White Blood Cell Segmentation by Distance Mapping Active Contour

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Abstract - **White blood cell segmentations are an important research issue in Hematology and related study field. Our research proposes a segmentation of nucleus and cytoplasm of peripheral white blood cell from color image slides. The segmentation is started by using a dilated perimeter of nucleus convex hull which propagated into a surrounding region in order to setup a color reference table of cytoplasm. Primary cytoplasm region was then estimated roughly. Distance mapping was applied to this primary area and used to create a gradient vector flow. The active contouring technique was then implemented according to the vector field and finally segmented the WBC boundary. The obtained segmentation outputs show that active contour which guided by the distance mapping from a surrounding area is able to extract nucleus and cytoplasm region efficiently.**

I. INTRODUCTION

Study and knowledge about white blood cell are widely recognized as an important research. It also realized as a one of many challenging and complicate investigation in Hematology and related field both cell component segmentation and cell classification for blood cell counting. White blood cell or Leukocyte is the most important cell in an immune system and can be found generally in the whole body. Its function is to eliminate a foreign body in blood circulation system. In general, an increasing or decreasing in a number of total white blood cells from normal level can be used statistically as an efficient primary indicator for an infection, inflammatory or disease in a human body. This figure can also be used for medical cure or follow up treatment and drug [1]. From the reason described above, the counting of white blood cell in order to specify a cell type and gain an amount of white blood cell in blood sample is necessary and very important. A normal stained blood sample slide will typically compose of red blood cell, white blood cell and plasma as a background. Each WBC cell has naturally different in both size and shape of nucleus. Some complications usually found during manual blood cell counting are mostly due to an unclear boundary between membrane both cytoplasm and plasma or cytoplasm and nucleus. Although the blood cell counting is realized as an important tank in blood component diagnosis, however this is a very time consuming process and quite inherent biasing from an expertise skill and experience, person by person [2,3]. These cause an implicit erroneous result unintentionally. An automatic blood cell counter by using computer vision technique can help to perform this medical test rapidly and accurately. Most available commercial automatic white blood cell analysis composed of three main steps including cell component segmentation, feature extraction and cell type classification. Among those described processing steps, blood cell segmentation plays an important role as the first essential step of blood cell counting process to separate a composition of white blood cell into nucleus region and cytoplasm region. A correction and accuracy of the following cell classification is

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affected from this segmentation. Several segmentation techniques were introduced and applied into these white blood cell images such as thresholding [3,4], scale-space analysis [5], component analysis [6], neural network [7], color-space fuzzy clustering [8,9], color shading [10], SVM [11], Multi-spectral segmentation [12], region growing [13] and active contour [14-18]. In this presentation, we propose a white blood cell component segmentation which focused on nucleus region and cytoplasm region by applying a novel active contour propagation in nucleus portion. We firstly identify the region of white blood cell nucleus and follow by morphology operation in order to locate a convex hull of nucleus. Perimeter of this ROI is enlarged into cytoplasm region in order to setup a reference color table of this region then a closing primary area of cytoplasm is obtained subsequently and converted into distance mapping for defining gradient vector flow. Cytoplasm active contour is activated from an initial and regularly expand to the gradient boundary. The final extracted results by our method show the segmentation between cell cytoplasm and image background satisfactorily and also obtain a promising separation at red blood cell touching region.

In this paper, a brief introduction of white blood cell counting and a short overview of this research were described in section I then followed by an implementation of convex hull and an estimation of primary cytoplasm region in section II. The propagation of active contour is explained in section III. Experimental results were shown in section IV, a discussion and conclusion is described in section V and VI, respectively.

II. NUCLEUS CONVEX-HULL AND CYTOPLASM REGION ESTIMATION

Some sample color image slides of peripheral white blood cell were sampling to test with our proposed technique in this experiment. Color image was binarized then thresholded and cropped respect to a nucleus position in order to cover region of a whole white blood cell. The nucleus area was identified and performed with boundary calculation. Since some of white blood cell is a multi-lobes nucleus type such as Eosinophile and Neutrophile, a morphology operation of convex hull technique seems to be suitable for our purpose. Convex hull of A in two dimension is defined as the smallest of convex set points C in polygon shape which can contain or envelop A. If B^i is a structural element where i = 1,2,3,4. An algorithm to find convex hull of set A or truly equated as an iteration of Hit-or-Miss Operation can be calculated as

$$X_k^i = (X * B^i) \cup A$$

when $i, k = 1, 2, 3, 4$ and $X_0^i = A$

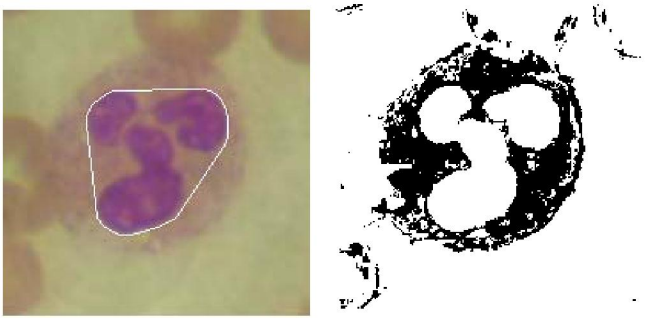
Let $D^i = X_{conv}^i$

As convergence condition $X_k^i = X_{k-1}^i$

Then, the Convex Hull of set A is determined as

$$C(A) = \cup_{i=1}^{4} D^i$$

In the image pre-processing step of our proposed research, we utilize an existent phenomenon that nucleus in adult white blood cell is naturally surrounded with cytoplasm region then an extension of its perimeter is implicitly invaded into this region. By using a group of color pixel data in this dilation ring as a reference table, cytoplasm region can be roughly estimated as a primary region [18] as shown in Fig. 1. Figure 1 shows the dilated nucleus boundary of cropped WBC image in (a) and the estimated cytoplasm area in (b).



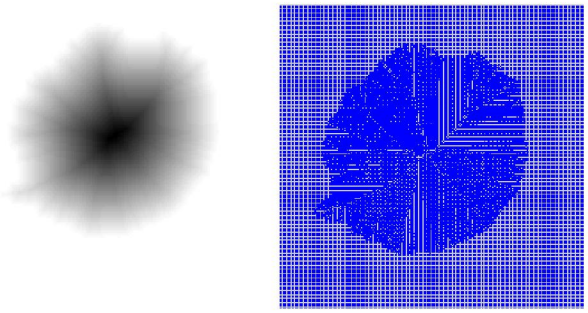
(a) (b)

Fig. 1. (a) dilated nucleus boundary, (b) estimated cytoplasm region.

III. ACTIVE CONTOURING PROPAGATION

The principle of cell segmentation technique that we apply in this research is the active contour algorithm which emphasize

on a segmentation of nucleus region and cytoplasm region. Primary cytoplasm as shown in Fig.1(b) was modified basically by a filling and closing morphology operation. By this implementation, a whole white blood cell area was obtained approximately and then can be transformed to get a distance mapping of binary image [16,17]. Flowing of gradient vector was then derived and later applied to dramatically induce model of active contour dynamics. Figure 2 shows the distance mapping of whole cell binary image (a) and gradient vector flow (b).



(a) (b)

Fig. 2. (a) whole cell distance mapping, (b) gradient vector flow

A parametric active contour model or snake can be defined as a boundary curve of V(s) in which s parameter is only 0 or 1. The curve shape can enlarge or contract on 2D image plane under the potency of two types of forces or energy function as internal and external [14]. The total snake energy function can define as

$$E_{snake} = E_{internal} + E_{external} \quad (1)$$

$$= \int_0^1 \left[E_{Int}(v(s)) + E_{Ext}(v(s))\right] ds$$

where E_{Int} and E_{Ent} are an internal energy function and external energy function respectively and v(s) = [X(s),Y(s)] is define as a position of snake when s ∈ [0,1]. The active contour model seeks to minimize this snake energy function.

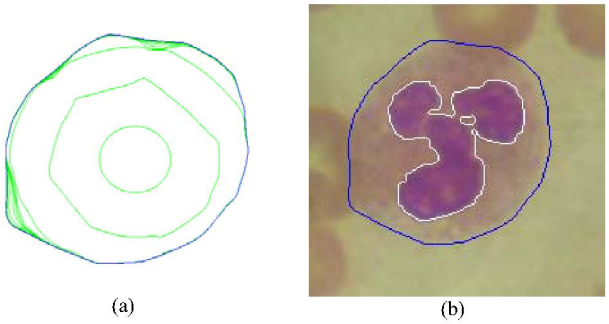
The internal energy function or internal force constrains the snake to be smooth by stretching and bending force energy while the external energy guides the snake to seek desirable image properties such as edge. The snake internal energy function, as shown in Eq.2., is basically composed of elasticity energy to control tension of snake and bending energy to control curvature or rigidity.

$$E_{Int} = \frac{1}{2}\left[\alpha(s) \cdot |v_s(s)|^2 + \beta(s) \cdot |v_{ss}(s)|^2\right] \quad (2)$$

The external forces or also known as an image energy are computed from the image data. In order to attract snakes to edge or ridge features in images, the external energy is needed. The typical external energy designed to lead an active contour toward object boundaries is equated as shown in Eq.3.

$$E_{Ext} = -|\nabla I(x,y)|^2 \quad (3)$$
$$= -|\nabla [G_\sigma(x,y) * I(x,y)]|^2$$

The derived term is an image energy which implemented by 2D Gaussian filter when *I(x,y)* is a grey-level image from distance mapping and σ is a standard derivation and ∇ is a gradient operator. The properties of contour depend on total snake energy function. The minimization of this energy dynamically forces the active contour model movement according to the gradient vector flow field and finally terminates at the image boundary. Figure 3 shows the contour series (a) and the final boundary (b).



(a) (b)

Fig. 3. (a) contour series, (b) final boundary

IV. EXPERIMENT AND RESULTS

Algorithm of our segmentation process is shown briefly in figure 4. The algorithm starts from nucleus position finding and image cropping then follows by convex hull identification and

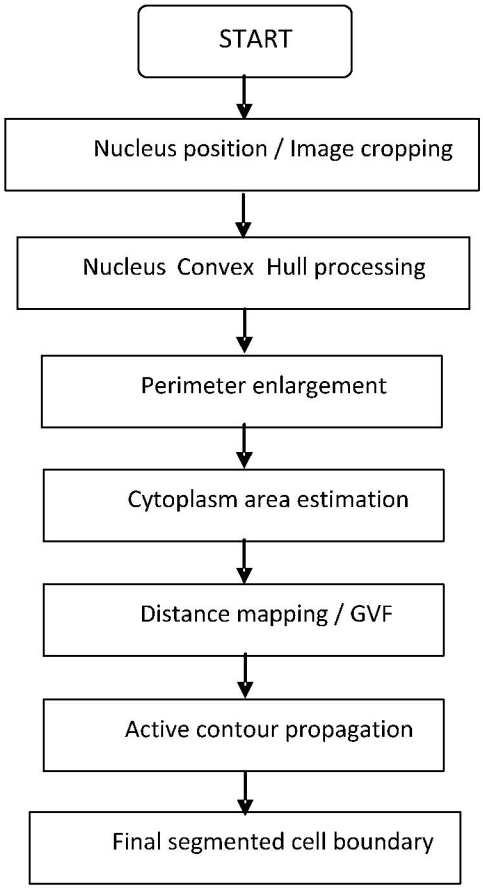
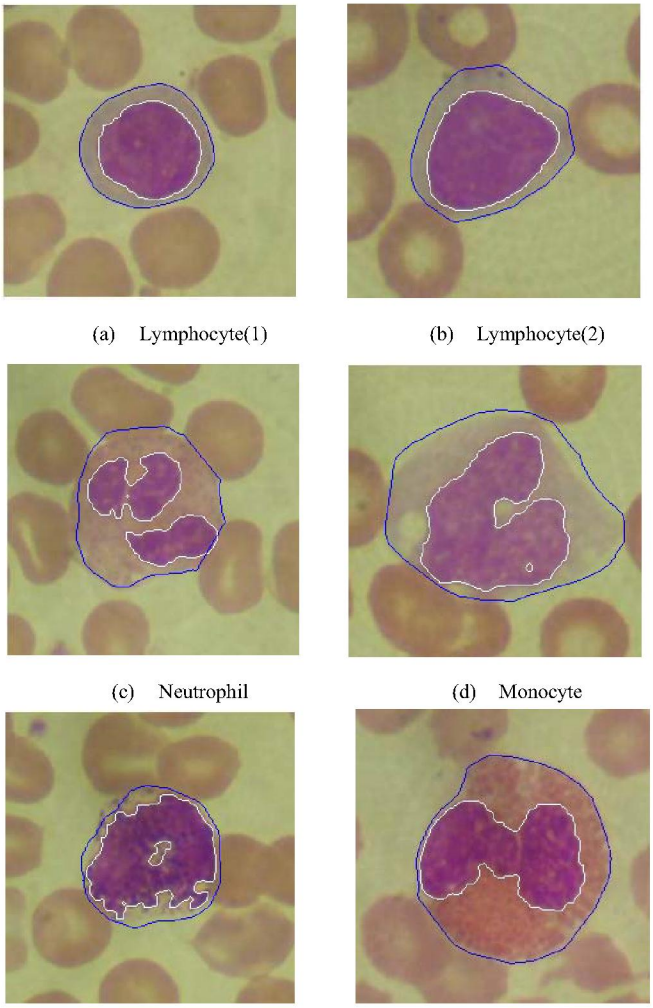


Fig. 4. Flowchart of segmentation steps

nucleus perimeter extension. The estimation of cytoplasm area is very careful step which its output is later mapped to create vector flowing gradient and guide the propagation of snake contour. Finally, the nucleus and cell boundary are segmented and able to apply for a further classification step. In this experiment, RGB color image slides of peripheral white blood cell as Lymphocyte, Monocyte, Neutrophile, Basophile and Eosinophile were sampling to test our proposed technique which some of them were RBC-touching. The final segmented results were also approved by a medical technology expert and shown in figure 5.



(a) Lymphocyte(1) (b) Lymphocyte(2)

(c) Neutrophil (d) Monocyte

(e) Basophile (f) Eosinophile

Fig.5. (a)-(b) Lymphocyte, (c) Neutrophile , (d) Monocyte, (e) Basophile, (f) Eosinophile,

V. DISCUSSION

From the experimental results of using active contour propagation to segment white blood cell, it is found that the cell segmentation by this technique is able to separate a nucleus area and cytoplasm area of WBC from an original blood cell slide image satisfactorily. For Lymphocyte and Eosinophile, the segmentation quite operates completely even though RBC touching occurs. Monocyte and Neutrophile still show some overlapping between cytoplasm boundary and RBC or over

extended contouring into plasma. In Basophile cell, the boundary between nucleus and cytoplasm are naturally unclear due to its granularity. These errors may overcome by an improvement in the primary cytoplasm area estimation step which is very important step and later used to calculate the distance mapping. If this estimation is close to a true cytoplasm area, the obtained GVF field will lead the snake contouring to fit with a true cell boundary properly. However, these inefficiencies may be also due to an unclear or a similarity of color component between cytoplasm region and plasma or red blood cell region in image slide. The color tone inconsistency also plays an important role in these problems. Clarified slide preparing and good quality of color staining process should be carefully concerned to minimize these problems. Further experiment should be emphasized on combination of GVF from distance mapping and edge detection or another powerful segmentation technique.

VI. CONCLUSION

Active contour algorithm with driven by a distance mapping from cytoplasm area estimation was performed in order to segment a cell component of white blood cell into nucleus region and cytoplasm region. The surrounding cytoplasm area was primary approximate by using an enlargement of nucleus convex hull. The segmentation results show that our proposed contouring technique is able to separate the nucleus and cytoplasm region promisingly.

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