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# Microscopic Image Processing System for Detecting Dengue Affected Blood Samples

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**Abstract**

Dengue has been identified as one of the severe disease in many countries around the world. The virus has been diagnosed as rapidly spreading disease and the effects of Dengue shock syndrome stage may lead to patient death. The objective of this paper is to design Microscopic Imaging Analysis System (MIAS) for detecting dengue affected blood sample by identifying and counting the Platelets in the given microscopic blood image. Image preprocessing techniques like segmentation and morphological operations have been performed on the captured microscopic images. Our automated system is implemented and the performance is compared with traditional methods like manual interpretation and automation system. The performance is estimated on the parameters accuracy, sensitivity and precision. The comparison results show the better accuracy and faster identification than the traditional methods.

***Key terms****: Microscopic Image, Blood Smear, Platelets count, Dengue virus*

## 1. Introduction

Dengue is one of the deadly illnesses caused by mosquitoes and found during the rainy seasons in most of the states in India recently. Dengue affected patients have to identified at right time and to be isolated for intensive treatment so as to avoid the spreading of the disease to others. Moreover the severe impact of such disease could lead to death [7]. The disease can affect any person irrespective of gender and age levels. Moreover dengue patients have to be carefully identified at the initial stage itself and to be treated effectively for the complete cure. Platelets are the third type of blood cells that are found small in size compared with other two types, White blood cell and Red blood cell. The major function of the platelets is keeping the blood clotting at some reasonable level. Reduction in such platelets can affect the blood clotting process. The clinical laboratory tests confirmed that the reduction of platelet counts for a dengue affected patients normally below 15 thousand [8]. Hence it is observed that counting of platelets with human resources is consuming much time and leads to a necessity for automation for counting platelets using image processing techniques. In this paper, we have discussed about the Basics of the proposed framework which identifies and counts the platelets from the given microscopic image. We have also concentrated on traditional preprocessing on images through histogram equalization, segmentation techniques. Segmentation techniques are used for the effective recognition of WBC and platelets. Morphological operation helps in extracting the platelets from the other blood cells. Morphological filter are very much useful in smoothing the given input images.

## 2. Related Works

Ilyas et al., [1] had worked on the effective segmentation on image and their contribution was in basic morphological operations and blob processing. They extracted the blood cells from the image and attempted to count the number of platelets present on it. Khan etal., [2] have developed an effective method for segmentation based on Ostu threshold algorithm and produced the better accuracy compared with manual counting on blood cells. Dey et al., [3] developed a method for color based segmentation using L*a*b image and performed morphological operations to extract platelets. Burduk et al., [4] worked on the watershed algorithm with mean

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shift threshold value and they extracted the platelets. Support vector Machine (SVM) is used for the segmentation of platelets in a faster manner. Prabakaran et al., [5] have contributed for feature extraction from the images with the morphological operations and they focused their work on circular Hough technique (CHT). The CHT detected the blood cells by estimating based on the average radius of blood cells and their results shows better performance on the high resolution images. Alomari et al., [6] produced a new approach for detecting White Blood Cells (WBC) and Red Blood Cells (RBC). The method developed for circular detection using Hough transform was named as Randomized Circle Detection (RCD) and produced the results with high accuracy. The study on various literatures gave an overall insight about the image processing and analyzing techniques.

## 3. Microscopic Image Analysis System

### Microscopic Image Acquisition

Microscopic images of blood samples can be collected from lab blood smear. For instant analysis of the blood samples, the images can be captures with the support of high resolution mobile cameras also. The hardware integration with mobile phones for instant microscopic image acquisition system can also be designed and developed and that is neglected in this work as we are focusing on the image processing for designing an efficient algorithm for detecting the dengue affected blood. Therefore we are making use of data collection for analyzing our system performance.

The first of our proposed work is collecting microscopic image samples for our trial based performance estimation. Hence the images may contain noises and can be removed by using median filters. This filtering technique is more efficient in not only reducing the noises and also helpful in preserving the noises [15], [16]. This makes use of neighboring pixels median value replacement strategy for effective removal of noises.

### Image Preprocessing

**Green Plane Extraction:** RGB Color image is divided into three components with respect to red, green and blue in separate plane. From this process, green plane is extracted with clear features which help in separating the platelets as identical components. Using the extraction G=Image (: 2), the green plane is separated. The other two planes are not suitable for our image analysis. The green plane image produced will give clear feature extraction.

**Contrast Adjustment:** As the image is not showing the sharp edges between black and white contrasts, we make use of Contrast Limited Image Histogram Equalization (CLIHE) which will focus on the selected areas of the image. The focused area is names as tiles of the image, and each tile is upgraded with enhanced contrast using CA=CLIHE(G).

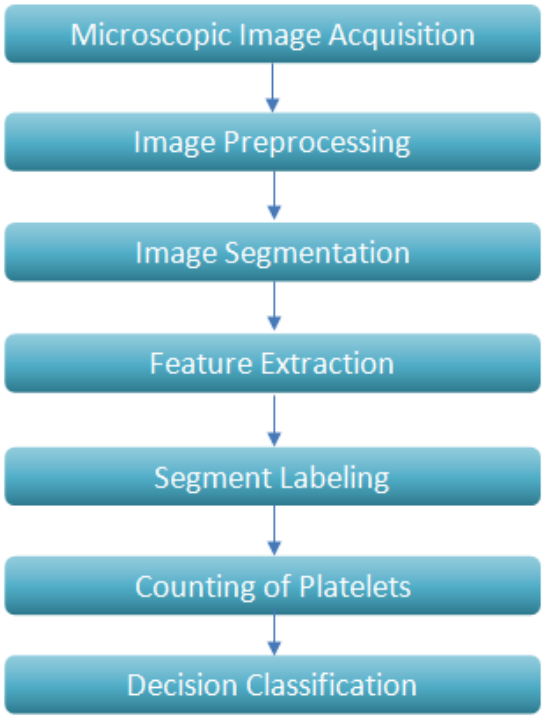


Figure 1: Research Methodology of MIAS

### Segmentation of Platelets

Image segmentation is performed using the simplest threshold method for segregating foreground and background of the given microscopic images. For the effective segmentation, the microscopic images are converted in to grey scale image and threshold technique can be used for creating binary representation of the same image [9]. This segmentation by threshold technique gives the extracted blood cell variations. The conversion of microscopic images into binary gray scale images by the simplest threshold classification. A high end value is added with every pixel of the image and the pixels having intensities above the threshold value is replaced with the black pixel and white pixel is assigned for the pixel position having intensity values less than the threshold. The pixel values having higher values above certain threshold can be taken as special pixels for feature extraction [10]. After the threshold segmentation, the input image *G(i,j)*is converted into binary image *H(i,j)* as:

$$H(i,j) = \begin{cases} 1, if\ Tlower \leq G(i,j) < Tupper \\ 0, if\ Otherwise \end{cases}$$

Segmentation removes the unwanted components from the blood samples and isolates the important components which are platelets. Clustering separates set of components from other regions based on the common characteristics [11]. The efficient clustering takes minimum distance between the data point and the corresponding clusters centroids.

$$Euclidian\ Distance = \sqrt{\sum_{i=1}^{n} (\mathrm{xi} - \mathrm{yi})^2}$$

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The classified pixels represents foreground of the image, whereas the remaining pixels are considered as the background of the image.

**Feature Extraction**

Feature extraction is carried out for finding the local features in the given image. Internal representations are created from the original image for ensuring the scale variations [12]. For the accuracy of our estimation, we prefer to choose scale space generation algorithm. After creating the scale space of the image, we are gradually making blur on the by step by step shrinking the image and by using the final blur images we are creating another set of images which are called "Difference of Gaussians (DoG). This DoG images are very much helpful in extracting the points of interest from the image space. Finding key points on images consists of two parts: coarsely locate the pixel maxima and minima. Then process through each pixel and check all the neighboring pixels, if the chosen intensity value is higher than the neighbors then the pixel is labeled as maxima, otherwise name it as minima.

**Image Labeling**

After the segmentation process, the image is divided into various components with respect to the segmented regions. The contrast adjusted image with black and white pixels is inverted to represent the background black cells to be converted in to inverted white cells. Flood fill morphological operation is performed on the produced binary image. This changes the connected background components into foreground pixels. Small gaps and little openings in the image are isolated using the identified fill hole function. In this process the identified little gaps are extracted from other blood cells, which results in isolating the affected platelets from the other blood cells.
The connected regions in the binary image can be named, refers to Image Labeling. Labeling groups the pixels into connected components based on the neighbor pixel intensity values. The connected pixels somehow have the similarity association with their neighbor pixels. The connected components are identified as the instances of platelets.

**Counting of Platelets**

Manual counting out platelets is a tiresome work which takes some human intervention and also consumes more time. The complexity grows with respect to the increasing size of the microscopic images [13]. This leads to the necessity for the automatic identification and counting of platelets in quicker and accurate way. Platelet is an important component to be identified in blood smear for determining the presence of possible factors that causes the dengue fever. A sequence of steps is carried out on the segmented image to count the platelets present. Our proposed algorithm is considering 8-neighborhood connectivity at the best case images and 4-neighborhood connectivity for the worst case in order to count the platelets. The identified count of platelets is multiplied with the calibration factor, usually by 20k for the microscopic images obtained through the 1000X magnification. The multiplication factor is taken as per the image acquisition methods in order to find the accurate blood cell counts from the given blood smear.

**Decision Classification**

Decision classification for dengue fever identification is very difficult as there are many ailments been an indicative factor. The major parameter for detecting dengue affected blood is identification of decreased platelet counts. Hence we need to count the ratio of affected blood cells with respect to the normal blood red cells. The decrease in the white blood cell count is an alarming factor for dengue symptoms. For better identification of dengue affected blood sample, we need to correlate with other data related with the symptoms of dengue. If-else vector based decision support system is used for combining both the decreased platelets count and the other symptoms observed on the patients [14]. Normally the symptoms related to dengue infection are abdominal pain, rash effect, severe headache, high fever, fatigue and continuous cough. The Decision Support System (DSS) asks for the impacts that the patients suffers as a sequence of binary questions. The if-else ladder is systematically devised so as to get the prompt classification tree which helps in making a final decision.

## 4. Results

We have analyzed the performance of our system with different kind of blood smear collected from various levels of dengue patients. Here we presented two different stages of dengue blood smear for our discussion. In figure 2, the analysis on a blood sample collected from the normal person is presented. Platelets in the blood smear are visible (image a). As this blood belongs to a normal healthy person, this shows 7 platelets count (image f). Platelets are usually 7 to 10 in count for a healthy person as per the sample size taken for our experiment.

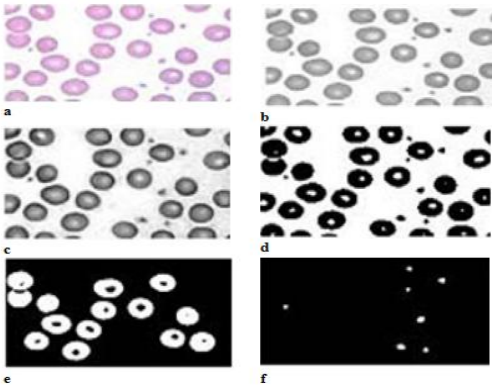


Figure 2: a. Original image b. Green plane c. Contrast adjustment d. Binary image e. except platelets f. 7--Platelet count

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For the second analysis, the blood smear taken from the dengue affected patient is considered. In this blood smear (figure 3), it is identified only 2 platelets in the same size of the microscopic image of the blood. We have performed our analysis on different samples and we end up with a result of different counts of platelets for different patients. It is observed that the platelet count will be in a range from 7 to 13 for those who are healthy and found not affected by dengue. For dengue affected patients the blood smear can contain fewer amounts of platelets ranging from 1 to 5 which significantly indicate the level of disease in the scale of severe dengue, highly affected, slightly affected, moderate symptom for dengue fever.

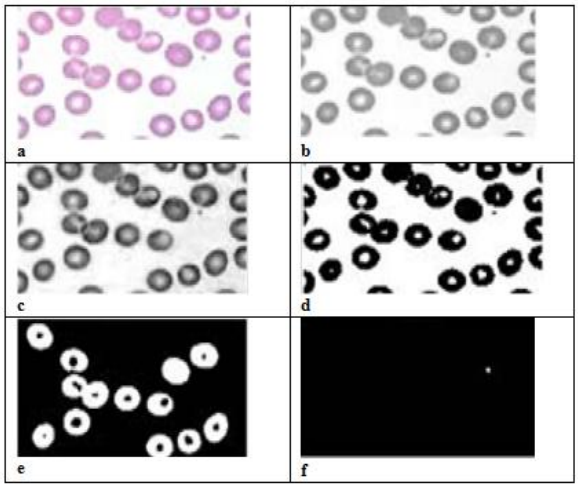


Figure 3: a. Original image b. Green plane c. Contrast adjustment d. Binary image e. except platelets f. 1--Platelet count

Normally the effectiveness of segmentation algorithms are evaluated with the sample images by the following measures: Probabilistic Rand Index (PRI), Variation of Information (VOI), and Global Consistency Error (GCE). Feature extraction procedures can be analyzed with respect to Error rate and Accuracy. The performance of the MIAS was evaluated against the parameters, Accuracy, Sensitivity and Precision. Accuracy is the significant measure to analyze the performance of most of the image retrieval systems. It can be defined as the ratio between the successful predictions of images to the total number of samples processed.

*Accuracy = 100 – Error*

Where

*Error = (100/40)* (Confusion_Matrix (1,2) + Confusion Matrix(2,1))*

In Confusion Matrix, the positions (1,1) and (2,2) show the original classification of platelet features while the positions (1,2) and (2,1) wrongly identified feature of the given blood smear.

Sensitivity analysis of the system describes the uncertainty in the obtained results, and classifies them with respect to different sources uncertainty of images. Uncertainty reduction needs to be focused in performance analysis in order to improve the robustness of the designed system.

Precision is the successful prediction of the count with respect to the original count, whereas specificity describes the true negative proportions that are identified correctly. Hence we have chosen only the precision parameter for our system analysis. Higher precision value refers to the low negative predictions. We obtained 0.78 precision rate which is better value compared with the existing approaches.

*Precision= True Prediction/ (True_Prediction+False_Prediction*)

Table 1: Comparison of MIAS with Traditional System

| Performance Analysis | Traditional Approaches | Proposed MIAS |
|---|---|---|
| **Accuracy** | **66** | **84** |
| **Sensitivity** | **71.3** | **68** |
| **Precision** | **64** | **78** |

## 5. Conclusion

The paper is aligned in the order starting from the introduction about the field of study, literature survey over recent researches, module wise description of our proposed system, experimental analysis and finally concluding with the results obtained. Our system includes various stages of image processing techniques and morphological operations for obtaining the better image enhancements which leads to the accurate identification of platelets in the microscopic blood smear. This automation of counting platelets reduces the manpower requirements and produces accurate results in fewer seconds. The limitation we found during our experiments was with the blood cells having high impact of overlapping. This could be an open issue for all the researchers in this field and we take this forward to give better results with such kind of image samples also in future.

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