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MODIFICATION OF IDTCS METHOD FOR TOUCHING LEUKEMIA CELL GROUPING

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Abstract. Morphological analysis and calculation of the number of white blood cells on microscopic images are stages in diagnosing leukemia. Constraints in developing a system for diagnosing leukemia are white blood cell segmentation and counting of the number single cells in touching cell. We propose to modify the Iterative Distance Transform For Convex Sets (IDTCS) method to separate the touching leukemia cells. The IDTCS method is used to determine markers for each cell in touching cells. The marker results from the IDTCS method are used as cell centroids and the next process is pixels clustering based on the nearest cell centroid using the euclidean distance function. The data used are microscopic images of Acute Lymphoblastic Leukemia (ALL). The experimental results show that using modified IDTCS method for clustering produces better accuracy compared to the K-Means clustering and Watershed methods.

Keywords: acute leukemia image; touching cell separation; iterative distance transform for convex sets (IDTCS); clustering; euclidean distance.

INTRODUCTION

Leukemia occurs because the production of white blood cells out of the spinal cord is immature and spread throughout the body. So it is very dangerous because it disturbs the stability of blood circulation. The importance of computerized based research on white blood cells will greatly help the medical field in diagnosing leukemia.

One important process in computerized systems in diagnosing leukemia in microscopic images is the process of segmenting white blood cells. A good segmentation process will produce good features to produce accurate diagnoses. Leukemia image segmentation research has been done in literatures (Labati, Piuri, & Scotti, 2011); (Zheng, Wang, Wang, & Liu, 2018); (Joshi, Karode, & Suralkar, 2013). The study used a peripheral blood smear dataset from ALL patients and not ALL patients collected at the Tettamaati Research Center, Monza, Italy research center (Labati et al., 2011). In literature (Putzu, Caocci, & Di Ruberto, 2014), the segmentation process uses Zack Algorithm for thresholding and uses the arithmetic process. In literature (Rezatofighi & Soltanian-Zadeh, 2011) used the Otsu thresholding, Gram-Schmidt orthogonalization, and the snake algorithm for white blood cell segmentation.

The obstacle in the process of leukemia white blood cells segmentation is the presence of touching cells. Because the next step in diagnosing leukemia from microscopic images is morphological analysis and calculation of white blood cell counts. Literature (Fatichah, Purwitasari, Hariadi, & Effendy, 2014) present white blood cells counting using features, K-Means clustering for separation the overlapping cells.

The segmentation used is the morphological iteration process of automatic erosion for tangent objects [5]. Research (Singhal & Singh, 2014) segmented morphology and thresholding methods. Research (Tian, Li, Zeng, Evans, & Zhang, 2019) in segmenting using K-Means clustering. The research (Tan, He, & Sun, 2010) conducted segmentation using fuzzy K-means clustering, thresholding and Zack algorithms. Research (Mohapatra, Patra, & Satpathy, 2014) in segmenting using the Shadowed C-means (SCM) and K-Means Clustering methods. The approach of the parametric model of the Gaussian mixture (GM) is used in cell segmentation (Cuevas & Sossa, 2013). In this study the concave method was used to determine the convexity and concomitance of overlapping cells (Zheng, Wang, Wang, & Chen, 2014). In research (Mandyartha & Fatichah, 2016) the watershed method was used in segmenting leukocyte cells.

Previous studies on the segmentation of touching leukemia cells still occur in the presence of oversegmentation and undersegmentation. It is necessary to develop a method of segmenting white blood cells to obtain an accurate area and number of single cells in the image of touching cells. The use of clustering methods such as K-Means for segmentation of touching leukemia cell have obstacles in determining the number of K and the results of clustering are not optimal if the centroid initialization is not correct. While the separation of touching

cells using the Watershed method still has oversegment. We propose to modify the Iterative Distance Transform For Convex Sets (IDTCS) method to separate touching leukemic cells. The IDTCS method is used to determine markers for each cell in the touching cell. The marker results from the IDTCS method are used as cell centroids and then grouping pixels based on the nearest cell centroid using the euclidean distance function. The data used for the experiment are microscopic images of Acute Lymphoblastic Leukemia (ALL) from M. Tettamanti Research Center for childhood leukemias and hematological diseases, Monza, Italy. The experimental results of the modified IDTCS for clustering were compared with the K-Means clustering and Watershed methods.

METHODS

A. White Blood Cell Segmentation

This stage is to get the area of white blood cells in leukemia microscopic images. A flowchart of touching leukemia cells separation using Modified IDTCS is shown in Fig. 1. Before the white blood cell (WBC) segmentation process is carried out, the preprocessing is done first. The stages of preprocessing include changing RGB to HSV images, thresholding using the Otsu method to get the object area of the blood cell to determine the value based on the histogram to select candidate cell objects is WBC.

B. Determining Cell Marker and Touching Cells Separation using Modified IDTCS

In detecting touching cell markers, the Distance Transform based method is used, namely the Iterative Distance Transform For Convex Sets (IDTCS) method (Fatonah, Tjandrasa, & Fatichah, 2018). Where the IDTCS method produces good accuracy to mark cells using the concavity concept. Concavity formula measure is used as research (Rosenfeld, 1985); in equation 1.

$$\boldsymbol{c(V)} = \max_{\boldsymbol{j=1,\ldots,m}} \frac{\boldsymbol{d(v_j \cap \partial O, v_j \cap \partial I)}}{\boldsymbol{l(v_j \cap \partial O)}} \quad (1)$$

Where $\boldsymbol{d(X,Y)} = \max_{\boldsymbol{x \in X}} \min_{\boldsymbol{y \in Y}} \|\boldsymbol{x} - \boldsymbol{y}\|$ and *l(L)* are lengths of the line segment L.

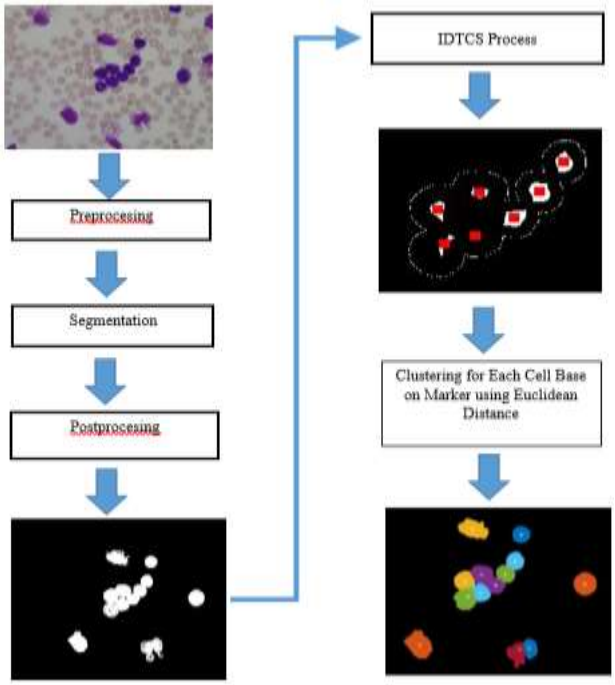

Figure 1. Flowchart of Touching Leukemia Cells Separation using Modified IDTCS Method

After getting the marker every single cell in the overlapping cell then the cell separation process or clustering is continued where the marker location is the cluster centroid.The process of separating the contacted cells is done by grouping pixels to the nearest centroid using the euclidean distance function as in equation 2.

$$\boldsymbol{Dist}(\boldsymbol{x},\boldsymbol{y}) = \sqrt{\sum_{i=1}^{n}(\boldsymbol{x_i} - \boldsymbol{y_i})^2} \quad (2)$$

Iterative Distance Transform For Convex Set (IDTCS) Algorithm
Input: Binary silhouette image $\boldsymbol{I}$
Output: Object marker (*M*)
Parameter: distance transform threshold $\boldsymbol{\rho_1}$ and concavity threshold $\boldsymbol{\rho_2}$.

1. Perform smart filling and smoothing object algorithm on $\boldsymbol{I}$
2. Initialize $\boldsymbol{I^{(0)}} = \boldsymbol{I}$
3. Compute distance transform of $\boldsymbol{I^{(t)}}$ and normalize to [0,1]
4. Create a new binary image by threshold the image using $\boldsymbol{\rho_1}$
5. Compute the concavity of all objects.
6. Mark the object if size of the concavity less than $\boldsymbol{\rho_2}$
7. Repeat step 3 to 6 until $\boldsymbol{I^{(t)}} = \boldsymbol{I^{(t-1)}}$

Figure 2. Psedocode of IDTCS method (Fatonah et al., 2018)

The IDTCS method process begins with the input of binary images with the output of the marker object, with the threshold parameter $\boldsymbol{\rho_1}$and the concavity threshold parameter $\boldsymbol{\rho_2}$. Then do smart filling to remove holes in the cell but do not remove holes between cells. Then smoothing, initialization, distance transform and normalization are done. Do the $\boldsymbol{\rho_1}$ threshold in the new binary image and do

the concavity process on all objects. Make a mark if the size of the object in concavity is less than the threshold concavity. Repeat the process from the distance transform to the threshold concavity $\boldsymbol{\rho_2}$ to get all the desired objects.

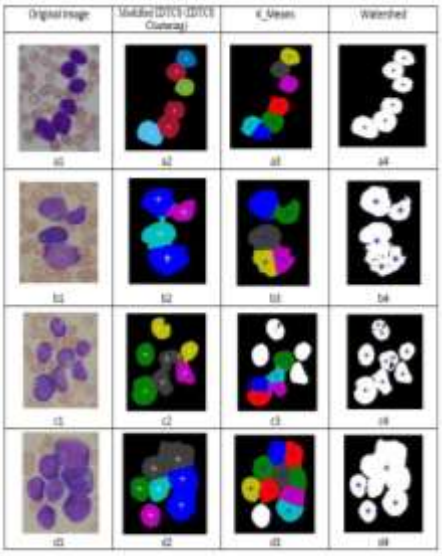

Figure 3. Examples of separation for touching leukemia cells (a1-d1) original Image, (a2-d2) Modified IDTCS, (a3-d3) Modified K-Means, (a4-d4) Modified Watershed

RESULTS AND DISCUSSION

The table of calculation of the number of cells in touching leukemia cells with the K-Means, Watershed, and IDTCS methods, is 23 images from ALL IDB data [16].

Methods	K-Means [4]	Watershed [13]	Modified IDTCS	IDTCS_Watershed
Correct cells	10	15	17	19
Oversegment	8	1	4	3
Under segment	5	7	0	1
Accuracy (%)	44	65 %	74%	83%

Table 1. Comparison of the results of the calculation of the number of cells in touching leukemia cells in ALL images using K-Means, Watershed, and IDTCS.

From Table 1, it can be seen that modified IDTCS results have higher accuracy compared to using the K-Means [4] and Watershed [13] methods. The results obtained by modified IDTCS were 73.3%, Watershed 63.3%, and K-Means 30%. Likewise with the occurrence of undersegment, using IDTCS is very small for undersegmentation compared to K-Means and Watershed method. Where modified IDTCS has 1 undersegmentation, while Watershed 4 undersegmentation and

K-Means 13 undersegmentation. For oversegmentation, IDTCS and Watershed tend to occur but K-Means are more likely to occur oversegmentation. The modified IDTCS, Watershed, have 7, 7, and 8 oversegmentation respectively.

CONCLUSIONS

In this study we propose the modified IDTCS method for counting and splitting touching cells in microscopic leukemia images. Where centroid cells have been found by the IDTCS method and then clustering the pixels with the closest centroid cell using the Euclidean distance to get the single cells. And by using the modified IDTCS method, the results are better than the watershed and K-Means methods. The comparison results of the three methods,are the modified IDTCS of 73.3%, Watershed of 63.3%, and K-Means of 30%. From the results obtained for cell counting and cell splitting, it is hoped that it will support accuracy in determining the overlapping cell counts so that it can support the pathologist in diagnosing acute leukemia. In the future research will be developed towards the cell area and the more accurate form of White Blood Cell (WBC) so that it supports the process of classification of acute leukemia types.

REFERENCES

Cuevas, Erik, & Sossa, Humberto. (2013). A comparison of nature inspired algorithms for multi-threshold image segmentation. *Expert Systems with Applications*, *4*(4), 1213–1219. https://doi.org/10.1016/j.eswa.2012.08.017

Fatichah, Chastine, Purwitasari, Diana, Hariadi, Victor, & Effendy, Faried. (2014). Overlapping White Blood Cell Segmentation And Counting On Microscopic Blood Cell Images. *International Journal on Smart Sensing & Intelligent Systems*, *7*(3).

Fatonah, Nenden Siti, Tjandrasa, Handayani, & Fatichah, Chastine. (2018). Automatic Leukemia Cell Counting using Iterative Distance Transform for Convex Sets. *International Journal of Electrical and Computer Engineering (IJECE)*, *8*(3), 1731. https://doi.org/10.11591/ijece.v8i3.pp1731-1740

Joshi, Minal D., Karode, Atul H., & Suralkar, S. R. (2013). White blood cells segmentation and classification to detect acute leukemia. *International Journal of Emerging Trends & Technology in Computer Science (IJETTCS)*, *2*(3), 147–151.

Labati, Ruggero Donida, Piuri, Vincenzo, & Scotti, Fabio. (2011). All-IDB: The acute lymphoblastic leukemia image database for image processing. *2011 18th IEEE International Conference on Image Processing*, 2045–2048. IEEE.

Mandyartha, Eka Prakarsa, & Fatichah, Chastine. (2016). *Three-level Local Thresholding Berbasis Metode Otsu untuk Segmentasi Leukosit pada Citra Leukemia Limfoblastik Akut*. https://doi.org/10.24002/jbi.v7i1.483

Mohapatra, Subrajeet, Patra, Dipti, & Satpathy, Sanghamitra. (2014). An ensemble classifier system for early diagnosis of acute lymphoblastic leukemia in blood microscopic images.

Neural Computing and Applications, *4*(7), 1887–1904.

Putzu, Lorenzo, Caocci, Giovanni, & Di Ruberto, Cecilia. (2014). Leucocyte classification for leukaemia detection using image processing techniques. *Artificial Intelligence in Medicine*, *6*(3), 179–191. https://doi.org/10.1016/j.artmed.2014.09.002

Rezatofighi, Seyed Hamid, & Soltanian-Zadeh, Hamid. (2011). Automatic recognition of five types of white blood cells in peripheral blood. *Computerized Medical Imaging and Graphics*, *3*(4), 333–343. https://doi.org/10.1016/j.compmedimag.2011.01.003

Rosenfeld, Azriel. (1985). *Measuring the sizes of concavities*. *3*(January), 71–75. https://doi.org/10.1016/0167-8655(85)90045-5

Singhal, Vanika, & Singh, Preety. (2014). Local binary pattern for automatic detection of acute lymphoblastic leukemia. *2014 Twentieth National Conference on Communications (NCC)*, 1–5. IEEE. 10.1109/NCC.2014.6811261

Tan, Tieniu, He, Zhaofeng, & Sun, Zhenan. (2010). Efficient and robust segmentation of noisy iris images for non-cooperative iris recognition. *Image and Vision Computing*, *8*(2), 223–230. https://doi.org/10.1016/j.imavis.2009.05.008

Tian, Kai, Li, Jiuhao, Zeng, Jiefeng, Evans, Asenso, & Zhang, Lina. (2019). Segmentation of tomato leaf images based on adaptive clustering number of K-means algorithm. *Computers and Electronics in Agriculture*, *6*(5), 1045–1160.

Zheng, Xin, Wang, Yong, Wang, Guoyou, & Chen, Zhong. (2014). A novel algorithm based on visual saliency attention for localization and segmentation in rapidly-stained leukocyte images. *Micron*, *5*(6), 17–28. https://doi.org/10.1016/j.micron.2013.09.006

Zheng, Xin, Wang, Yong, Wang, Guoyou, & Liu, Jianguo. (2018). Fast and robust segmentation of white blood cell images by self-supervised learning. *Micron*, *10*(7), 55–71. https://doi.org/10.1016/j.micron.2018.01.010