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Fuzzy C means Detection of Leukemia based on Morphological Contour Segmentation

Viswanathan P[a,*]

[a]*Associate Professor, Information Technology, VIT University, Vellore and 632014, India*

Abstract

Due to complex nature of blood smear images and imitation of similar signs of other disorders makes difficult to detect leukemia. It also needs more time to diagnose and sometimes susceptible to errors. In order to solve this issues fuzzy C means cluster optimization of leukemia detection based on morphological contour segmentation is proposed in this paper. This paper introduces the new approach for leukemia detection which consist of (1) contrast enhancement to highlights the nuclei, (2) morphological contour segmentation, and (3) Fuzzy C means detection of leukemia. The contract enhancement is done by simple addition and subtraction operation to separate the nuclei. The morphological contour segmentation detects the edges of nuclei and eliminate the normal white blood cells from the microscopic blood image. Then the texture, geometry, color and statistical features of nuclei is evaluated to determines the various factors of leukemia. Finally it is trained by Fuzzy C mean clustering of single row feature vector of each cell is used to classify leukemia from white blood cells. This makes the proposed algorithm better results in accuracy and time consumption when compare to normal hematologist's visual classification.

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Keywords: Contrast; curve; contour; morphology; texture; geometry; color; fuzzy; cluster.

1. Introduction

Leukemia is a type of blood cancer occurs in white blood cells(WBCs) generated from the bone marrow. It disrupts the balance of the blood system diagnosed through highly trained specialists using expensive laboratories. But this way of evaluation reported that, 50% of patients are misdiagnosed in regard of subtypes. Diagnostic problem arises due to imitation of similar signs in other disorders [1] and complex nature of blood smear images. Hence the variation in slide preparation techniques, needs more work to meet real clinical demands.

The acute leukemia segmentation and classification techniques are based on four main categories such as threshold, boundary, region and hybrid. Most of the techniques combines boundary and region criteria [1]-[16]. Threshold based methods such as Otsu and histogram [9][12] segments the WBCs directly from the blood smear image using the intensity level. Contour based methods identifies the irregularities of the nucleus boundary [6] combined with selective

* Corresponding author. Tel.: +0-915-004-1131 ; fax: +0-000-000-0000.
E-mail address: pviswanathan@vit.ac.in

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filtering [5] segment leukocytes from other blood components. The region and hybrid segmentation are based on multiresolution analysis extract the expected maximization of hue, saturation, and value [14] color space to identify the cytoplasm and nucleus of the WBCs. Mostly color image segmentation is more reliable image segmentations compare to gray-level images. Watershed segmentation algorithm and unsupervised color segmentation provided good segmentation of nuclei [10] to detect acute leukemia. Mostly automated classifier systems [3] are based on two new features, such as cell energy and Hausdorff dimension to classify cancer cells. But the common drawback observed from these systems are, due to similar gray level and texture among the interested objects may result in segmentation error. To avoid that supervised learning technique is used but requires sufficient number of training samples to be trained. The main objectives of the paper is to excludes the influence of subjective factors and increases the accuracy of identification process of leukemia at earlier stage by Fuzzy C means detection using contour and morphological processing. The paper is organized as follows to present the various process of leukemia detection. The introduction and literature is discussed in section I follows with contrast enhancement and nuclei extraction in section II. Then in section III illustrates the process of segmentation of nuclei and section IV presents the the Fuzzy C mean detection of leukemia. Finally experimental result analysis of segmentation of nuclei and leukemia from microscopic blood image is discussed in section V and conclusion with future work is derived in section VI.

2. Nuclei Separation

The preprocessing of microscopic blood image by contrast stretching enhances the global uniformity, local sensitivity and geometry of the blood cells. It is performed by morphological addition and subtraction operation illustrated in algorithm (1) provides less computation complexity. The proposed algorithm improve the contrast of the blood cell which reflects in projection of nuclei in the WBCs. The contrast is stretched with 50% makes further process to accurately target on nuclei of WBCs in blood microscopic image.

Inputs: Color Image I(x, y) **Output:** Contrast Enhanced Image C(x, y)

(1) The Blood cells image I(x,y) is initially converted to gray scale image g(x,y) by using equation (1) to define the nuclei of the WBCs as dark region.

$$g(x, y) = 0.2989 * I(:, :, 1) + 0.5870 * I(:, :, 2) + 0.1140 * I(:, :, 3) \tag{1}$$

(2) Contrast stretching is applied to improve image contrast done by stretching the range of intensity values. The lower and upper limits is defined as a =0 and b=255, histogram (h) of the original image is evaluated using equation (2) by no of pixels(N) is used to initialize the limit of lower(c) and upper(d) in histogram. Then image g(x,y) contrast is stretched to L(x,y) using equation (3).

$$h = \frac{g(x, y)}{N} \tag{2}$$

$$L = (g(x, y) - c)\left(\frac{b - a}{d - c}\right) + a \tag{3}$$

(3) Histogram equalization(H) of equation (4) is used for adjusting the image intensities which enhances the contrast of the nuclei where l is the level of intensity.

$$H = floor(g_l - 1) \sum_{i=0}^{g(x,y)} h(l) \tag{4}$$

(4) Addition process $R_1 = L + H$; Brightens the image except nuclei, such that the resultant pixels exceeding the intensity value of 255 is reduced to 255.
(5) The subtraction process $R_2 = L - H$; Highlight all the objects and its borders in the image including the cell nuclei.

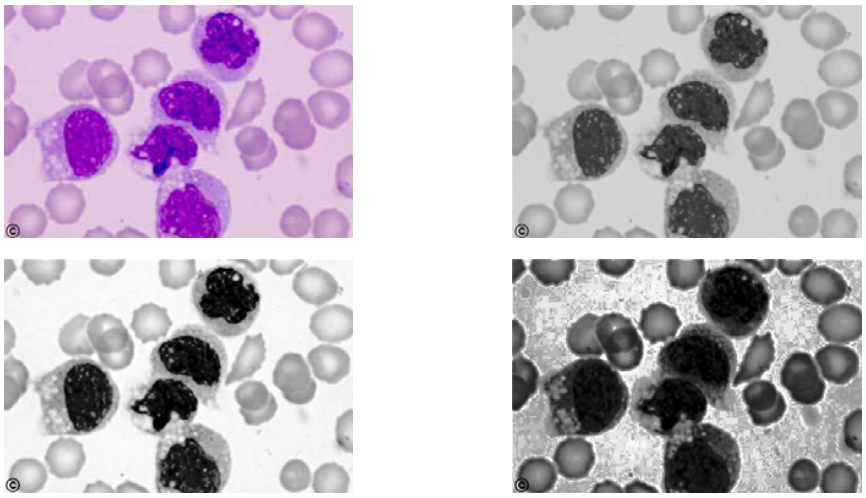

Fig. 1. (a) Original Image (b) Gray level Image (c) Linear Contrast Stretched Image (d) Histogram Equalized Contrast Enhanced Image.

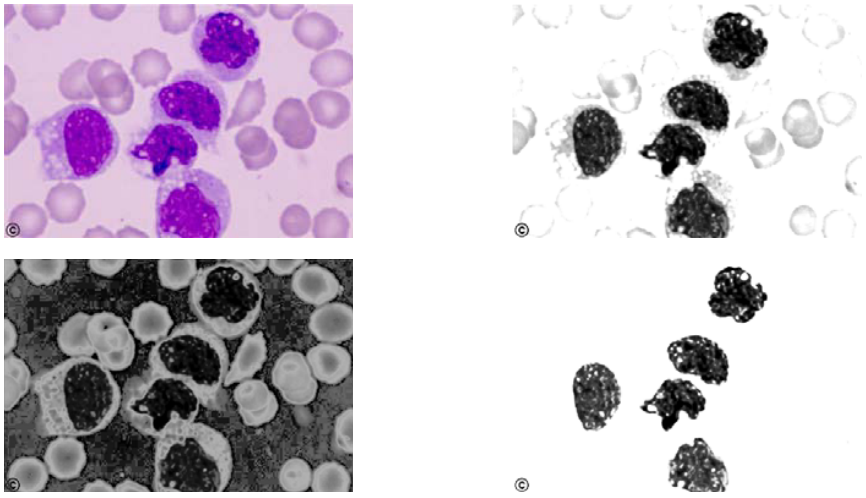

Fig. 2. (a) Original Image (b) Addition processed Image (c) Subtraction processed Image (d) Addition of (b) & (c) image.

(6) $R_3=R_1+R_2$; Removes the other blood components and retains the nuclei with less distortion on the nuclei part of the white blood cells.

Contrast Enhanced Image $C(x, y)=R_3$

Algorithm 1: *Contrast Enhancement*

3. Morphological Contour Segmentation of Nuclei

The subsequent feature extraction will highly depends on the accurate segmentation of nuclei from WBCs. It is a challenging problem for segmentation of nuclei from the microscopic images since it is having a complex appearance of cells structure with uncertainty and inconsistencies. In order to solve this issues, segmentation based on global and

local curvature properties is proposed in this paper is illustrated in algorithm (2). The curvature properties is used for accurate extraction of maximum curvature points and absolute value of the curvature. The round corner is determined by means of low curvature when maxima tends to have absolute curvature smaller than triangulation T. The sharp corner determines high curvature when maxima tends to have an absolute curvature larger than T. If T satisfies the Delaunay criterion then the interior circumference of the circle through the vertices does not contain any points. If all triangles satisfy the Delaunay criterion, then the triangulation T is called Delaunay triangulation. It is applied to all points of maximum curvature to find candidate edges which potentially segments the nuclei.

Inputs: Enhanced Contrast Image C(x, y), Color Image I(x,y) **Output:** Segmented region S(x, y)

(1) The RBC is evaluated by the equations (5) and (6) with the difference between RED and BLUE components in I(x,y) of $d = R_I - B_I$.

$$b = \sim \left(\begin{cases} 0 \ if \ \ \mathrm{C(x,y)<0.9} \\ 255 \ otherwise \end{cases} \right) \ in = b \rightarrow 0 \tag{5}$$

$$D = \left(\begin{cases} 0 \ if \ \ \mathrm{d<0.05} \\ 255 \ \ otherwise \end{cases} \right) \oplus h \ ind = D \rightarrow 0 \tag{6}$$

(2) The RBC components is eliminated by filling with compliment of equation(7) on $Iout\,(in) \rightarrow C(x, y)$, $Iout\,(ind) \rightarrow 255$.

$$W = \sim \left(\begin{cases} 0 \ if \ \ \mathrm{Iout<0.8} \\ 255 \ \ otherwise \end{cases} \right) \oplus h \ indice = W \rightarrow 1 \tag{7}$$

(3) The small components are removed by erosion followed by dilation of equation (8).

$$W_c = ((W \ominus s) \oplus s) \oplus h \tag{8}$$

(4) Detection of WBC by reshaping C(x,y) according to indice with difference of R and B and find diff $\rightarrow$ 1 and WBC is segmented by HSV conversion with erosion using equation(9).

$$W_s = HSV(W_c) \ominus s\,[rc] \tag{9}$$

(5) Extract the curves and edges from binary edge map in all directions and estimate the curve point using equation (10).

$$[\mathrm{I\ \ J}] = ((\mathrm{W}_s(\mathrm{p}\,(1) - \mathrm{G} \rightarrow \mathrm{p}\,(1) + \mathrm{G}) \rightarrow (\mathrm{W}_s(\mathrm{p}\,(2) - \mathrm{G} \rightarrow \mathrm{p}\,(2) + \mathrm{G})) \rightarrow 1$$

$$size(r, 1) > 0 \rightarrow p = [r(1), c1)]; cur = p$$

$$size(I, 1) > 0 \rightarrow p = p + [I(i), J(i)] - G - 1; cur = [cur; p]$$

$$[dist, i] = \min((I - G - 1)^2 + (J - G - 1)^2)$$

Repeat the step to extract edge on another direction

$$curve = cur - Gif size(cur, 1) > \frac{size(BW, 1) + size(BW, 2)}{25} \tag{10}$$

where G is Gap size=5, p is the position of the maximum curvature point on the contour, and R is a coefficients.

(6) The corners of the curves is evaluated using equation (11).

$$cor = \frac{x'y'' - y'x''}{(x'^2 + y'^2)^{1.5}} \tag{11}$$

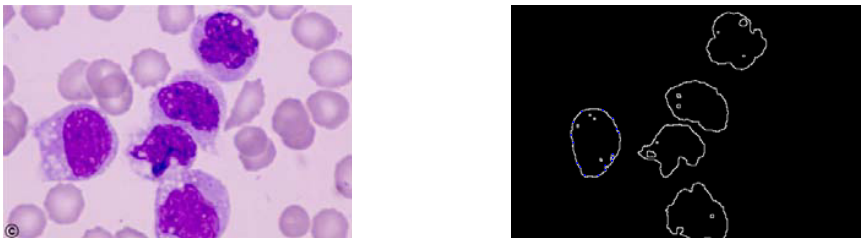

Fig. 3. (a)Original Image (b) Nuclei Edge Detected Image.

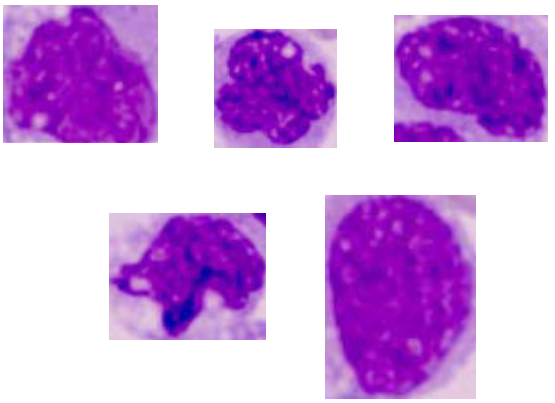

Fig. 4. Segmented Nuclei from WBCs

where x and y represent the x coordinates and y coordinates of the boundary points respectively. $x^{'}$ and $y^{'}$ represent the first derivatives, $x^{''}$ and $y^{''}$ represent the second derivatives.

(7) The region of interest (ROI) is maximum curvature point which is defined as the segmentation of contour between two nearest curvature minima points denoted by L_1 and L_2. The ROI of each maximum curvature point is used to calculate a local threshold using equation (12).

$$T(p) = R \times \frac{1}{L_1 + L_2 + 1} \sum_{i=p-L_2}^{p+L_2} |cor(i)| \tag{12}$$

Algorithm 2: *WBC Segmentation*

4. Fuzzy C mean Detection of Leukemia

The Fuzzy C mean (FCM) clustering algorithm cluster the feature points to the degree specified by membership grade. It partition the collection of n feature vector extracted from the segmented nuclei. The cluster center of each group is evaluated using equation (13) .

$$c_i = \frac{\sum_{j=1}^{n} u_{ij}^{m} x_j}{\sum_{j=1}^{n} u_{ij}^{m}} \tag{13}$$

It minimize the dissimilarity measure of the objective function equation (14). The partitioning is initialized by membership value u between 0 and 1 and updated for every iteration by using equation (15).

$$O_i = \sum_{i=1}^{c} \sum_{j=1}^{n} u_{ij}^{m} d_{ij}^{2} \quad where \quad d_{ij} = \| c_i - x_j \| \tag{14}$$

$$u_{ij} = \frac{1}{\sum_{k=1}^{c} \left(\frac{d_{ij}}{d_{kj}} \right)^{2/(m-1)}} \tag{15}$$

The result of FCM classification of normal and leukemia is shown in figure (5) provide accurate variation to identify the leukemia cells.

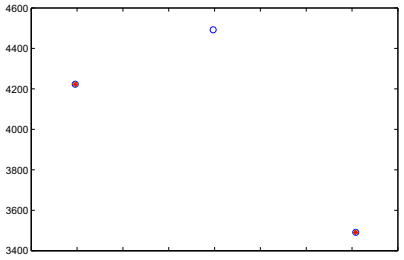

Fig. 5. Fuzzy C Means classification of Normal and Leukemia Cells

5. Experimental Result

The proposed technique is applied on microscopic blood image of Acute Lymphoblastic Leukemia Image Database (ALL-IDB) for image processing dataset. The blood image is preprocessed as shown in Fig(2) having good contrast enhancement used to highlight the affected WBC. Then it is further processed with addition and subtraction operation with morphological operation to remove the other smaller components as shown in Fig (3). The Nuclei is segmented by curve and corner detection as shown in Fig (4) provides the accurate detection of nuclei and WBCs of the microscopic blood image. Fig 4(a) to 4(e) is the segmentation of WBCs and nuclei from image shown in Fig (3a) shows varying degree of lobulation characterized by delicate folding or increasing of nuclear membrane is processed to segment leukemia from blood images as shown in table (1). It is further classified by Fuzzy C mean clustering as shown in figure (5). The obtained results is further correlated with different validation of sub images as shown in Fig(5) with

Table 1. Difference between Normal Monocyte and Acute leukemia

Value/Type	Normal monocyte		Acute leukemia	
Cell parts	Whole Cell	Nuclei	Whole Cell	Nuclei
Perimeter	527.09	407.811	3.534	3.326
Diameter	170.414	132.834	1.142	0.986
Density	218.284	109.548	123.058	80.643
Cytoplasmic Ratio	4:1 → 2 : 1		7:1 → 3 : 1	

distribution of nucleus and whole to determine acute leukemia and normal monocyte. Thus the system presented enabled detection of leukemia provided better performance when compared with some of the existing systems. From the experimental analysis it demonstrates that the proposed algorithm presents accuracy of 98% and provided an effective reliable source of detection for leukemia cell type.

6. Conclusion

The proposed approach identified leukemia WBCs from a whole slide image facilitated the work flow to have tedious and monotonous detection of leukemia. The nuclei and leukemia segmentation based on morphological contour processing is enhanced and provided accurate segmentation of WBCs from the blood microscopic images. It is added with Fuzzy C mean classification trained with the extracted features row vector like perimeter, density and percentage from segmented nuclei with WBC provided accurate evaluation of leukemia. It ensures that proposed system provided accurate segmentation of leukemia from blood sub images. Thus the proposed approach provided viability of larger scale automated solution for detection and classification of normal and abnormal WBCs with less computation time and error rate. It can be further extended with soft set rules in future work to classify the types of cancer cells affected in WBCs.

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