

# Automated RBCs Segmentation & Counting using SCILAB

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**Abstract**—The deficiency of red blood cells (RBC), that constitutes 99 percent of blood cells and specialized as oxygen carrier, causes various blood disorders. The estimation and counting of RBCs plays a crucial role in medical diagnosis and pathological study. The main problem arises when massive amounts of blood samples are required to be processed by the haematologist. The time and skill required for the task limits the speed and accuracy with which the blood sample can be processed. This project aims to provide a fast and cost-effective solution to diagnose and count the RBCs. It is user friendly software based on SCILAB, which is free and open source software, helps us to reduce the cost of the system. The objective of this system is to segment and count the number of red blood cells present in the blood smear sample image. The process is initiated by image acquisition and image enhancement process, segmentation, counting and displaying the RBCs count.

**Keywords**—Red blood cells; SCILAB; RBCs count; Image Processing; Biomedical.

## I. INTRODUCTION

Here in this research based project we proposed a software based solution related health industry which will assist the medical laboratory technician (MLT) to detect and find a blood cell count and produce an accurate cell count report. This would be very helpful to a physician in identifying the cause of his patient's diseases. To count the blood cells in a clinical laboratory different two methods and techniques are used. One is the old conventional method of cell counting under the microscope and the other is to produce cell counting report by latest but very expensive haematology analyzer. But both these methods have its own different drawbacks and limitations.

### A. Limitations with Existing Methods

The main problem with the method of counting manually under the microscope is accuracy, this method needs a real experienced laboratory technician who is trained enough to produce an accurate cell counting report, and even if the laboratory technician is well trained and experienced still we one can't neglect the chance of error in the report due to error caused by apparatus, personal errors, statistical errors etc. While on the other hand latest haematology analyzer somehow error free and fast but it is widely unavailable and very expensive machine, and the remote rural areas are resource less to provide it in hospital laboratory. So as a result of the problem this research based project proposed a new method of cell counting which is easy to use, don't need fully experienced men to handle, much more accurate than the manually counting method and is very economical way of cell counting.

## II. METHODOLOGY

The functioning in the proposed method is totally based on computer vision technologies via image processing techniques. The input images that are taken through a microscope camera are similar to what the laboratory technician observes under the microscope. Digital image processing was extensively used in this work. It is the key performance index to establish the ability of the proposed method.

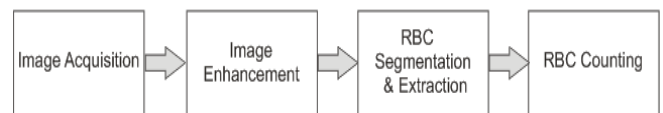


Fig 1: A proposed RBCs counting procedure

### A. Image Acquisition

In image acquisition, we used sample images from an online medical library as an input image. These images can be acquired by the user through a simple user interface, from their computers. As these images contain noise and are not fit for direct processing they need to be enhanced for further analysis.

### B. Image Preprocessing

This is a preprocess step of an image sequence before feeding into the segmentation process. The image is first converted to its corresponding grey level images. Median filtering is used to remove noise which is added at the time of capturing the microscopic blood images. This noise can be the dust particles that are present on the blood slide while preparing the slides.

### C. Histogram equalization

When the original coloured (RGB) image of blood is converted into grayscale intensity values of pixels, the gray level histogram can represent the distribution of pixel intensities of that image. We can easily see the frequencies of all intensity, and on bases of gray level values in the histogram the image can be analyzed. The histogram study of gray level intensities is important to make a line between blood cells and the background. Between the two peaks of the histogram the threshold value lies somewhere. The obtained histogram is divided into three different sections one section for RBC, the other is for WBC in the blood and third is the background of these blood cells indicated by (a), (b) and (c)

respectively. And so the threshold value lies between the area (a) and (b) that is between the peaks of WBC and the RBC. To segment the region of interest this threshold value is used. Basically the method of converting gray scale image into the easily handled binary image is called thresholding of the image. The advantage of this thresholding is to separate the blood cells from the back ground.

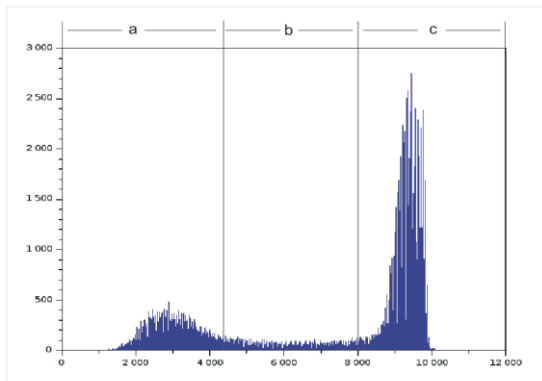


Fig 2: Histogram of an image

**D. Conversion to Binary Image**

Binary images are those images having only two pixel intensity values, zero (pure black) and 1 (white). By thresholding the unwanted area in color images or images with gray level pixel intensity binary images can be formed. In this proposed method development with the help of threshold value obtained from the histogram peaks the binary images is formed to separate white and red blood cells. If the result is satisfied the pre-processing phase completes here, but if more filtration is needed the image has to pass from all above processes again until we obtained our required image.

**E. Morphological Operations**

Mathematical morphology will be used to segment RBC based on elimination WBC appearance. Morphological image processing is based on a strong mathematical concept which been used to change the size, shape, structure and connectivity of objects in the image. It involves binary erosion, dilation, opening, closing and reconstruction. The technique also extended the use in greyscale image. Erosion plays the role to shrinks and thins objects in image while dilation used to grows and thickens objects in image. Next, morphological opening is the combination process of erosion and continued by dilation while morphological closing is using the concept of dilation and continued by erosion. In other words, the functions of morphological opening are to removes, break and diminished the connection or objects which not contain the structure elements. In contrary, morphological closing functions to join, fill and build connection and objects in the image. Using the closing image transformation with defined SE (Structure Element) unwanted edges, typically generated, are removed.

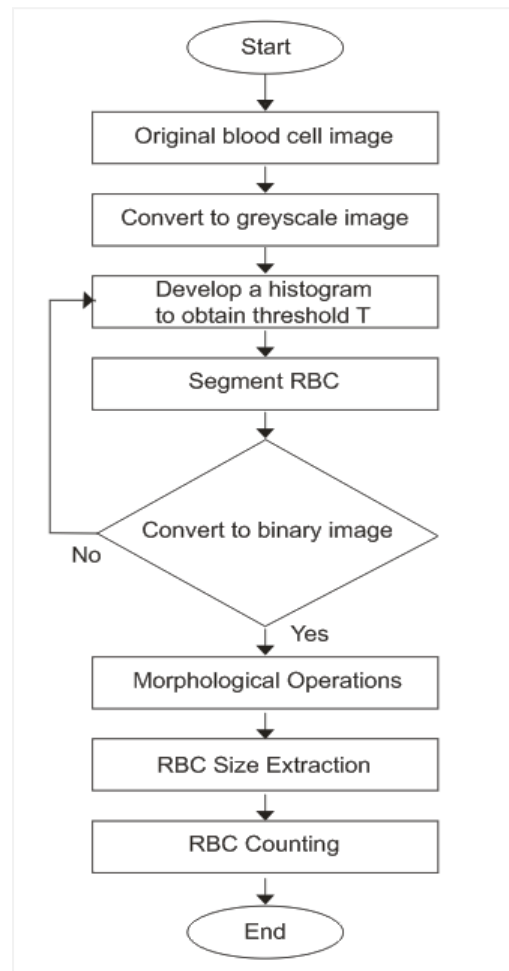


Fig 3: Flow chart of software program

**F. RBC Extraction and Counting**

A normal blood cell is primarily one of two major particles: a RBC with a normal Probability Distribution Function (PDF) around 6.08.5 m or a WBC (7-18 m) which includes a nucleus and cytoplasm is about 1-3 times bigger than normal and mature RBCs. Moreover, WBCs are classified into five main shape groups with varying degrees of non-convexity. We use size characteristics as an effective factor to distinguish between the two main types of RBC and WBC cells. After morphological closing on the image we have an image with some broken edges and filled cells. We remove the broken edges from the image so that we are left with the filled cells only. Now the actual size extraction algorithm starts. We find the area of all the regions that are filled and then find the statistical parameters like mean, median, standard deviation etc. Since most of the regions are single cells it is expected that the mean value of the regions will give an idea of size of single cells in an image. Using this concept we have made three ranges,

- Single Cell Size = (Mean Standard Deviation) to (Mean + Standard Deviation)
- Double Cell size = (Mean + Standard Deviation +1) to (2\*Mean + Standard Deviation)
- Triple Cell Size = (2\*Mean + Standard Deviation+1) to (3\*Mean + Standard Deviation)

- We then find out number of regions falling in each range  
 From the above we can count easily by
- No. of Single cells = No of regions in single cell image x 1
  - No. of Double cells = No of regions in double cell image x 2
  - No. of Triple cells = No of regions in triple cell image x 3
  - Total Count = No. of Single cells + No. of Double cells + No. of Triple cells.

Using the above method some cells whose edge is not completely detected are left out.

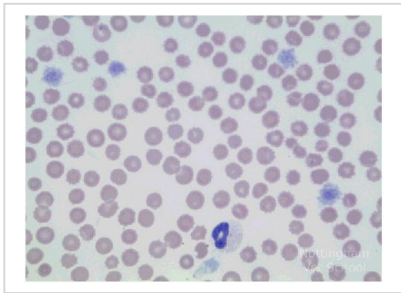


Fig 4: Input Image

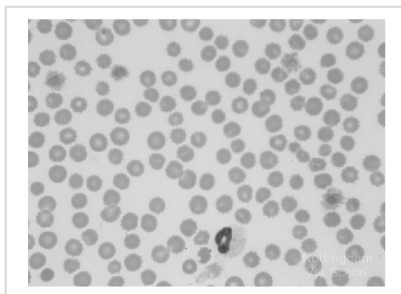


Fig 5: RGB to gray conversion

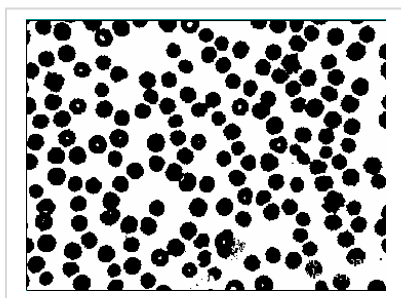


Fig 6: Binary image after grey thresholding

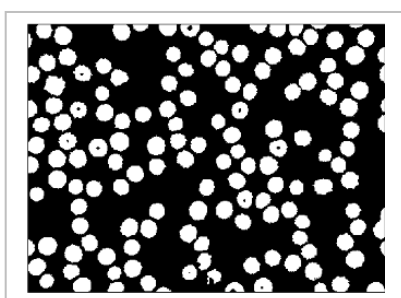


Fig 7: RBC segmented image

### III. RESULTS & DISCUSSIONS

The results are presented and the graphical user interface (GUI) is developed to provide user friendly for analysis. This GUI was developed using GUI builder which is one of the toolbox that have been used in the SCILAB.

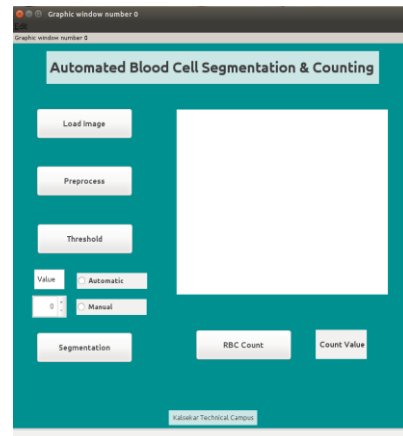


Fig 8: Final GUI

Figure shows the GUI for estimating the number of red blood cells in blood smear image. An important part in this estimating process is radius of red blood cells. Each image has different radius that need to determine before proceed to the estimating process. Table 1 presents the radius parameter for each 5 set of images collected from different sources.

Image	Min Radius	Max Radius
1	36	40
2	32	40
3	26	34
4	18	24
5	11	20

Table 1: Training data

Image	Manual Counting	Computer Counting
1	20	19
2	60	59
3	34	35
4	102	95
5	60	54

Table 2: Accuracy of 5 image samples

From this image samples, the average computational time by this system is 5 seconds per sample. Table 2 shows a comparison between manual counting and estimation by computer for 5 image samples. The average of accuracy of these 5 image samples is 95%.

The system used was run on an Intel Core 2 Duo CPU, with Ubuntu 14.04 operating system using SCILAB 5.5 for programming. The following toolboxes used with SCILAB for image processing and making GUI.

- Scilab Image Processing (SIP) Toolbox
- GUI Builder Toolbox

Complete system according to proposed method of blood cell counting has a microscopic camera over a microscope, and a PC as shown below in the fig. 9.



Fig 9: Complete system for blood cell counting

#### IV. CONCLUSIONS & FUTURE RECOMMENDATIONS

Proposed method of cell counting is fast, cost effective and accurate to produce blood cell report. It gives 94-96% accurate results for red blood cell count which an important test carried out to diagnose diseases. A count for the WBC can also be conducted after thorough research. The RBC count only helps in partial diagnosis of blood; the counting of white blood cells will improve it further. By improving our proposed algorithm we can also detect malaria parasite through computer vision technologies and techniques of image processing techniques. But this procedure would need a little advance microscope then the ordinary used in the clinical labs to achieve 100% accurate results.

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Sufiyan Ashfaque Siddique, completed BE in ECE from A. I. Kalsekar Technical Campus under Mumbai University. He is part of FOSSEE textbook program in IIT Bombay, in which he has contributed many codes written in Scilab and Python. His research interests are in software systems and algorithm, open source technologies, image processing, embedded system.



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