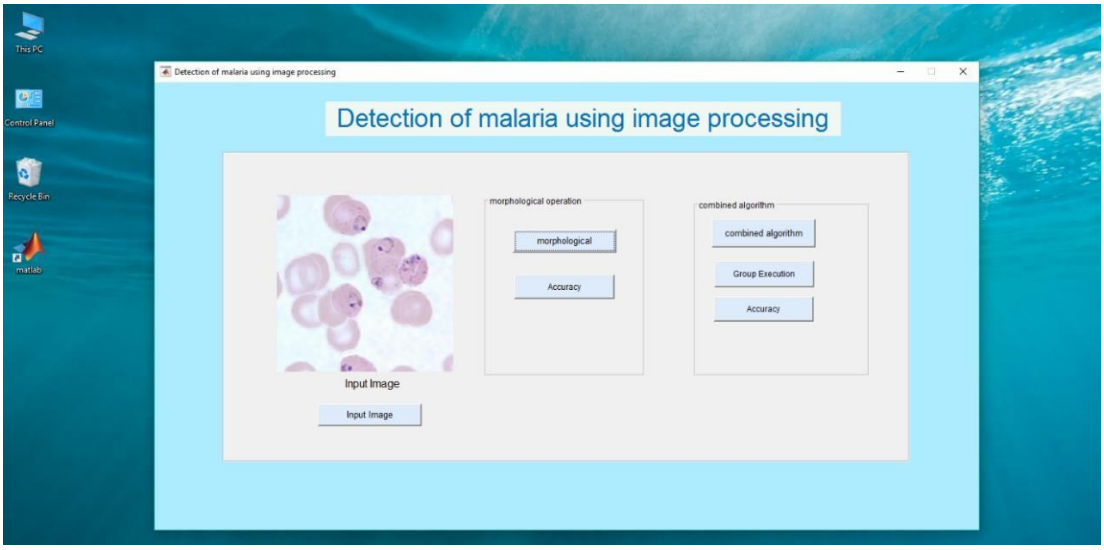
Distribution after applying SVM

Output of Morphological Operation

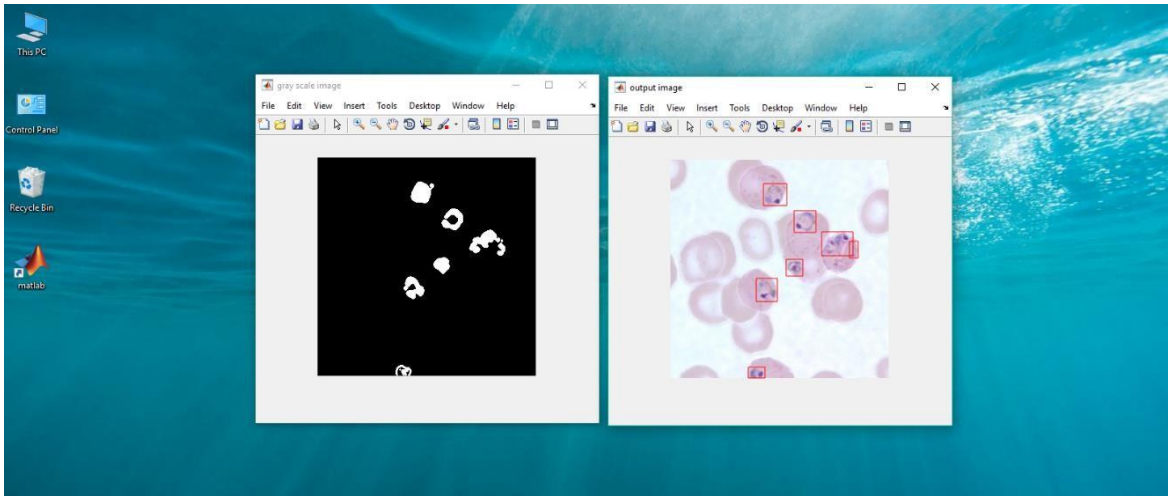
- Home Page



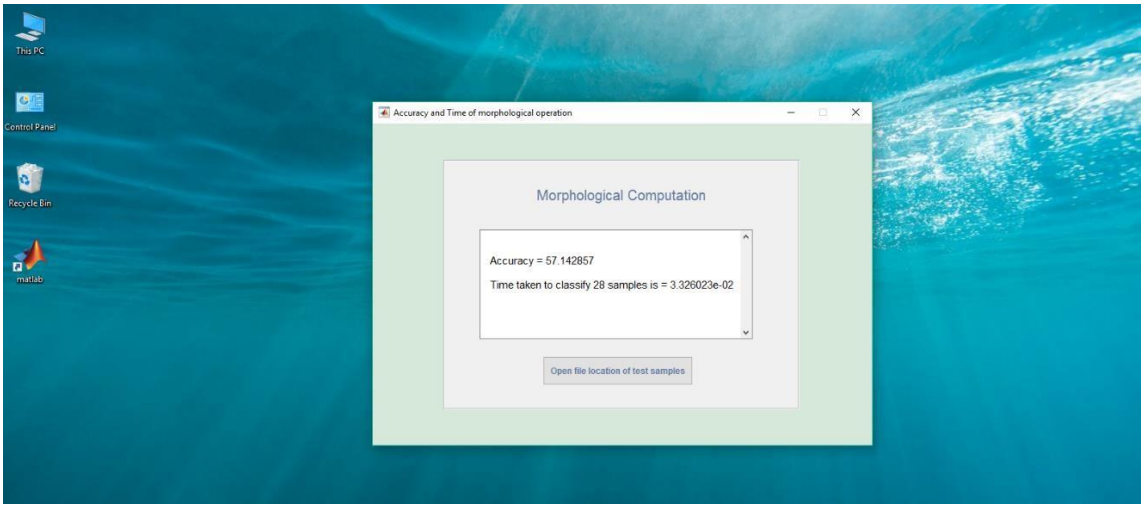
- Input Image Section



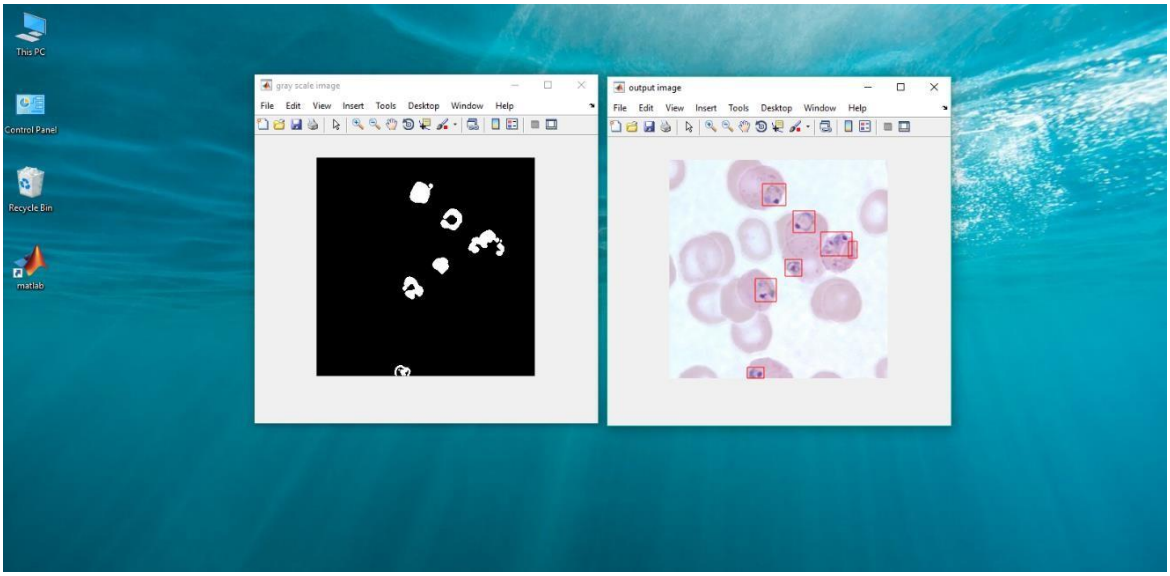
- Morphological Operation



- Accuracy of Morphological Operation



Output of Color Based Discrimination



color based algorithm

- Group Execution

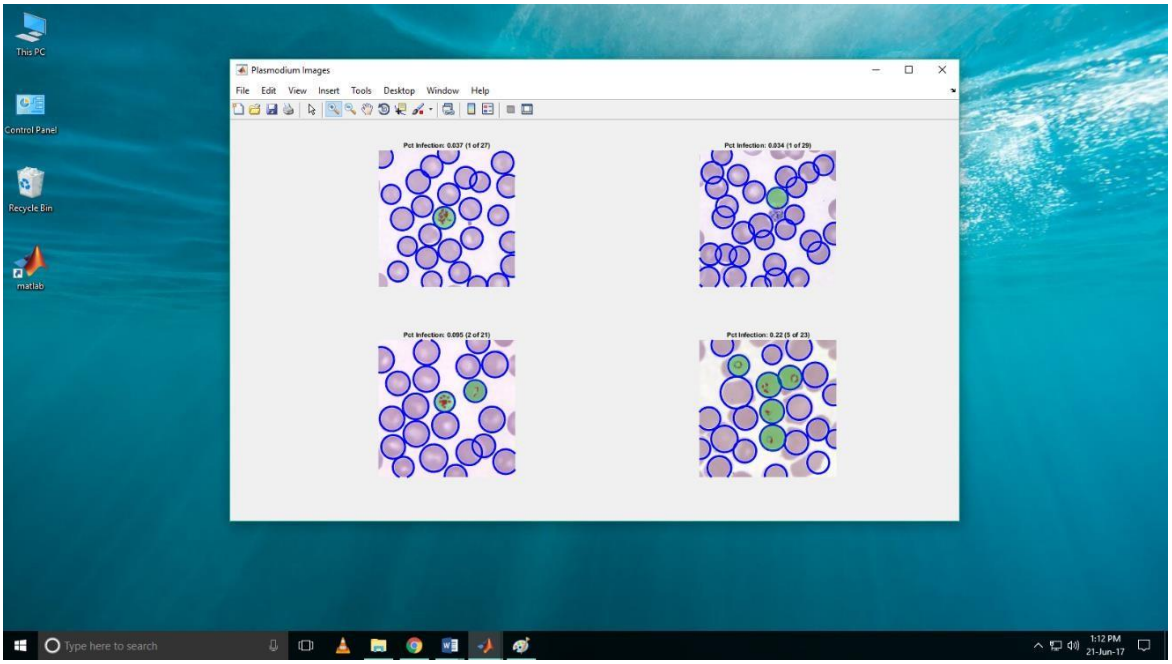
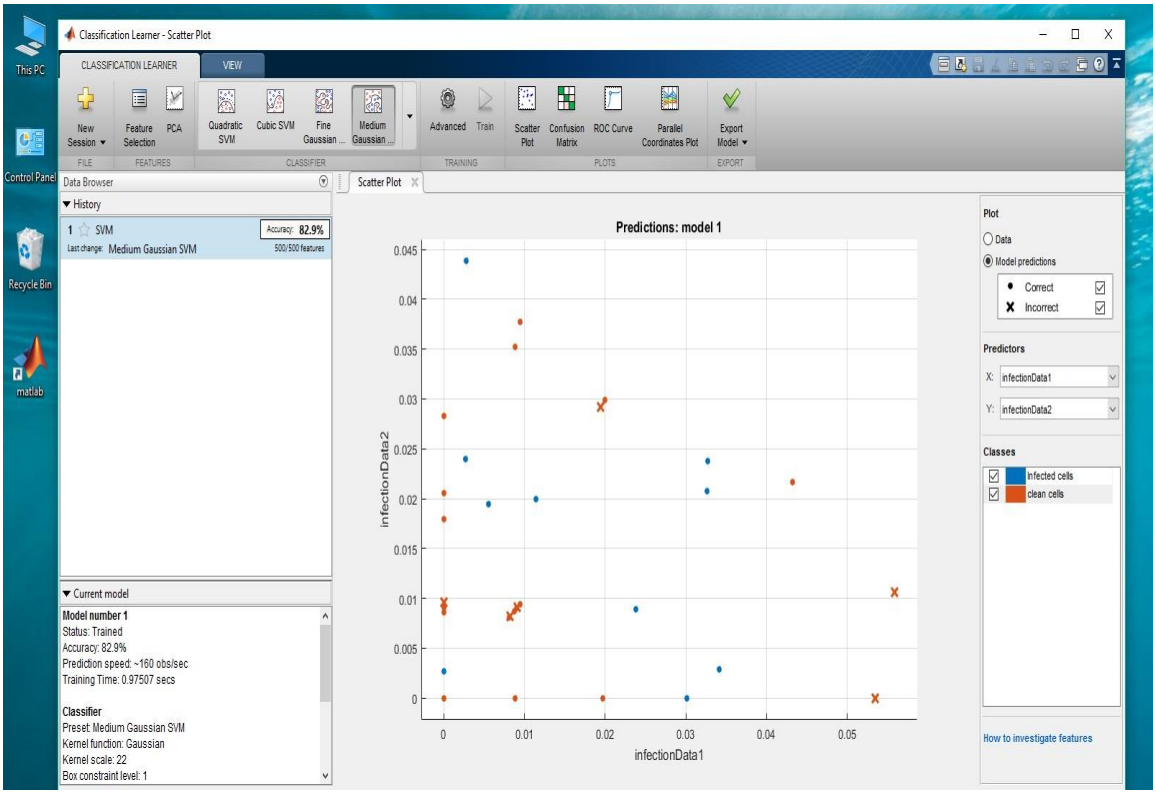


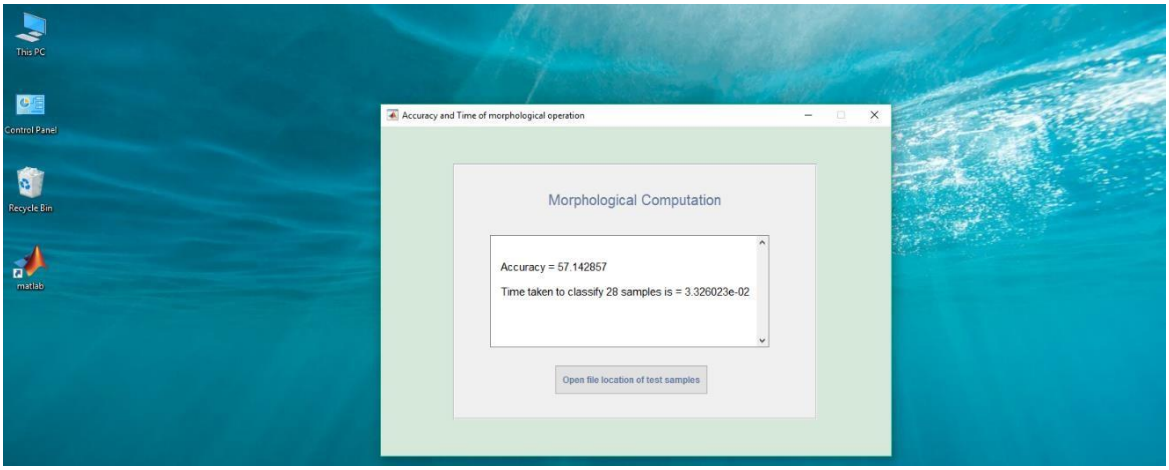
Fig: multiple image execution

- Accuracy of colour based algorithm

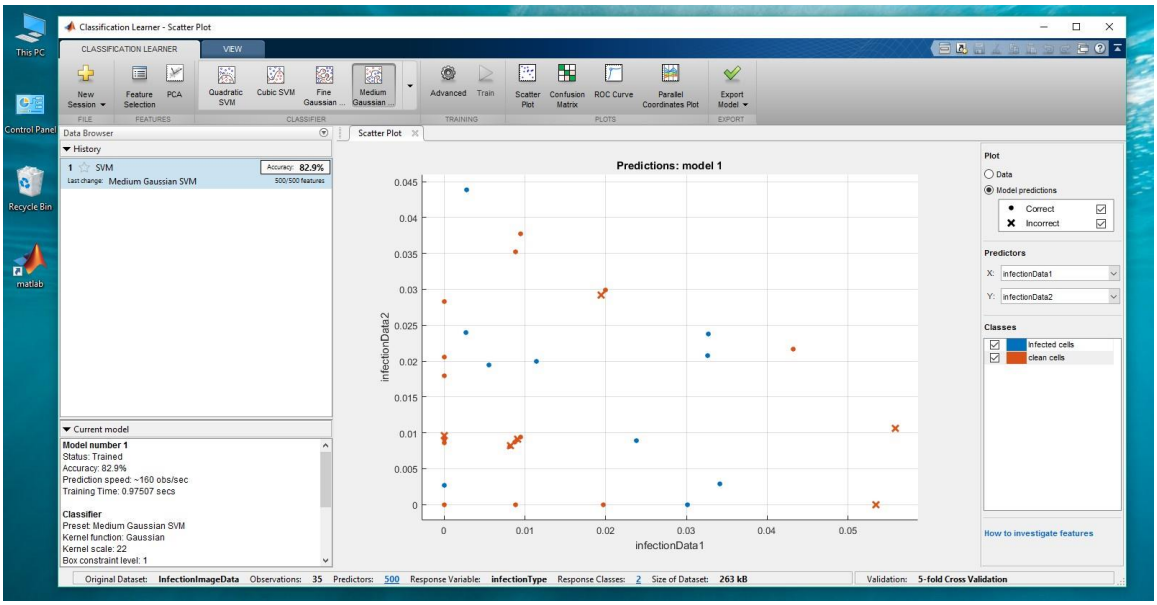


Comparative Result and Graph Analysis

- Accuracy of morphological Operation



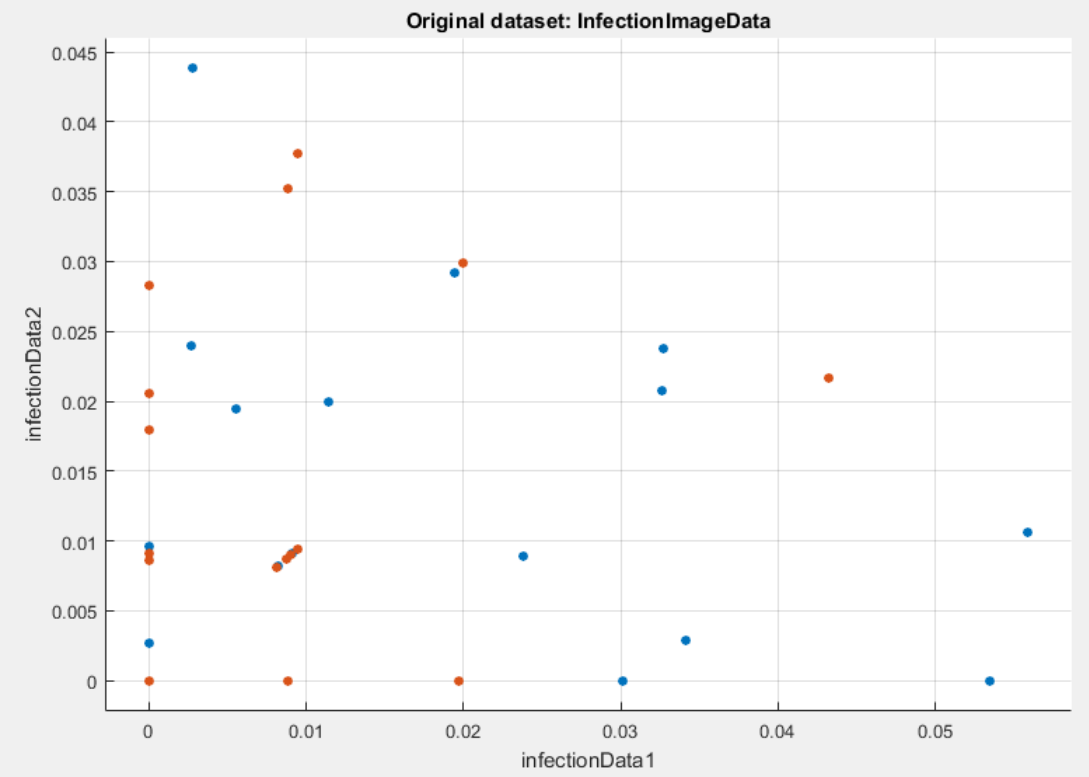
- Accuracy of Color based Algorithm



Sl. No.	Method	Accuracy(in percentage)
1	Morphological operation	**57.14**
2	Colour based discrimination	**82.9**

As we can see the accuracy found in morphological operation i.e., 57.14 is significantly lower than the accuracy of colour based discrimination 82.9

Blue dots in the plane tells about the infected cells and orange dots tells about the clean cells from original data set.



Conclusion and Future Scopes

The detection of malaria parasites is done by pathologists manually using microscopes. so, the chances of false detection due to human error are high, which in turn can result into fatal condition. this seminar curbs the human error while detecting the presence of malaria parasites in the blood sample by using image processing and automation. we achieved this goal using image segmentation smoothing processing techniques to detect malaria parasites in images acquired from giemsa stained peripheral blood samples. the system in a robust manner so that it is unaffected by the exceptional conditions and achieved high percentages of sensitivity, specificity, positive prediction and negative prediction values. and the extraction of red blood cells achieves a reliable performance and the actual classification of infected cells.

Our project focuses on detection of malaria detected cells, future work can be carried out to predict different stages of infected cells, different kinds of diseases like H1N1, Dengue etc. using machine learning techniques.

References

Alexei and Baakdah, F. a. (2019). Malaria Detection by Third-Harmonic Generation Image Scanning Cytometry. Analytical chemistry, 2216--2223.

Bashir, A. a. (2017). Detection of malaria parasites using digital image processing. 2017 International Conference on Communication, Control, Computing and Electronics Engineering (ICCCCEE), (1--5) IEEE.

Breman, J. G. (2016). Conquering the intolerable burden of malaria: what's new, what's needed: a summary. The American journal of tropical medicine and hygiene, 1-15.

Chavan, S. N. (2016). Malaria disease identification and analysis using image processing. International Journal of Computing and Technology (IJCAT), 10.

Diaz, G. a. (2018). Infected cell identification in thin blood images based on color pixel classification: comparison and analysis. Iberoamerican Congress on Pattern Recognition, 812--821.

Edison, M. a. (2011). Digital analysis of changes by Plasmodium vivax malaria in erythrocytes. 11-15.

Frean, J. (2010). Microscopic determination of malaria parasite load: role of image analysis. Micrsocopy: Science, technology, Applications, and Eductaion, 862-866.

Halim, S. a. (2006). Estimating malaria parasitaemia from blood smear images. International Conference on Control, Automation, Robotics and Vision, 1--6 IEEE.

Kurer, D. A. (2018). Detection of malarial parasites in blood images. International Journal of Engineering Science and Innovative Technology (IJESIT), 3(3) pp: 651--656.

Kwenti, T. E.-A. (2017). dentification of the Plasmodium species in clinical samples from children residing in five epidemiological strata of malaria in Cameroon. Tropical medicine and health, 14.

Roy, K. a. (2018). Detection of malaria parasite in giemsa blood sample using image processing. International Journal of Computer Science and Information Technology, 55-65.

Somasekar, J. a. (2018). Computer vision for malaria parasite classification in erythrocytes. International Journal on Computer Science and Engineering, 3(6) pp: 2251--2256.

Suradkar, P. T. (2017). Detection of malarial parasite in blood using image processing. International Journal of engineering and innovative Technology (IJEIT), 2(10), pp: 124-126.

Suryawanshi, S. a. (2018). Comparative Study of Malaria Parasite Detection using Euclidean Distance Classifier & SVM. International Journal of Advanced Research in Computer Engineering \& Technology (IJARCET), 2(11) pp:2994—2997.

Varma, S. L. (2019). Detection of Malaria Parasite Based on Thick and Thin Blood Smear Images Using Local Binary Pattern. Computing, Communication and Signal Processing, 967--975