An Anemia Recognition System Based on Blood Smear Image

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Abstract

Anemia diseases have become a worldwide disease. In today’s medical technology in diagnose for Red Blood Cells (RBC), medical personnel take the blood sample of patients and through the microscope to observe the blood smear. Blood cell images play an important role in helping diagnosis of the anemia. According to the quantity, size and the contour of the RBC and RBC’s disc, the professional can diagnose whether the patient have the symptoms. The Genetic Algorithm Based Parameter Detector (GABPD) helps decide each feature optimal parameter value to recognize the RBC.

The research using different 45 blood smear test images and the total number of the RBC is about 1150. The experimental illustrates the RBC can be correctly segmented by the proposed method and the RBC recognition rate can reach 90%. The conclusion is that the sleep quality of the college students seems poor, and going to PE class turns out to be the main way of doing exercise.

Keywords: RBC, Anemia, Image Segmentation.

Introduction

Anemia diseases have become a worldwide disease. Caused by the body can’t produce enough hemoglobin. When the symptom happens, the person will feel weak and exhausted, depressed mood and irritability anxiety. Other symptoms include fatigue, dizziness, syncope, apathy, anxiety. If symptoms are mild, diet therapy can recover, else if symptoms are serious, the need for medical treatment. For these symptoms, the patient’s Red blood cells (RBC) are abnormal and more fragile. In today's medical technology in diagnose for RBC, medical personnel take the blood sample of patients and through the microscope to observe the blood smear. Blood cell images play an important role in helping diagnosis of the anemia. According to the quantity, size and the contour of the RBC and RBC’s disc, the professional can diagnose whether the patient have the symptoms. Figure 1 is the blood image including normal and abnormal (Drepanocyte type) cells.

Anemia can separated for many types, such as bad hematopoietic (aplastic anemia, thalassemia), hemolytic damage (hemolytic anemia) or excessive bleeding (iron deficiency anemia), anemia occur according to different regions and environment, in some Southeast Asian countries, or the Mediterranean countries, the incidence of thalassemia is relatively higher. Therefore, to develop an automatic computer processing software to process blood smear images can help the professional observe the diseases occur in the parts of body and diagnosis the critical diseases. However, in many blood smear images, red blood cells often overlap and make the recognition difficult. This paper purpose an efficient segmentation method, which combine two methods, erosion and dilation operations method and watershed segmentation. Through the purposed method, we can disconnect the adjacent cells. Then biconcave disk segmentation can achieve from the object histogram equalization and threshold definition. The recognition optimal parameter can obtain through the Genetic algorithm based parameter detector (GABPD). The purposed system can provide the amount of RBC, the biconcave disk area and the RBC type of recognition with useful parameters to help medical do more accurate diagnosis.

Related Work

Image segmentation is one of the most widely studied in image analysis. Many of image segmentation methods have
been proposed such as [1][5]. One of the popular methods for image segmentation is using the statistical model, such as the 

Gamma correction is a nonlinear operation used on gray-level images analysis. The Gamma correction image be 

\[ I_{\gamma}(x,y) = 255 \times \left( \frac{I(x,y) - I_{\min}}{I_{\max} - I_{\min}} \right)^\gamma. \]  

(1)

Where the input image I is assumed to be a gray-level image range from 0 to 255, \( I_{\max} \) and \( I_{\min} \) stand for the maximum and minimum gray value in I. The difference of \( \gamma \) value is shown in Fig. 2.

**Local Gamma Correction**

Uneven illumination always affects image quality seriously in practice. To weaken illumination effect on image quality, we use the Local Gamma Correction method [12]. The image \( I_{\gamma} \) divide into m equal sized blocks \( [I_1, I_2, \ldots, I_m] \). Then respectively to calculate \( I_{\text{local}} \), the function as follows:

\[ I_{\text{local}}(x,y) = \begin{cases} \frac{I(x,y) - I_{\text{local min}}}{I_{\text{local max}} - I_{\text{local min}}} \\ \frac{I(x,y) - I_{\text{local min}}}{I_{\text{local max}} - I_{\text{local min}}} \\ \frac{I(x,y) - I_{\text{local min}}}{I_{\text{local max}} - I_{\text{local min}}} \\ \frac{I(x,y) - I_{\text{local min}}}{I_{\text{local max}} - I_{\text{local min}}} \end{cases} \times 255 \quad \text{if} \quad I(x,y) \geq \gamma I_{\text{local min}} \quad (2)

Where \( I_{\gamma} \) is the gamma correction image, \( I_{\text{local}} \) is the gray level pixel in each blocks correspond \( I(x,y) \). \( I_{\text{local min}} \) and \( I_{\text{local max}} \) stand for the maximum and minimum gray value in \( I_{\text{local}} \). \( I_{\text{local min}} \) stand for the mean value in \( I_{\text{local}} \).

**Otsu’s thresholded method**

Otsu’s method [13] is used to automatically perform histogram shape-based image threshold, or reduce the gray-level image to a binary image. The procedure is very simple. The algorithm assumes that the image to be thresholded contains two classes of pixels, then decide the optimal threshold to separate two classes by statistical. The Otsu’s method is an unsupervised method of automatic threshold selection for different image segmentation. For these reasons, we decided to apply the Otsu’s method for image binarization.

The local gamma correction image \( I_{\gamma} \) uses it to specify the threshold \( T_o \). The pixel \((i,j)\) in a binary image \( I_{\text{local}}(i,j) \) is following as:

**Fig. 1. The correspond curve of different \( \gamma \)**

**Fig. 2 Gamma correction image with different \( r \)**
\[ I_{\text{cell}}(i, j) = \begin{cases} 0, & I_i(i, j) \geq T_n \\ 1, & I_i(i, j) < T_n \end{cases} \] (3)

**watershed**

The watershed algorithm [14][16] is usually implemented by simulating a flooding process. During the processing, the image is taken as a surface of mountainous terrain, and the gray value of each pixel denotes the altitude of that point. In this terrain, there exist deep valleys (minima), high ridges (watershed), and steep or gentle hillsides (catchment basins). Firstly, holes are pierced in each minimum, and then this surface is slowly immersed into a lake. Starting from the minima of lowest altitude, water will progressively fill up the different catchment basins.

**Methods of Segmentation**

In diagnosis anemia from the blood smear images, some of cells overlap and make the diagnosis difficult. This paper purpose an automatic processing system to help the medical personal which combine two steps, segmentation and recognition. In this chapter we introduce the segmentation part, including RBC segmentation and biconcave disk segmentation.

Then we separate the single cells image and multi-connected cells image from the binary image. In the multi-connected cells, the cells overlapped with others need to be segment. In here, the method of erosion and dilation operations used to disconnect the multi-connected cells. However, if the cells’ overlapping region too much, the erosion and dilation operations can’t work effectively. Therefore, we use watershed algorithm to solve the above problem. Watershed method can produce good results for separating the high overlapping cells. However, the problem of over-segmentation is usually unavoidable in watershed, so we use the region-merging to combine the fragment regions to meaningful regions after the watershed method.

1. **Preprocessing**

In the preprocessing step, because a given frequency luminance is more important in distinguishing visual features and grayscale, we convert the original RGB image to grayscale image. Then use gamma correction method and local gamma correction method to improve the contrast of the image.

Uneven illumination always affects image quality seriously in practice. If only use the gamma correction on an uneven illumination image, image may have the miscarriage of justice on the binarization step. Local gamma correction image divide into several equal sized blocks. Then respectively use gamma correction method on each region. In this way, the above problem could be solved. To separate the object and background, we use Otsu’s method after doing gamma correction and local gamma correction. The Otsu’s method is an unsupervised method of automatic threshold selection for image segmentation. After the preprocessing, the original image converts into binary image. Fig. 3 shows the image of the preprocessing steps.

2. **Cells segmentation**

Because of some pictures take from different angles, cells overlap with others, so directly calculate the cells area is inaccurate. Therefore, we separate the single cells image and the multiple-connected cells image and then do the follow-up segmentation methods on the multiple-connected cells image. In order to know each of the single cell area, we filling in the each cell to let the area be stuffed. In this step, we evaluate the single cell area interval from the images. It means when the cells area is located in this interval, we define it single cell. But if the cells area over the interval, we define it multiple-connected cell.

To consider the different of the blood cell images, we define \( Q \pm k \times \sigma \) for the single cell area interval. Where \( \sigma \) stand for the standard deviation of all of the cells area in image, \( k \) is the constant which optimal value defined by genetic algorithm.

The single cells area upper bound \( T_{sc} \) and lower bound \( B_{sc} \) is defined as:

\[
T_{sc} = Q + k \times \sigma \\
B_{sc} = Q - k \times \sigma
\] (4) (5)

According to the definition of the single cells area, two output images \( I_{sc} \) and \( I_{mc} \) being generated. That \( I_{sc} \) is the image which consists of the single cells area between \( T_{sc} \) and \( B_{sc} \). \( I_{mc} \) is the image which consists of the cells area over \( T_{sc} \) and need segmentation process.

In this section, we use a series of \( I_{mc} \) \( \ominus \) and \( I_{mc} \oplus \ominus \) operations on the \( I_{mc} \) image. Where \( \ominus \) stands for the 3×3 structure element of 4-neighbors as erosion and \( \oplus \) stand for dilation.

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Fig. 3 (a) Original image, (b) Grayscale image, (c) Gamma correction with (b), (d) Local gamma correction with (c), (e) Binary image

Fig. 4 The 3×3 structure element of 4-neighbors
For $I_{MC}$, the erosion and dilation operations steps as follows:

Step1: For each overlapping cell do $I_{MC} \ast$ b iteratively $r/2$ times.

Step2: Then do $I_{MC} \oplus$ b with all the cells. When the disconnect cells intersect with others, retain the intersect regions and avoid connection.

Step3: Repeat step 2 until dilation $r/2$ times.

The number of erosion times is equal to dilation times and it decides based on the single cell radius $r$. The radius $r$ can be calculated from single cells upper bound area $T_{sc}$ refer as (4). By observation, we define $r/2$ times because of avoiding iteration too many times leading the cells contour deformation.

$$r = \sqrt{T_{sc}/\pi}$$  \hspace{1cm} (6)

But not all the multi-connected cells could be separated by the above steps. When the two cells have too much overlapping region, the erosion and dilation operations can’t disconnect effectively. Therefore, we use watershed algorithm to solve the above problem.

The watershed algorithm used to split the overlapping object. Watershed algorithm produces good results for gray level images with different minima and catchment basins. However, the problems of over-segmentation are usually unavoidable, so we use the watershed algorithm on the overlapping cells which can’t be separated by erosion and dilation operations. In this way, it can minimize the over-segmentation regions. The $I_{MC}$ image cells can’t disconnect by erosion and dilation operations as shown in Fig. 5 (a) and the image after watershed algorithm as shown in Fig. 5 (b).

The watershed algorithm causes the over-segmentation unavoidably. Region-merging can eliminate false boundaries and spurious regions by merging adjacent regions that belong to the same object. Therefore, we merge the over-segmented regions into more meaningful regions. The region-merging steps as follows:

Step1: Calculate each region area from the over-segmentation image.

Step2: Find the min region $R_1$ in each region.

Step3: Find the minimum region adjacent with $R_1$ defines to $R_2$.

Step4: If $R_1 + R_2 < T_{sc}$, merge the two regions $R_1 \cup R_2$.

Step5: Repeat step 1-4 until no region can be merged.

The merging image shows in Fig. 5 (c). After the region-merging, the RBC segmentation is finish.

Fig. 5 (a) The image which cells can’t be disconnected, (b) The image of watershed with (a), (c) The image of region-merging with (b)

3. RBC’s biconcave disk segmentation

The normal RBC is shaped as biconcave disk, means the disk that is thinner in the center area then on the outside. The professor can diagnose whether the patients’ Suffering from anemia diseases by observe the biconcave disk size and the shape of RBC. In this paragraph, we use two steps to extract the disc in the RBC. Because the biconcave disk color is closer to the center area color in grayscale image, some disks may lost by directly using the Otsu’s method on the grayscale image. Therefore, we raise the RBC region contrast respectively in order to retain the disc area not lost after binarization.

Object histogram equalization with Otsu

We can get the each RBC location from the chapter 3.1, then respectively to do the function in each RBC region:

$$I_n(i,j)=255 \times \frac{I_n(i,j)-I_{\min}}{I_{\max}-I_{\min}}.$$  \hspace{1cm} (7)

Where $I_n$ is the region n of the RBC with grayscale image, $I_{\max}$ and $I_{\min}$ stand for the maximum and minimum gray value in $I_n$. $I_n$ is the object $I_n$ using histogram equalization.

According the above method, we extract the region inside the RBC. But some of the regions are not the disks instead of the noises. Therefore, according to the difference of gray-level color, we can decide whether the extract regions correspond with the biconcave disk. While the degree of difference is higher than threshold $T$, we define the region as center area and if lower than $T$, we define as biconcave disk. The function as follow:

$$T=\frac{\text{Mean}_{\text{center}}-\text{Mean}_{\text{disk}}}{\sigma_{\text{center}}+\sigma_{\text{disk}}} 	imes k.$$  \hspace{1cm} (8)

Where $\text{Mean}_{\text{center}}$ and $\text{Mean}_{\text{disk}}$ is the mean of gray-level pixel in center area and biconcave disk. $k$ stand for the constant and $\sigma_{\text{center}}$ and $\sigma_{\text{disk}}$ stand for the standard deviation of the center area and biconcave disk.

Recognition

In this chapter, we extract the non-overlapping RBC image $I_{SC}$ and do the shape features recognition.

Fig. 6 is the most common four different types of RBC, normocyte, acanthocyte, drepanocyte and teardrop. If the blood smear images contain the cells except normocyte type, we speculate the patient is likely to infect blood diseases. We define eight features $F_1$-$F_8$ from each cell and count each RBC types features representative. Then calculate feature distance difference between the identified RBC and each types features.

(a)  (b)  (c)
representative. Each feature has its own weight. Through genetic algorithm based parameter detector (GABPD) to decide the optimal weight value for these eight features to help us identify the RBC.

![Image](image.png)

(a) Normocyte (b) Acanthocyte (c) Drepanocyte (d) Teardrop

Fig. 6 The four types of the RBC samples.

The eight features we define as follows:

\[ F_1 = \frac{A_c}{(\frac{D_c}{2})^2 \times \pi} \]  \hspace{1cm} (9)
\[ F_2 = \frac{A_c}{(\frac{D_c}{2})^2 \times \pi} \]  \hspace{1cm} (10)

Where \( P_c \) stand for the perimeter and \( D_c \) stand for the longest distance of the cell, \( A_c \) stand for the cell area. \( F_1 \) and \( F_2 \) are the area ratio. The value of \( F_1 \) and \( F_2 \) fall into the range \([0,1]\). While the value of \( F_1 \) or \( F_2 \) closer to 1, the cell is closer to rotundity. As a rule, the normocyte features \( F_1 \) and \( F_2 \) values are closer to 1. Compare to normocyte, the acanthocyte feature \( F_2 \) and the Drepanocyte feature \( F_1 \) usually have lower value.

\[ F_3 = \frac{L_{q1}}{L_s} \]  \hspace{1cm} (11)
\[ F_4 = \frac{L_{q3}}{L_s} \]  \hspace{1cm} (12)

We divide the cell of long axis into quartiles, where \( q1, q2, q3 \) stand for the each point of equal diversion. \( L_{q1}, L_{q2}, L_{q3} \) represent the line which perpendicular to the \( q1, q2, q3 \) and stretch to the edge of the area. \( L_s \) is known as short axis. The illustration shows in Fig. 7(a). The difference of \( F_3 \) and \( F_4 \) can help to separate the teardrop type. As a rule, the teardrop cell difference usually higher and others type difference usually lower.

Feature 5 to 8 is the area out of the cell which through the minimum bounding rectangle to surround the cell. We divide the rectangle to four regions by center of the rectangle stretch the line which perpendicular to the edge. Then count the non-cell pixels from each region and sort these non-cell regions in ascending assigned \( A_5, A_6, ..., A_8 \). The illustration shows in Fig. (b). The ratio of each regions to the cell area be define as feature \( F_5, F_6, ..., F_8 \). The purpose of each outside region divided by the cell area is normalization to \([0,1]\). As a rule, the teardrop types and drepanocytes types of features \( F_5-F_8 \) difference usually higher than normocyte type and acanthocyte type.

\[ F_5 = \frac{A_5}{A_c} \]  \hspace{1cm} (13)
\[ F_6 = \frac{A_6}{A_c} \]  \hspace{1cm} (14)
\[ F_7 = \frac{A_7}{A_c} \]  \hspace{1cm} (15)
\[ F_8 = \frac{A_8}{A_c} \]  \hspace{1cm} (16)

After computing eight feature values from all the RBC, we take a part of blood cells as the training data. Then, we classify the training data into four types of blood cell. We compute the average value for each feature and each type gain eight average feature values, and then we take these feature values as the type feature. Each feature has different weight, exponential weight and constant weight. By genetic algorithm, we can obtain the best weight of the training data. Then calculate feature distance difference between the RBC and each types features representative from the training data. Then we have four distance difference from the four types of blood. We define the RBC belong minimum distance difference type.

![Image](image.png)

(a) The illustration diagram of the each axis, (b) The illustration diagram of the outside regions

1. **Genetic algorithm based parameter detector (GABPD)**

In the research, Genetic Algorithm Based Parameter Detector (GABPD) is used to determine the most optimal weights. In this chapter, we define the GABPD and the process of GABPD, including initial, crossover, mutation, selection. The method used on two parts, RBC segmentation and recognition.
In GABPD, an initial population consisting of $N$ chromosomes is specified and then the fitness of each chromosome is calculated for further operation. In order to evolve the optimal solution, the genetic algorithm is used to include repeatedly mutation, crossover and selection operations.

In crossover operation, similarly a random number generator is used to designate $N'$ pairs of chromosomes from the $N$ reserved chromosomes. For each chromosome pair, each bits randomly decide crossover or not.

In mutation operation, for each of the $N$ reserved chromosomes, the GABPD uses a random number generator to specify one bit $b$ for each of $s_1, s_2, ..., s_k$. Then, $b$ is replaced by $\neg b$ to generate a new chromosome, where $\neg$ signifies the operator “NOT.”

In the selection operation, GABPD select chromosomes as parents from the chromosomes reserved in the previous iteration and the chromosomes are created in the mutation and crossover operations. GABPD iteratively performs these three operations — mutation, crossover, and selection, until one chromosome in the population satisfies the predefined fitness or that the number of iterations is greater than a given number MAX_NO_RUN. Finally, the GABPD extracts the most fitted chromosome and assigns the values decoded from the chromosome to produce the values.

### 2. RBC segmentation and recognition parameter

In RBC segmentation, the Gamma correction value $r_j$, local Gamma correction value $r_k$ and the single cells area threshold constant $k$ are determined by GABPD. The chromosome is combined with three binary substrings which are $s_{r_1}, s_{r_2}, s_K$, $n_{r_1}, n_{r_2}, n_K$ denote the number of bit of $s_{r_1}, s_{r_2}, s_K$ and $n_{r_1}, n_{r_2}, n_K$ are the number that bit value is 1 in the substring. The corresponding relation between each chromosome and parameters $r_1, r_2, k$ are defined as follows:

$$y_1 = \frac{y_{k1}}{y_{r1}}$$ (17)

$$y_2 = \frac{y_{k2}}{y_{r1}}$$ (18)

$$k = \frac{y_{k1}}{y_{r2}}$$ (19)

fitness is the Relative Area Error (RAE) [17].

In recognition phase, each feature $F_i$ contains different proportion of weights including constant weight $w_i$ and exponential weight $r_i$. The chromosome is combined with 16 binary substrings $S_1$-$S_{16}$, where $S_1$-$S_{k}$ stand for the binary string of parameter $r_1$-$r_k$ and $S_1$-$S_{16}$ stand for the binary string of parameter $r_1$-$r_{16}$. Besides, the number of bits of substring are $n_{r_1}$-$n_{r_16}$ and $n_{1}^{r_1}$-$n_{16}^{r_1}$ is the number that bit value is 1 in the substring. The corresponding relation between each chromosome and parameter $w_i$-$w_{16}$, $r_1$-$r_{16}$ are defined as follows:

$$w_i = \frac{n_{1}^{w_i}}{n_{1}^{w_i} + n_{k}^{w_i}} \ell = 1, 2, ..., 6$$ (20)

$$r_i = \frac{n_{r_i}^{r_i}}{\sum_{i=1}^{16} n_{r_i}^{r_i}} i = 9, 10, ..., 16$$ (21)

The fitness defined as follows:

$$f = \min \left( \frac{\sum_{i=1}^{16} y_i}{\sum_{j=1}^{k} y_j} \left| F_i - F_{j,k} \right| \right) \quad j = 1, ..., 4, k = 1, 2$$ (22)

$F_{i,j,k}$ stands for all the $j$ RBC types, each type divide to $k$ cluster, each cluster has $i$ features. $F_i$ stands for the eight feature in each cells, $j$ stand for the RBC types, total have four types, $k$ stand for each RBC types divide into two cluster.

#### Experimental results

We select 45 microscopic images be the test images. For 36 microscopic images are consisted of each 680x512 pixels with 24-bits and else 9 microscopic images consisted of different size pixels with 24-bits and the total number of cells in test images is nearly 1150 cells.

#### Evaluative criteria

For the RBC segmentation, Misclassification Error (ME) [17], Relative Area Error (RAE) [17], Modified Hausdorff Distance (MHD) [17], and Relative Distance Error (RDE) [18] are often adopted to evaluate the segmentation errors. For the normalization, we not consider the cells which are incomplete or touch to the side.

In the biconcave disk segmentation, there is no other purposeful method cab be compared. In here, we use two criteria, Recall and Precision to evaluation our segmentation method, the corresponding relation between each ground-truth and our method are defined as Table 1.

<table>
<thead>
<tr>
<th>TABLE I. TP, FP, FN, TN DEFINITION</th>
<th>Ground-truth</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Our method</strong></td>
<td><strong>Ground-truth</strong></td>
</tr>
<tr>
<td><strong>True</strong></td>
<td><strong>TP</strong></td>
</tr>
<tr>
<td><strong>False</strong></td>
<td><strong>FP</strong></td>
</tr>
<tr>
<td><strong>True</strong></td>
<td><strong>FN</strong></td>
</tr>
<tr>
<td><strong>False</strong></td>
<td><strong>TN</strong></td>
</tr>
</tbody>
</table>

Recall : $\frac{TP}{TP + FN}$ (23)

Precision : $\frac{TP}{TP + FP}$ (24)

In order to evaluate our proposed methods, the experimental results divide into three parts, RBC segmentation, biconcave disk segmentation and RBC recognition.
**RBC segmentation**

The test images were used to compute the optimal values of parameters are $r_1=2.7$, $r_2=2.8$, $k=1.6$. Fig. 9 shows five different test images compare to others method (including Level-set [191719, 0] and Fuzzy C-means (FCM) [181]), the figure that contains less number of cells and has the less overlap proportion is shown in Fig. 8 (a), and the performance of level-set and FCM of Fig. 8 (a) are both have ideal performance. In the other hand, the blood cell which has a higher overlap proportion is both hard to use the level-set and FCM to separate the cells and the figure is shown in Fig. 8 (b). However, the method we proposed that can segment well. Compare with other methods, the upper bound of $T_{SC}$ defined in our method will obvious affect the accuracy of segment. If the image that contains more connected RBC or has less cell components, the first quartile $Q_1$ which the difference of variance will become large, and increase the error amount with $T_{SC}$ and affected the accuracy of segment directly.

![Fig. 8](image)

**Fig. 8** Different test images segmentation by Level-set, FCM and our purposed method.

Fig. 9 demonstrates that the ground-truth image and segmented images by using level-set method, FCM method and our purposed method respectively. In the Fig. 9 (c), level-set method cannot effectively segment the cells and some overlapped cells cannot separate into distinct cells. Although FCM method is more accurate than level-set method as Fig. 9 (d), it will produce excessive noise. However, our purposed RBC segmentation method as Fig. 9 (e), can more successfully segment the cells than Level-set method and less the noise being generated. Table II shows the averages of ME, RAE, MHD and RDE segmenting errors.

![Fig. 9](image)

**Fig. 9** The ground-truth image and segmented images by using level-set method, FCM method and our purposed method respectively

**TABLE II. THE AVERAGE OF ME, RAE, MHD AND RDE**

<table>
<thead>
<tr>
<th>Method</th>
<th>ME</th>
<th>RAE</th>
<th>MHD</th>
<th>RDE</th>
</tr>
</thead>
<tbody>
<tr>
<td>FCM method</td>
<td>0.457</td>
<td>0.298</td>
<td>22.954</td>
<td>21.620</td>
</tr>
<tr>
<td>Level-set method</td>
<td>0.451</td>
<td>0.352</td>
<td>20.646</td>
<td>20.680</td>
</tr>
<tr>
<td>Our purpose method</td>
<td>0.226</td>
<td>0.107</td>
<td>12.240</td>
<td>14.238</td>
</tr>
</tbody>
</table>

**Biconcave disk segmentation**

In the biconcave disk segmentation experiment, the system random select 9 images to calculate the sensitivity and accuracy. Through experiment, the best perform accuracy while $k=1.2$, Table III shows different parameter $k$ correspond the average sensitivity and accuracy and $T_{IV}$ is the parameter $k=1.2$ correspond 9 test images accuracy.

**TABLE III. DIFFERENT PARAMETER $k$ CORRESPOND THE AVERAGE ACCURACY**
TABLE IV. THE SENSITIVITY AND ACCURACY WITH 9 TEST IMAGES

<table>
<thead>
<tr>
<th>Test images</th>
<th>Recall(%)</th>
<th>Precision(%)</th>
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<tbody>
<tr>
<td>1</td>
<td>79.72</td>
<td>60.38</td>
</tr>
<tr>
<td>2</td>
<td>90.73</td>
<td>47.06</td>
</tr>
<tr>
<td>3</td>
<td>86.74</td>
<td>50.54</td>
</tr>
<tr>
<td>4</td>
<td>84.02</td>
<td>68.5</td>
</tr>
<tr>
<td>5</td>
<td>79.45</td>
<td>66.29</td>
</tr>
</tbody>
</table>

TABLE V. THE WEIGHT OF \(w_i - w_0\) AND \(r_i - r_0\)

<table>
<thead>
<tr>
<th>i</th>
<th>(w_i)</th>
<th>(r_i)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.1818</td>
<td>0.125</td>
</tr>
<tr>
<td>2</td>
<td>0.1591</td>
<td>0.175</td>
</tr>
<tr>
<td>3</td>
<td>0.0682</td>
<td>0.2</td>
</tr>
<tr>
<td>4</td>
<td>0.1136</td>
<td>0.1</td>
</tr>
<tr>
<td>5</td>
<td>0.09</td>
<td>0.15</td>
</tr>
<tr>
<td>6</td>
<td>0.1591</td>
<td>0.175</td>
</tr>
<tr>
<td>7</td>
<td>0.1136</td>
<td>0.025</td>
</tr>
<tr>
<td>8</td>
<td>0.1136</td>
<td>0.05</td>
</tr>
</tbody>
</table>

We get the 16 values \(w_i - w_0\) and \(r_i - r_0\) as identification of parameters. In the experiment, we random select 285 cells to be the test data, the results obtained recognition accuracy up to 90% (256 cells).

Conclusions

For assisting the medical analyzes properties of cells and counts the number of cells, in this paper, an automatic segmentation by erosion and dilation operations and watershed segmentation, and recognition system by using GABPD provide useful data for medical personal do a more accurate determination for the symptom. The experimental results demonstrate that the system can effectively segment cells from an image than other compared methods.

Reference


