Red blood cell counting using fuzzy based segmentation

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Abstract- Counting of red blood cells (rbc) in blood cell images is very important to detect as well as to follow the process of treatment of many diseases like anaemia, leukaemia etc.The traditional method of manual counting under a microscope yields inaccurate results and put an intolerable amount of stress to medical laboratory technicians. Due to high vulnerability in human error and large time consumption, better and more effective image processing software is needed. As a solution to this problem, this paper proposes an image processing technique for counting the number of red blood cells using fuzzy based segmentation.

Keywords: RBC, Fuzzy Clustering, Image segmentation, Cell Count

I. INTRODUCTION

Blood is a connective tissue consisting of cells suspended in plasma. Blood's major functions are to transport various agents such as oxygen, carbon dioxide, nutrients, wastes and hormones. The most abundant small reddish cells are erythrocytes and called red blood cell. An erythrocyte is a discoid cell with a thick rim and a thin sunken center [1]. RBCs' two principal functions are to move oxygen from lung to tissues elsewhere and transport carbon dioxide from tissues to the lung.Red blood cells, also known as enthrocytes are the most important and numerous blood cells in human body. Main function of RBCs is to carrying oxygen and delivering it to the cells in the body [2]. They are minute disc shaped. They does not contain nucleus but a protein called hemoglobin. Both inner and outer layers of cell are made of protein that gives red color to blood. Hemoglobin actually does the work of grabbing and carries oxygen. Usually level of hemoglobin is tested in blood test. Decrease in level may cause severe diseases including anemia, blood loss, leukemia and malnutrition.

A life span of RBC is of around 120 days for normal individual [3]. A normal RBC count for an adult male is between $4.6x10^{12}$ and $6.2x10^{12}$ per liter of blood. Production of red blood cells takes place in the bone marrow from precursor stem cells. Typical red blood cell count (RBC) levels are:

- 4.2 to 5.4 million cells per micro liter for women
- 2.6 to 4.8 million cells per micro liter for children
- 4.5 to 6.2 million cells per micro liter of blood for men.

In diagnosis of several diseases, major step is automated detection and counting of red blood cells. In the conventional procedure, haematologist manually counts and classifies the cells with the help of a microscope. The task is to measure the red blood cells and assess the size and shape of red blood cells. But this procedure is time consuming, complex and tedious . Also, the accuracy of recognition is affected by subjective factors like experience and fatigue due to human tiredness. As a solution to this problem, to provide automated, cost-effective and efficient alternative to detection and counting of RBCs,image processing techniques are used [3].

II. LITERATURE REVIEW

Carrying out literature review is very significant in any research project as it clearly establishes the need of the work and the background development. It generates related queries regarding improvements in the study already done and allows unsolved problems to emerge and thus clearly define all boundaries regarding the development of the research project.

Venkatalakshmi [4] attempted the process of red blood cell counting through Hough Transform. The pre-processing stages include capturing of an image via camera featured with microscope. However, this input is available on web for research applications. For image saturation the author implemented conventional HSV transformation but this technique does not consider non-linear characteristics of the capturing device. Pulse coupled neural network for blood cell segmentation and counting was proposed by Vinod V. Kimbahune et al. [5]. The technique was used to denoise the image and clipping of some parameters that were considered as hindrance in blood cell counting. S. Chinwaraphat et al. [6] used modified fuzzy clustering for white blood cell count. The research proposes a segmentation of nucleus and cytoplasm of white blood cell slides. The segmentation is performed firstly by using a standard FCM clustering technique to classify the image of blood sample slide into 4 primary groups as white blood cell nucleus, white blood cell cytoplasm, plasma and red blood cell. Morphological operations were used for the counting and segmentation of blood cells by Y. D. Ma et al. [7]. It is based on the feature of cell's logical and morphological information. By using of mathematical morphological logical operation and laplacian filter,the method is realized with the MATLAB 5.10.G.P.M Priyankara et al. [8] on white blood cell count research also studied white blood cells in deep prior to their research.

III. PROPOSED METHODOLOG

There are five steps involved in the process of estimating the red blood cells. These are input image acquisition, preprocessing, segmentation, feature extraction and finally the counting for RBCs. In the preprocessing step the original blood smear image is converted into saturation image using Gamma Correction. Segmentation is done by Fuzzy segmentation method. Next, feature extraction is accomplished through morphological operations in order to differentiate red blood cell other cells (WBC and platelets) and background. The final step is to find out the number of red blood cell from the blood smear image by using morphological operations.

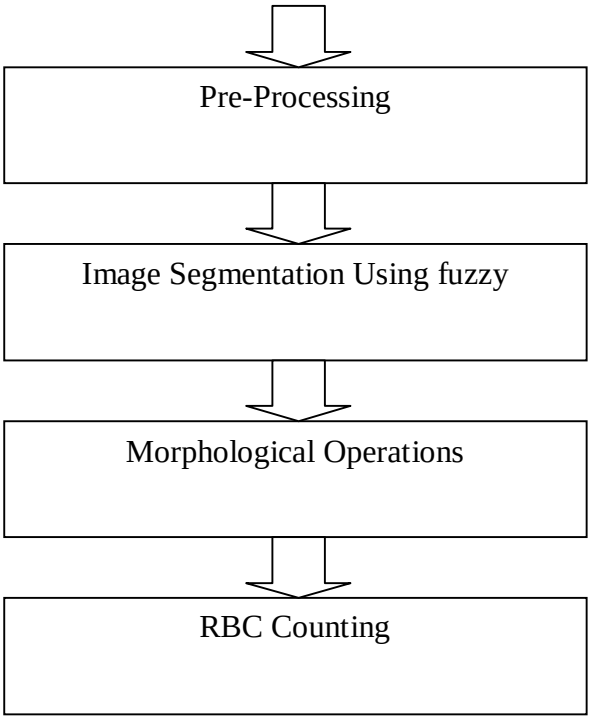


Figure 1Flowchart for RBC counting

A. Preprocessing-

Image pre-processing is a technique of adjusting images suitable for the next step of computational process. It is done in such a way that image quality improved for the success of the other processes. Pre-processing techniques usually include enhancing contrast, removing noise, isolating regions and use of different color models Grayscale image, hsv image. Original

blood cells images are in color. To ease the process of ratio determination, the original images will be converted into grayscale color. Grayscale represents the intensity of the image. Acquired images have low contrast as all blood elements colors close to background color. Also noise is included due to clustered white blood cells. To overcome or reduce such effects contrast enhancement is done. In this work we use simple image processing technique to enhance the image. We first convert the input image into HSV image. From this HSV image, we precede the analysis of the saturation component S, because the S image shows clearly the bright objects such as WBC and platelets. So it is easy to distinguish the red blood cells. A color's identity may be represented in terms of a set of color space parameters termed a gamut.Many range have been researched for color image processing including RGB, YUV, YCrCb, HSI and the related HSV range [9][10].

B. Image segmentation-

The next stage deals with image segmentation. Segmentation partitions an input image into foreground and background region.

Fuzzy C-Means Clustering-

Fuzzy C-Means iteratively moves the cluster centers to the "right" location within a data set. Objective function based fuzzy clustering algorithms such as the fuzzy c-means (FCM) algorithm has been used extensively for different tasks such as pattern recognition, data mining, and image processing and fuzzy modeling. Applications have been described from different areas such as financial engineering, direct marketing and systems modeling. Fuzzy clustering algorithms partition the facts and figures set into overlapping groups such that the clusters describe an underlying structure within the facts and figures. In order to get a good presentation from a fuzzy clustering algorithm, a number of matters should be considered. These concern the shape and the volume of the clusters, the initialization of the clustering process, the circulation of the data patterns and the number of clusters in the data. One of the most widely used fuzzy clustering algorithms is the Fuzzy C-Means (FCM) Algorithm. Let $\{\mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_N\}$ be a set of N data objects represented by n-dimensional feature vectors.

$$\mathbf{x}_k = [x_{1k}, \ldots\ldots, x_{nk}]^T \in R^n$$

A set of N feature vectors is then denoted as a $n \times N$ datamatrix

$$X = \begin{bmatrix} x_{11} & x_{12} & \cdots & x_{1N} \\ \vdots & \vdots & \vdots & \vdots \\ x_{n1} & x_{n2} & \cdots & x_{nN} \end{bmatrix}$$

The FCM algorithms are best described by recasting conditions in matrix-theoretic terms [38]. Towards this end, let U be a real $c \times N$ matrix, $U = [u_{ik}]$. U is the matrix representation of the partition $\{Y_i\}$ in the situation

$$u_i(y_k) = u_{ik} = \begin{cases} 1; & y_k \in Y_i \\ 0; & otherwise \end{cases} \quad (4.9)$$

In equation (4.9), u_i is a function such that: $u_i: Y \rightarrow \{0, 1\}$. In conventional models, u_i is the characteristic function of, Y_i: in fact, u_i and Y_i determine one another, so there is no harm in labelling u; the i^{th}hard subset of the partition (it is unusual, of course, but is important in terms of understanding the term "fuzzy set").

C. Morphological Operations-

Binary Morphology: In binary morphology, everything could be defined using the set operations. Since we are dealing with bimodal images, a pixel could be either 1 or 0. So, a bimodal image can be thought of set of 2-tupples, in which its elements are (row, column) coordinates of the non-zero elements of the image. Formally, let **I** and **B** are the sets corresponding to the image and structuring element, then **I** = {(x, y) | I[x, y] <> 0, ∀x,

$y \in I_R\}$ where I_R is the set of all possible (row, column) elements over and image I. **B** can be defined in a similar manner. There are two basic operations in morphology, which are called *dilation* and *erosion.*The dilation of **I** by **B** is denoted by **I**⊕**B** and it is defined as

$$\mathbf{I}\oplus\mathbf{B} = \{c \mid c = i + b, \text{ where } i \in \mathbf{I}, b \in \mathbf{B}\} \quad (4.13)$$

The translation of set **B** by **t** is defined as follows:

$$\mathbf{B_t} = \{c \mid c = b + t, \forall b \in \mathbf{B}\} \quad (4.14)$$

Dilation operation is defined as follows:

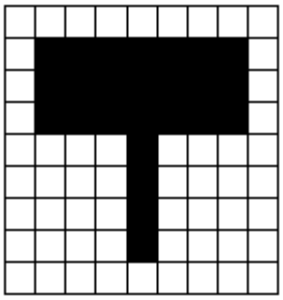
$$Dil(I,B) = \bigcup_{t \in I} I \oplus B_t \quad (4.15)$$

In the same sense, erosion and erosion operations are defined as in Equations 4.15, 4.16 respectively.

$$\mathbf{I}\Theta\mathbf{B} = \{c \mid c = i - b, i \in \mathbf{I}, b \in \mathbf{B}\} \quad (4.16)$$

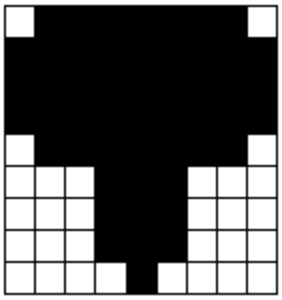
$$Ero(I,B) = \bigcap_{t \in I} I\Theta B_t$$

Implementation of the morphological operations on images is very similar to the filtering image via given kernel. Instead of taking weighted sum, the formulas given are used to evaluate the point at kernel center.

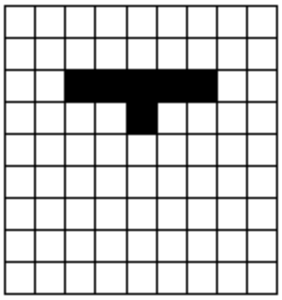


(a)

(b)



(c)



(d)

Fig2. Example of basic morphological operations: a) Original image b) structuring element called simple cross, c) dilation of a) by b), d) erosion of a) by b).

By using the primitive operations, several morphological operations can be defined. Most frequently used morphological operations could be listed as *Hit-Miss, Open, Close, Boundary, Convex Hull, Skeleton, Thin, Thick, Prune* and *Distance Transform* operations.

IV. SIMULATION RESULT

Simulation is carried out using MATLAB 2010a.

A. CELL Count- The steps of proposed algorithm yields following results. The original image is a digital image captured with microscopic device attached. The following results were obtained via simulation of proposed architecture.

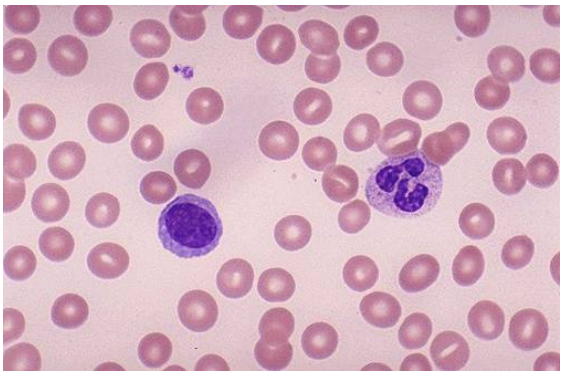


Fig3. Original image representing various elements of blood

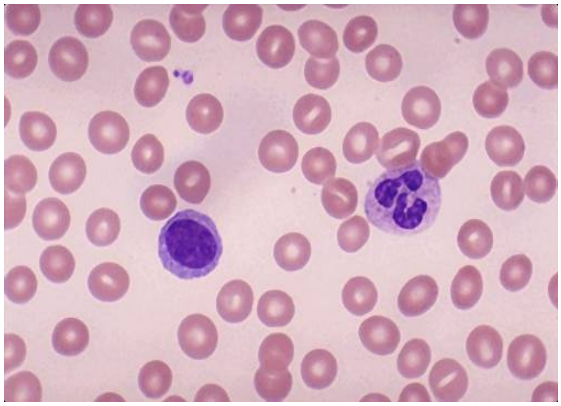


Fig 4. The image is filtered with a median filter as the stage of pre-processing.

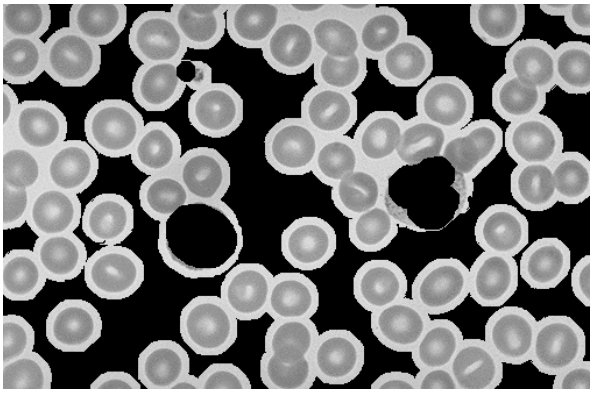


Fig7. Image with removed background of a blood cell after saturation

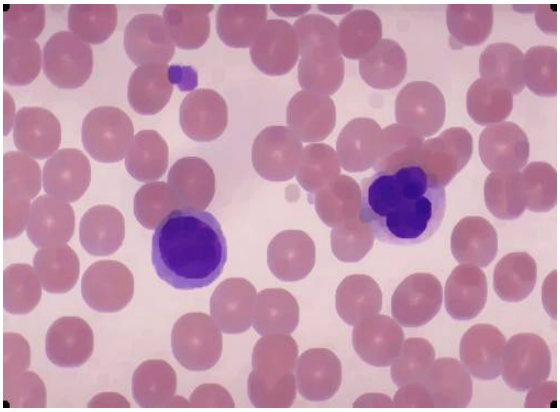


Fig 5. The conversion of original image as the Eroded image.

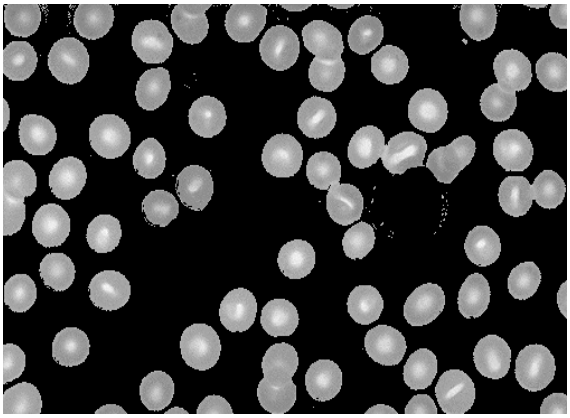


Fig 8.Removal of white blood cells and platelets as second stage of saturation

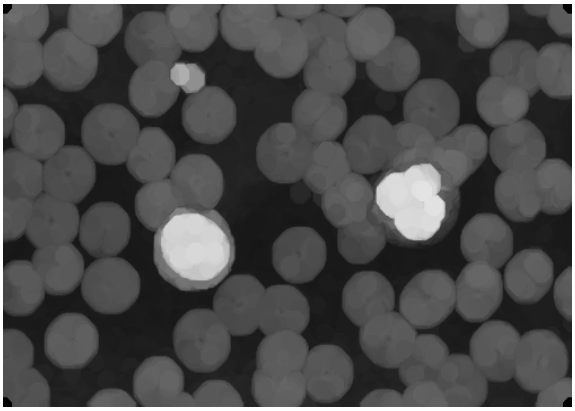


Fig6.Calculation of Saturation component using HSV component algorithm

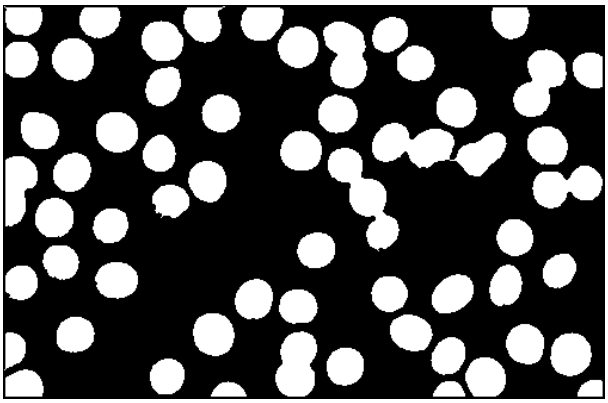


Fig9. Conversion of a saturated image into binary image

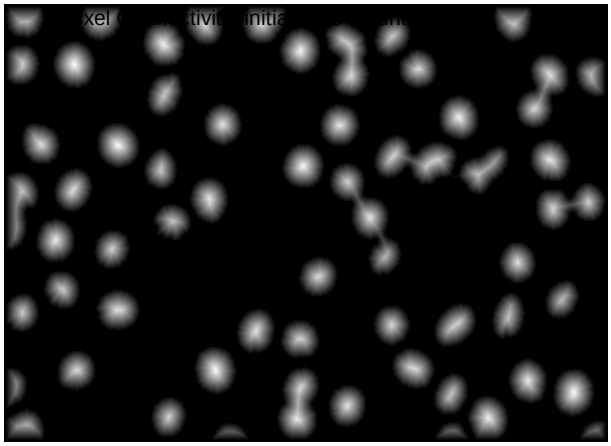


Fig10.Connectivity of Pixels through centroid calculation of cells

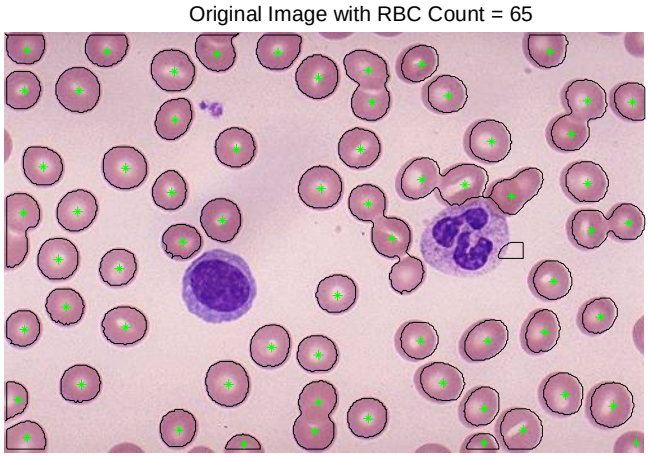


Fig11.Counting of cells for test input.

V. CONCLUSION

The approaches of cell count are autonomic in nature and accuracy depends on algorithmic capability of various methods. The two stage fuzzy clustering and morphological operations are efficient on their part and customizes the image in various states that collectively determines the accuracy and precision in blood cell count. The pre-processing stage, clipped the un-necessary background of image and filtering of white blood cells and platelets were performed based on nature of their classification.

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