Automatic Detection of Sickle cell in Red Blood cell using Watershed Segmentation

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Abstract: Red Blood Corpuscles are the major cellular component of human blood which is responsible for gaseous exchange between living cell and external environment. In normal physiological condition, an RBC is circular in front view and biconcave in side view. In this paper image processing techniques applied on RBC cell to count the normal and abnormal cells using Watershed Segmentation. Then form factor calculated for each cell to differentiate between normal and abnormal cell. Also Contour plot of RBC cell drawn to highly visualize the RBC cell, Sickle cell, and Target Cell. Simulation of this technique is done on MATLAB 2013a.

IndexTerms: Peak Signal to Noise Ratio (PSNR), Mean Square Error (MSE), Red Blood Corpuscles (RBC), Sickle Cell Anemia (SCA), edge detection, Root Mean Square Error (RMSE).

I. INTRODUCTION

The erythrocytes are the most numerous blood cells in the human body, and it also called red blood cells. The red blood is a cell that functioned as carry oxygen throughout our body [1]. According to American Cancer Society (2009), the normal red blood cell in our body is divided into four categories of ages, which are newborn, children, women and men. The average amount of red blood cells each category is about 4.8-7.2 million per cubic millimeter, about 3.8–5.5 million per cubic millimeter, about 4.2-5.0 million of these cells per cubic millimeter and 4.6-6.0 x 106 per cubic millimeter respectively. Red blood is measured by the amount of hemoglobin in our blood. The level of hemoglobin in blood will affect our health tremendously. One may suffered fatigue and short of breath when the level of hemoglobin is too low and not enough to supply oxygen to our tissues [2].

Background of SCA
SCA is a haemoglobinopathy that is hereditary and characterized by presence of structurally abnormal haemoglobin (HbS) [3]. In an adult human RBC, there is haemoglobin which is constituted by Haem molecule and 4 globin chains mostly 2α and 2β chains. Substitution of the amino acid valine for glutamic acid at the 6th position of β chain produces HbS which is due to point mutation of the gene forming beta globulins chain [4].

- If both parents are carrying this faulty gene, child is homozygous→ child will suffer from full blown SCA All the adult type haemoglobin (HbA) is replaced by abnormal haemoglobin (HbS).
- If 1 of the parent is carrying this abnormal gene, the child id heterozygous →(50% HbA is replaced by HbS→ child will have sickle cell trait i.e. the child will be a carrier but not sufferer.

In the proposed algorithm images are first denoised by using the imfilter in MATLAB then they are segmented and the results are compared by using certain parameter. Those parameters are:

1. **MSE: Mean Square Error (MSE):** MSE is computed by averaging the squared intensity of the original (input) image and the resultant (output)images as given[5]

$$\text{MSE} = \frac{1}{M*N}\sum_1^M\sum_1^N e(m,n)^2$$

M: numbers of rows of original image
N: number of column of original Image
e(m, n): Error Difference Between Original and Filtered Image

2. **Peak Signal to Noise Ratio (PSNR):** PSNR is the ratio between the maximum possible power of a signal and the power of corrupting noise that affects the fidelity of its representation. PSNR is usually expressed in terms of the logarithmic decibel scale. PSNR is an approximation to human perception of reconstruction quality. A higher PSNR generally indicates that the reconstruction is of higher quality [6]., PSNR can be defined as

$$\text{PSNR} = 10\log_{10}\frac{Imax^2}{MSE}\ \text{dB}$$

3. **Root Mean Square Error (RMSE):** It considers the quality of the removed noise. The root mean square error is defined as

$$\text{RMSE} = \text{sqrt(MSE)}$$

Value of RMSE should be low for an efficient filter.

The paper is organized as follow; section II starts with literature Survey, section III starts with the Proposed Methodology in which proposed block diagram, proposed algorithm is given. Section IV illustrates the results in which MSE and PSNR calculated for filter section and determine number of normal and abnormal cell using watershed segmentation. The conclusions are drawn in section V.

II.LITERATURE SURVEY

In the literatures, normal and abnormal RBC cells detection and counting have been proposed.
Mahmood et. al [2]

Blood cell segmentation and identification is a vital in the study of blood as a health indicator. In this paper provide userfriendly software based on MATLAB allowingfor quick user interaction with a simple tool for thesegmentation and identification of red and white blood cells from a provided image. In order toperform the segmentation, used color based segmentation using InternationalCommission on Illumination L*a*b* (CIELAB) color space.

Rakshitet. al [4] presents the detection of abnormal cells using image processing. Here some pre processing done using weiner filter and Sobel Edge detection method and calculate form factor using regionprop commands.

Maitraet. al [7]

This paper presents a methodology to achieve an automated detection and counting of red blood cells in microscopic images using Hough Transform.

Vijayaraniet.al[8]

Edge detection refers to the process of identifying and locating sharp discontinuities in an image. In this paper, two edge detection algorithms namely canny edge detection and Sobel edge detection algorithm are used to extract edges from facial images which is used to detect face. Performance factors are analyzed namely accuracy and speed are used to find out which algorithm works better.

Arunaet. al [9] this paper presents an approach to detect the shape of sickle cells presents in RBCs by finding the highest, lowest and mean radius of each type pf cell by comparing it with standard cell size and mark the cells by a red circles for identification.

Vinutha H Reddy [10], this paper introduces an cost effective automatic RBC and WBC counting accurately using image analysis technique for remote or rural areas using telemedicine approach independent of specialist to generate patient RBC and WBC report.

Sreekumar et. al [11], this paper presents a simple method to count the red blood cells and identify sickle cells using circular hough transform an image processing technique.

In this Paper, we are taking motivation from this paper and proposed Watershed Segmentation for counting normal and abnormal cell also plot the contour plot for better visualization of normal cells, Sickle cells, and target cells.

III.PROPOSED METHODOLOGY
A.   Overview

In proposed methodology, the colored blood smear image is taken as an input. Then preprocessing is done on image to remove unwanted noise from it. Then segmentation applied on image to find certain objects of interest which may be depicted in the image. In this paper, watershed segmentation applied because it is more popular in the field like biomedical, medical image. It is based on the geography. Image is taken as geological landscape; the watershed lines determine boundaries which separate image regions.

Each cell in RBC image is labeled and for calculation of form factor region props command is used to calculate the area and perimeter. After that based on Form Factor value

counting of Normal and Abnormal cells is done. For a normal RBC cell the form factor around or near to 1 and for sickle cells its value less than 0.5.
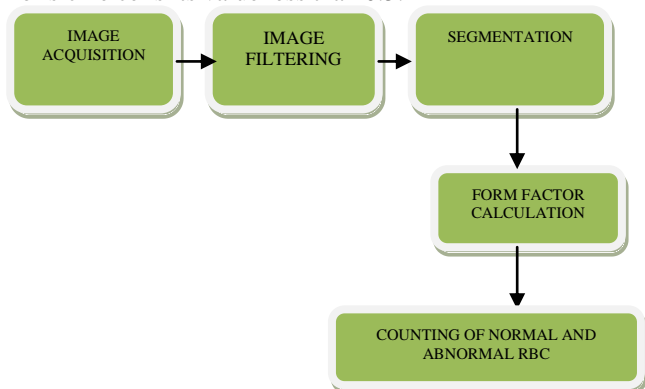

Figure 1: Proposed Block Diagram for Watershed Segmentation

B.   For Contour Plot

For Contour plot some preprocessing applied on image to remove noise. A contour plot displays the isolines of matrix Z. where Z is interpreted as heights with respect to the x-y plane. Z must be at least a 2-by-2 matrix that contains at least two different values. The x values correspond to the column indices of Z and the y values correspond to row indices of Z.
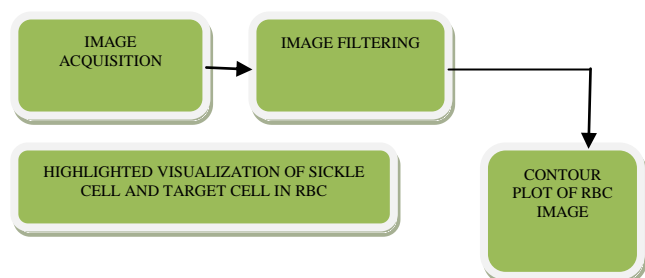

Figure 2: Proposed Block Diagram for Contour Plot

For normal RBC the contour plot is a circle and for other sickle cell the irregular shape. Also using Contour plot got the highlighted visualization of sickle cell and target cell.

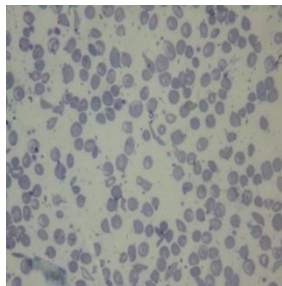### PROPOSED ALGORITHM FOR WATERSHED SEGMENTATION

1. Input the Sullied and magnified human blood image and convert to binary image.
2. Image filtering algorithm applied to remove noise or unwanted spots.
3. Watershed segmentation applied on image to separate the image from its background.
4. Form factor is calculated for each cell. Form Factor defines as $(4*pi*area/Perimeter^2)$

PROPOSED ALGORITHM FOR CONTOUR PLOT

1. Input the Tainted and magnified human blood image and convert to gray Scale Image.
2. Image filtering algorithm applied to remove noise or unwanted spots.
3. The contour plot of image is drawn.

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4. Then in contour plot, we can see highlighted normal RBCs and Sickle cells.
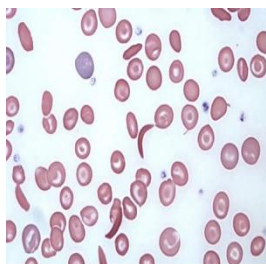
IV. SIMULATION RESULTS
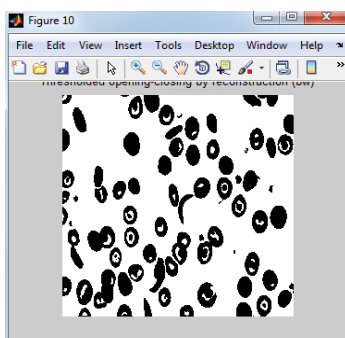

Input Image (Real Image)
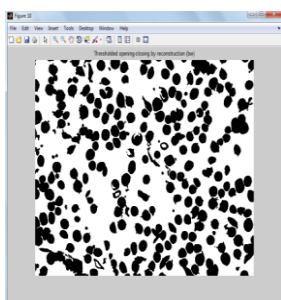
After preprocessing image

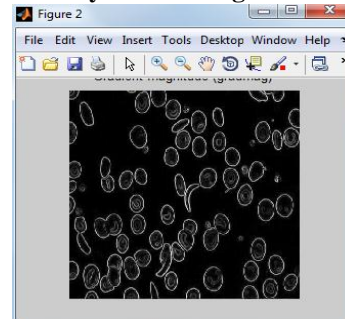Input Image (Synthetic Image)

After preprocessing image

Table 1: MSE, PSNR and RMSE

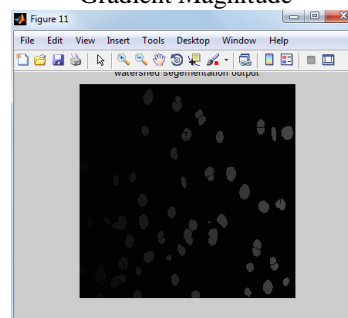|	MSE	PSNR	RMSE
After applying filter operation (Synthetic Image)	0.17	55.82dB	0.41
After applying filter operation (**Real Image**)	0.035	62.69dB	0.19

The Detection of Sickle Cell Anemia simulation results shown below:

1.   Simulation   Results   using   Watershed Segmentation
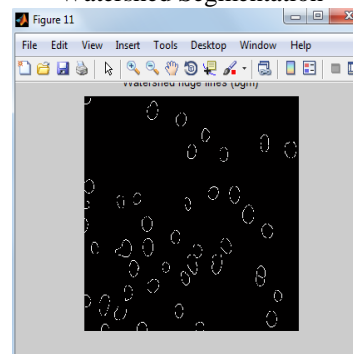
a.   Synthetic Image Simulation
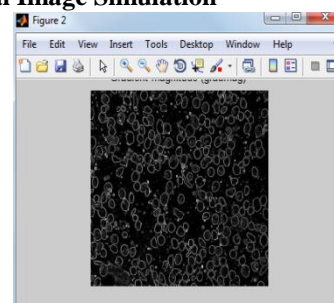

Gradient Magnitude
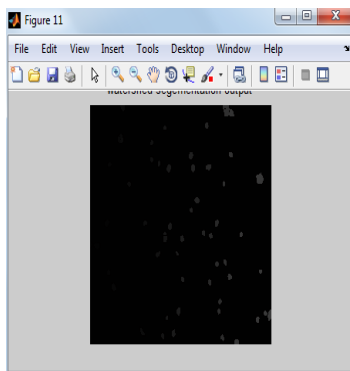

Watershed Segmentation

Watershed Ridge lines

Table 2: Results for Synthetic Image Cells

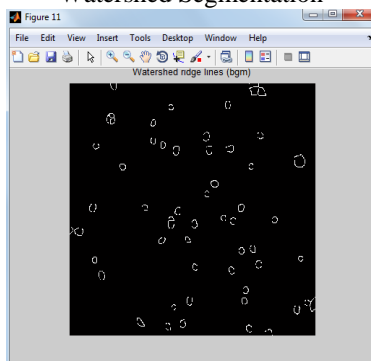|	Total Number of Count	Normal RBC Cell	Abnormal RBC Cell
Water shed Segmentation	70	63	7

b.   Real Image Simulation

Gradient Magnitude

490

Watershed Segmentation

Watershed Ridge Lines

Table 3: Results for Real RBC cell

	Total Number of Count	Normal RBC Cell	Abnormal RBC Cell
Water shed Segmentation	58	54	4

2.   Simulation Results for Contour Plot
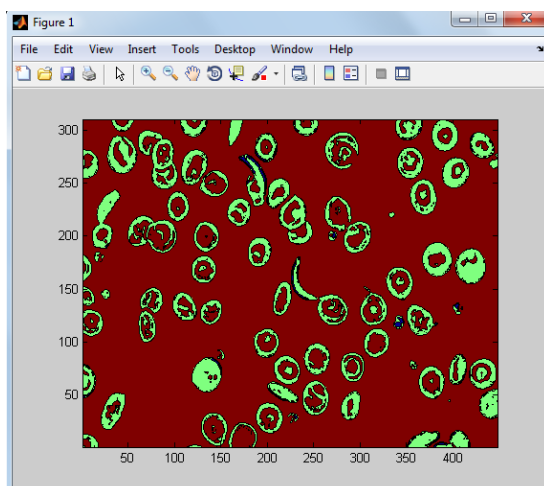
Synthetic RBC image Contour Plot

V.CONCLUSION AND FUTURE SCOPE

In our work, sickle cell anemia detected and counted. In the simulation results firstly certain parameter MSE, PSNR, and RMSE calculated to measure the quality of image after filter operation. After that watershed segmentation is applied on the pre processed image and their simulation results shown, also calculated normal and abnormal RBC cell. A Contour plot of cells was drawn to highly visualize the normal, sickle and target cell.

In future scope we can work to detect the Target cell in RBC cell because a Target cell shows the Abnormalities of hemoglobin, the protein in red blood cells that carry oxygen.

VI. ACKNOWLEDGMENT

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