shape analysis, blood cells

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BLOOD CELLS ANALYSIS BASED ON SIMPLE GEOMETRICAL SHAPE DESCRIPTORS

In the paper we present some results concerning application of simple shape parameters that are successfully used to distinguish between normal and pathological blood cells. All descriptors are based on shape area and its perimeter. We use five parameters that are automatically calculated for objects pointed out in the analyzed image with the help of our software. The experiments performed on the same set of tested images as in [3] let us draw the same conclusions as those reported in [3] where fractal analysis to shape has been used.

1. INTRODUCTION

Nowadays shape analysis methods are used very often to solve many practical problems [2]. Every year more and more scientists, working in image processing, try to explore information that is hidden in a picture. Shape analysis methods play an important role for object recognition, matching, registration and classification. State of the art of the discipline is presented e.g. in [5], [6] and in the ample literature given there.

In this work we analyse images, available at http://www.hematologica.pl, which show healthy blood cells and pathological ones. Parameters (described in the next section) characterize blood cell shapes adequately and give us the possibility of recognition, registration and classification of different abnormal blood cells. The aim of this work is to check experimentally usefulness of some parameters to description of abnormal blood cells which can characterize some pathologies related to changes in shapes of blood cells. The main our assumption is that blood cells are treated as 2D objects. Other approach to the problem is presented in [3], where fractal dimension to differentiate between normal and pathological blood cells has been used.

2. SHAPE DESCRIPTORS

Denote by X a figure on the plane. Let A(X) and P(X) are respectively the area and the perimeter of the figure X. The first parameter used for description of a shape is

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$$\frac{O_{\min}}{O_{\max}} \tag{1}$$

where O_{min} (O_{max}) is minimal (maximal) distance from a center of gravity to the boundary of *X*, respectively.

The center of gravity $(\overline{x}, \overline{y})$ of *X* we compute by the formula

$$\overline{x} = \frac{\sum_{i,j:(x_i,y_j)\in X} x_i}{A(X)} \quad , \qquad \overline{y} = \frac{\sum_{i,j:(x_i,y_j)\in X} y_j}{A(X)}$$
(2)

The second parameter is related to a circle. It expresses deviation of X from a circle and is given by

$$\frac{4\pi A(X)}{\left(P(X)\right)^2}\tag{3}$$

The choice of this coefficient is natural because it is easy to see that normal cells are like discs in contrast to pathological ones. For any disc the parameter defined by (3) equals to 1 while for any other figure it has the value less than 1. The smaller that number is, the greater the deviation is. This number is called circularity. In the literature [2] that parameter has the form

$$\frac{1-4\pi A(X)}{\left(P(X)\right)^2}\tag{4}$$

The third parameter, which describes a shape, represents a figure deviation from its convex hull. It is defined as a quotient of a shape area to its convex hull area i.e.

$$\frac{A(X)}{A(conv(X))} \tag{5}$$

where A(conv(X)) denotes the area of the convex hull of the figure X.

In the literature [2] that descriptor is called convexity. For a convex figure that parameter is equal to 1, but for not convex one it is less than 1. We compute convex hull by means of Graham algorithm [1]. The next parameter used in this work is similar to the previous one. Instead of the area A(X) we use the perimeter P(X) i.e.

$$\frac{P(conv(X))}{P(X)} \tag{6}$$

where P(conv(X)) denotes the perimeter of the convex hull of the figure X.

It characterizes how strongly a contour of X is winding. For blood cells we can observe that the contour of normal blood cells is not winding in contrast to abnormal ones. The value of that parameter is less or equal to 1. The smaller that number is, the greater the winding is. The name for that parameter is rugosity. The last descriptor in this article is given by the formulas:

$$a(X) = \lambda(X) + \sqrt{\left(\lambda(X)\right)^2 - \frac{A(X)}{\pi}}, \quad b(X) = \frac{A(X)}{\pi a(X)}, \tag{7}$$

where

$$\lambda(X) = \frac{1}{3} \left(\sqrt{\frac{A(X)}{\pi}} + \frac{P(X)}{\pi} \right)$$

The parameter a(X) (b(X)) is the length of the long (short) semi-axes of the ellipse with the area A(X) and the perimeter P(X), respectively. How we can see all the parameters described above are based on area and perimeter of a given figure. The area is calculated with the help of the algorithm described in [2]. It is a recursive algorithm, which fills a given contour with the selected color and counts marked pixels. The perimeter is calculated using the following formula:

$$P(X) = \sum_{i} \sqrt{(x_{i} - x_{i-1})^{2} + (y_{i} - y_{i-1})^{2}}$$
(8)

where (x_i, y_i) is a sequence of contour points of the figure *X*.

In Fig.1 some of shape parameters are presented. Basing on definitions of parameters given above we have prepared suitable software which has been used for performing analysis described in Section 3. The program finds the outer contour of a shape pointed out in the image and calculates those five parameters.



Fig.1. Examples of different geometrical parameters for figure X: **a**) O_{min} and O_{max} distances; **b**) the convex hull; **c**) a(X) and b(X) are respectively lengths of the long and short semi-axes of an ellipse having area A(X) and perimeter P(X)

3. ANALYSIS OF BLOOD CELLS

For analysis we have chosen very good quality original images from [4]. One of the images showing normal and pathological blood cells (indicated by the arrow) is presented in Fig. 2. At first color 8-bits images had been changed into gray-scale bitmaps and then after sharpening and contrast enhancement we have obtained images which could be analyzed by our software. Image processing has been performed with the help of Photoshop program. Fig. 3 shows the image after processing. In Fig. 4 we have chosen 10 blood cells. Those numbered from 1 to 5 are classified as normal while those from 6 to 10 are pathological ones. All parameters calculated for chosen blood cells are presented in Table 1.



Fig.2. Original image with normal and pathological blood cells. Arrow indicates the two sample pathological cells (reproduced with permission from [4])



Fig.3. Image after processing with the help of Photoshop program



Fig.4. Blood cells chosen to analysis are numbered

No.	Blood cell	O _{min} /O _{max}	Circularity	Convexity	Rugosity	A(X)	b(X)	b(X)/a(X)
1	Normal	1,124	0,952	0,973	0,944	16,631	11,558	0,695
2	Normal	0,368	0,944	0,978	0,946	17,564	11,854	0,675
3	Normal	0,440	0,933	0,976	0,946	17,815	11,543	0,648
4	Normal	0,483	0,916	0,965	0,932	17,363	10,648	0,613
5	Normal	0,480	0,901	0,969	0,930	19,786	11,604	0,586
6	Pathological	0,534	0,524	0,794	0,802	25,807	6,372	0,247
7	Pathological	0,635	0,585	0,822	0,856	20,634	5,849	0,283
8	Pathological	0,604	0,601	0,841	0,851	21,459	6,309	0,294
9	Pathological	0,466	0,385	0,734	0,764	30,178	5,248	0,174
10	Pathological	0,425	0,719	0,907	0,865	22,849	8,679	0,380

Tab.1. Results of blood cells analysis

4. CONCLUSIONS

From Table 1 it is easily seen that circularity, convexity and rugosity significantly differentiate between normal and pathological blood cells. Circularity e.g. for normal blood cells is greater than 0.9 while for pathological ones that parameter is distinctly smaller than 0.9. The parameter which even better indicates differences between normal and pathological blood cells is the ratio b(X)/a(X). The value of that parameter is nearly two times smaller for pathological blood cells in comparison with normal ones. Similar results we have also obtained for a number of different images. Using the parameters mentioned above and additionally a fractal dimension, as it has been showed in [3], it is possibly to classify blood cells. Next, the process of recognition and registration of pathological blood cells in the images one can make automatically. However much more images should be analyzed to obtain statistical verification of the results reported here.

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