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FOURIER ANALYSIS IN CLASSIFICATION OF BLOOD CELLS

In the paper we present some results concerning the usage of Fourier analysis which we can successfully apply to distinguish between normal and pathological blood cells. We use special area function and different number of Fourier descriptors that are automatically calculated for all objects pointed out in an image. Calculations are performed with the help of the software made by the first author. Experiments performed on the same set of tested images as in [3] and [5] draw as to the same conclusions as there in [3] where the fractal analysis to shape has been used and in [5] where simple geometrical shape parameters have been applied. Other application of Fourier analysis one can find in [9].

1. INTRODUCTION

Currently shape analysis for the sake of many applications [2] attracts attention of many researches. One of the ways to describe shapes is Fourier analysis [7],[8],[9]. We recall some details concerning Fourier analysis in the next section. Approximating certain function by Fourier series we obtain some numbers (Fourier coefficients) and the amplitude spectrum by means of which we can characterize a shape. The amplitude spectrum allows us, for example, to differentiate between normal and pathological blood cells.. In this work we will determine one healthy blood cell as a reference one and we will investigate deviation between the other normal blood cells and the reference one and deviation between abnormal ones and the reference cell. We analyse images available from [4] which show healthy blood cells and pathological ones. The main our assumption is that blood cells are treated as 2D objects.

2. FOURIER ANALYSIS

Suppose that, we have a periodic piecewise continuous and differentiable function $f(x)$ defined on $[0,2\pi]$. We can approximate such a function by Fourier series in the following way:

$$f(x) = \frac{a_0}{2} + \sum_{k=1}^{\infty} (a_k \cos kx + b_k \sin kx) \quad (1)$$

where the Fourier coefficients are:

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$$a_k = \frac{1}{\pi} \int_{-\pi}^{\pi} f(x) \cos kx dx \quad \text{and} \quad b_k = \frac{1}{\pi} \int_{-\pi}^{\pi} f(x) \sin kx dx \quad (2)$$

We can also compute a sequence $\{A_k\}$, called the amplitude spectrum, by the formula:

$$A_k = \sqrt{a_k^2 + b_k^2} \quad (3)$$

In practice, we apply the discrete version of Fourier transform, namely we consider the value of the function $f(x)$ at N points:

$$x_r = \frac{2\pi r}{N} \quad (4)$$

Then we can write the formula:

$$f(x_r) = a_0 + \sum_{n=1}^{[(N+1)/2]-1} (a_n \cos x_r n + b_n \sin x_r n) \quad (5)$$

$$a_0 = \frac{1}{N} \sum_{r=0}^{N-1} f(x_r), \quad a_n = \frac{2}{N} \sum_{r=0}^{N-1} f(x_r) \cos x_r n, \quad b_n = \frac{2}{N} \sum_{r=0}^{N-1} f(x_r) \sin x_r n \quad (6)$$

where $r=0,1,\dots,N-1$ and $n=0,1,\dots,[(N+1)/2]-1$.

To distinguish between shapes we use normalized amplitude spectrum $\{A_k / A_0\}$ which we obtain from contour function related to the shape (e.g. area function) described in the next section.

3. AREA FUNCTION

In this section we describe one of the contour function which can be used for classification of shapes. Construction of the function is the following. First suppose that, we have all contour points $\{P_i\}$ which are extracted with the help of the algorithm presented in [2]. Denote by X a figure on the plane and by $A(X)$ its area. We search the center of gravity (center of mass) (\bar{x}, \bar{y}) of X :

$$\bar{x} = \frac{\sum_{i,j:(x_i,y_j) \in X} x_i}{A(X)}, \quad \bar{y} = \frac{\sum_{i,j:(x_i,y_j) \in X} y_j}{A(X)} \quad (7)$$

Then to determine the starting point we choose a point of the contour for which its distance from the center of gravity is maximal. Next, we rotate the shape around (\bar{x}, \bar{y}) to obtain the starting point lying on the horizontal line. In Fig. 1 the construction of the area function is showed.

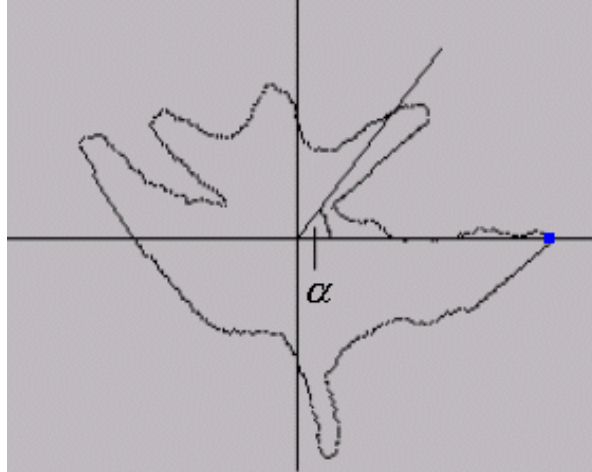


Fig.1. Construction of area function

The black square in Fig.1 denotes the maximal distant point from the center to the contour. Further changing the angle α from 1° to 180° we write down the following formula (area function):

$$f(\alpha) = \frac{A(\alpha)}{A(X)} \quad (8)$$

where $A(\alpha)$ denotes the part of area of X contained between the arms of the angle α . Dividing $A(\alpha)$ by the area of the whole figure X , we get the normalized function which does not depend on the size of the shape. Of course, we must use this function with the same angle for all compared figures. Moreover, the angle should not be too large, because in this situation we obtain only few points representing the function and finally not precise representation of the given shape. The area function can be used for analysis of any, but coherent shapes.

4. ANALYSIS OF BLOOD CELLS

The analysis have been done for images of very good quality from [4]. One of the images showing normal and pathological blood cells (indicated by the arrow) is presented in Fig. 2. Color 8-bits images first have been changed into gray-scale bitmaps and then after filtering that is after sharpening and contrast enhancement we have obtained images which could be analysed by our software. Image processing with the help of Photoshop program has been performed. In Fig. 3 we can see results after processing.

We have chosen 10 blood cells and additionally one as the reference one (indicated by 0). Those numbered from 1 to 5 are classified as normal while those from 6 to 10 are pathological ones. The choice is shown in Fig. 4. Results from analysis for different number of coefficients and different angles have been gathered in Table 1.

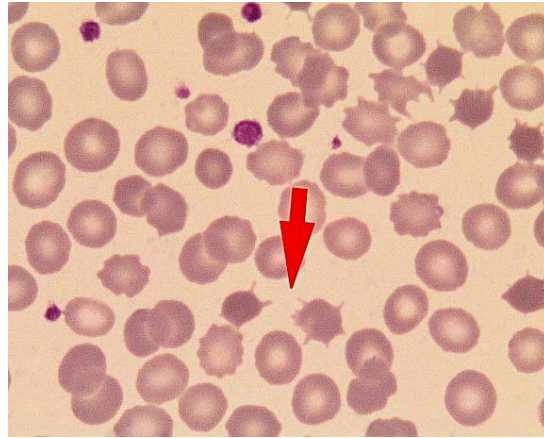


Fig.2. Original image with normal and pathological blood cells. The arrow indicates two pathological cells (reproduced with permission from [4])

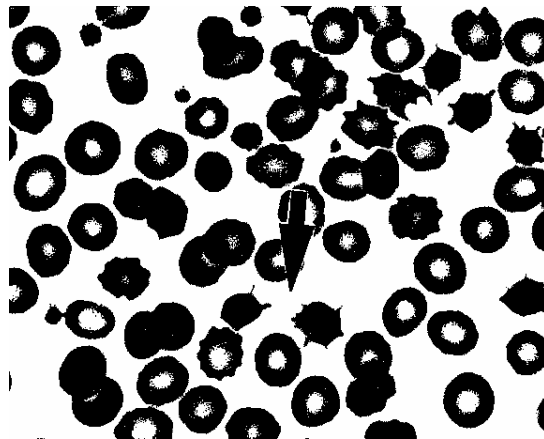


Fig.3. Image after processing with the help of Photoshop program

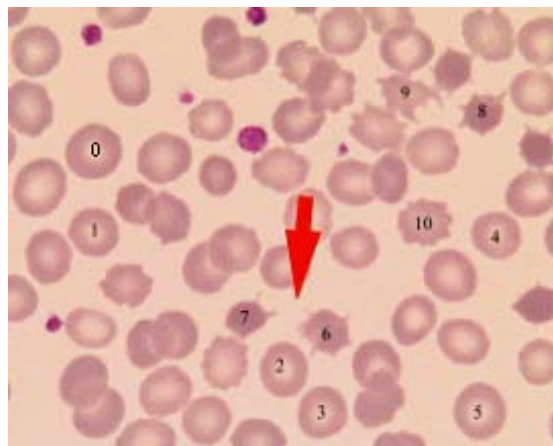


Fig.4. Blood cells chosen to analysis

After obtaining numbers $\{A_k / A_0\}$ we calculate an error, which is an Euklidean metric (see [6]). This metric denotes the difference between reference and the analysed blood cell.

$$error = \sqrt{\sum_{j=1}^n \left(\frac{A_j}{A_0} - \frac{A'_j}{A'_0} \right)^2} \quad (9)$$

where n denotes the number of Fourier coefficients and primed Fourier coefficients correspond to actually analysed blood cell.

Take notice of that summing is from j=1. That is why the numbers A_0 / A_0 and A'_0 / A'_0 are of course equal to 1. Numbers $\{A_k / A_0\}$ are obtained for reference cell while $\{A'_k / A'_0\}$ are from actually analysed blood cell. Of course the less an error is the more similar blood cell is. Below we present the table with results.

Tab.1. Results of blood cells analysis

No.	Blood cell	$A=1^\circ, n=50$	$\alpha=1^\circ, n=10.$	$A=5^\circ, n=30.$	$\alpha=5^\circ, n=10$
1	Normal	0.1334	0.0486	0.2281	0.0509
2	Normal	0.1073	0.0622	0.2063	0.0749
3	Normal	0.1597	0.1093	0.2211	0.1282
4	Normal	0.1525	0.0558	0.0909	0.0556
5	Normal	0.0781	0.0451	0.0636	0.0444
6	Pathological	0.3273	0.2270	0.2743	0.2262
7	Pathological	0.5319	0.3446	0.4670	0.3359
8	Pathological	0.4048	0.2572	0.3007	0.2441
9	Pathological	0.5889	0.5420	0.5607	0.5406
10	Pathological	0.2056	0.1534	0.2524	0.1740

5. CONCLUSIONS

From Table 1 it is easily seen that the amplitude spectrum distinguishes between normal and pathological blood cells very well. For example errors in the first column ($\alpha = 1^\circ, n= 50$) for normal blood cells are less than 0.2 while for pathological ones errors are considerably greater. Similar results we have also obtained for a number of different images. Using the error mentioned above and additionally the fractal dimension, as it has been showed in [3] or some of parameters presented in [5], it is possibly to classify blood cells much better and thereby to automatize of the process of recognition of pathological blood cells in the images. However much more images should be analysed to obtain statistical confirmation of the results reported here.

It is also worth to mention that for 2D objects, possibly scaled, rotated or moved we obtained very good results in classification purposes from Fourier analysis. The last conclusion follows from experiments, not reported here, which had been performed for different shapes related not only to blood cells. However the results of experiments are dependent on the choice of the starting point which means that the area function is not defined uniquely. That is the main disadvantage of the Fourier method when used in shape analysis.

BIBLIOGRAPHY

- [1] JANKOWSKI M.: Elements of computer graphics, Wydawnictwo Naukowo-Techniczne , Warszawa 1990, pp. 65-67, (in Polish).
- [2] KINDRATENKO V.: Development and application of image analysis techniques for identification and classification of microscopic particles, Universiteit Antwerpen, Ph.D. Thesis, Antwerpen 1997, (<http://cgi.nesa.uiuc.edu/People/kindr/phd/index.html>)
- [3] KOTARSKI W., WIDUCH S.: Shape analysis of blood cells based on fractal dimension, Journal of Medical Informatics & Technologies, Vol. 2, pp. 177-182, 2001.
- [4] LEWANDOWSKI K., HELLMAN A.: Atlas of HAEMATOLOGY, Medical University of Gdańsk, Poland, Medyczne Wydawnictwa Multimedialne 2000, (<http://www.hematologica.pl>)
- [5] KOCJAN K., KOTARSKI W., WIDUCH S.: Blood cells analysis based on simple geometrical shape descriptors, Journal of Medical Informatics & Technologies, Vol. 2, pp. 177-182, 2001.
- [6] ŻAKOWSKI W, KOŁODZIEJ W.: Mathematics, academic books, part II, Warszawa 1993, pp. 285-287.
- [7] LONCARIC S.: A survey of shape analysis techniques, pp. 1-46, 1998 (<http://www.citeseer.nj.nec.com>).
- [8] VELTKAMP R.C, HAGEDOOM M.: State of the art. in shape matching, pp.1-26, 1999, (<http://www.citeseer.nj.nec.com>).
- [9] BARTON S.: Identification and recognition of leaves and general 2-D objects, (http://www.mapleapps.com/categories/data_analysis_stats/imageprocessing/html/leaves.html)