

UDC 004.048+004.932

EVOLUTIONARY APPROACH TO IMAGE PROCESSING ON THE EXAMPLE OF MICROSECTIONS

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Abstract

This paper offers a new approach to color image processing and segmentation on the basis of evolutionary models. We developed a set of objective functions for estimating the quality of segmentation taking into account the type of histological research. Experimental research was carried out on the example of histological images. The results of this research confirmed the efficiency of the developed evolutionary processing and segmentation algorithms.

Keywords: image processing and segmentation, effective algorithm, histological section

General Problem Statement

Computer systems of diagnostics (CSD) based on visual information analysis are used in many fields of science for solving such problems as face image identification, text recognition, medical and technical diagnostics, safety systems, etc. Computer-aided systems of image processing and analysis help to accelerate visual information processing, increase the accuracy of objects detection and recognition. Existing models, algorithms and computer-aided systems developed on their basis often use manual parameter tuning and heuristic algorithms for image processing. As a rule it reduces the quality and adequacy of image processing and segmentation [6, 7, 12, 15, 17, 20-23]. Therefore, in spite of the present numerous researches, the problem of color images processing and segmentation remains very important; and first of all it concerns adaptive methods.

In order to eliminate the above drawbacks we suggested [2, 3] a modification of the evolutionary approach to the development of effective algorithms for histological sections images processing. To solve a particular problem we need, at least, to do the following [1, 4, 8, 9, 11, 14]: 1) to develop a presentation (encoding) of a potential solution (chromosome); 2) to define genetic operators of crossover and mutation; 3) to define a fitness-function which allows estimating the quality of solution; 4) to develop a general evolutionary algorithm of task solution.

Potential solution (chromosomes) are represented as directed acyclic graphs, where internal nodes are standard image processing operators, terminal nodes are output image planes, and input nodes are input image planes. It allows describing practically any image processing algorithm, which is the sequence of standard operators. Functional and terminal sets, crossover and mutation problem-oriented operators are developed in [2, 3, 13, 16, 19]. The crossover operator is implemented with the exchange of graph paternal individuals fragments; the set rules [2, 3] must be used. A mutation, as usual, is executed by the casual change of this graph [2, 3, 14]. Algorithm generation is based on the conception of teaching with a teacher which uses the training set.

The Problem of Image Processing Optimization

The task of effective image processing and segmentation algorithm synthesis consists in generating such a sequence of processing operators with the proper parameters which gives the quality estimation criterion maximal for some image types. Processing accuracy is determined by means of calculating the objective function F , which is defined by comparing the segmented image M_k with the image from the training set G_l [5].

To solve the above problem step-by-step image processing procedure is proposed:

$$M_n = operate(S_{i_n}, P^{S_{i_n}}, N_n), \quad (1)$$

where M_n is an intermediate image at the n^{th} stage of processing; S_i is image processing operation (IPO); P^S is a set of IPO parameters values; n is the number of image processing operation; i – IPO number from the set of accessible operations; N_n is a set of intermediate images (obtained at the previous stages) which is the basis for constructing the image M_n :

$$N_n = (n_1, n_2, \dots, n_{z(S_n)}) \quad (2)$$

As it is not known which particular color model will provide the most effective segmentation procedure, we propose to represent the input image as a set of color planes:

$$I = \{C, R, G, Blue, H, Light, S, L, a, b, u, v\} \quad (3)$$

Every color plane contains the values of image pixels in one of color models (CM): RGB, HLS, Lab and Luv.

So, the first 12 color planes are fixed as follows:

$$\begin{aligned} M_0 &= C; & M_1 &= R; & M_2 &= G; \\ M_3 &= Blue; & M_4 &= H; & M_5 &= Light; \\ M_6 &= S; & M_7 &= L; & M_8 &= a; \\ M_9 &= b; & M_{10} &= u; & M_{11} &= v. \end{aligned} \quad (4)$$

Thus, to solve the given problem it will be enough to apply two sequential operations to one of color planes:

$$M_{12} = operate (ClipLo, (CL), (field)), \quad (5)$$

$$M_{13} = operate (ClipHi, (CH), (12)), \quad (6)$$

where *ClipLo* is a threshold limitation operation, when all CM pixel values with the number *field* ($field \in \{0, 1, 2, \dots, 11\}$) less than the value of the parameter *CL* ($CL \in [0 \dots 255]$) are set to 0, and the other save their values; *ClipHi* – all pixel values, which exceed the value of the parameter *CH* ($CH \in [0 \dots 255]$) are set to 0, the other are set to 1.

The above operations result in the binary image M_{13} .

Fitness-Function for Histological Sections Images

The structure of chromosomes (which are potential solutions in searching for rational parameters of microsections colored images segmentation) can be represented as follows:

$$Chr_i = [field, CL, CH]. \quad (7)$$

The segmentation must result in a set of homogeneous image areas, comparable by their accuracy to the results of the visual analysis made by a human expert. A fitness-function must compare the processed image with an image from the training set (referred to a certain class). Segmentation stage is completed successfully if the methods of segmentation show the results similar to the standard results obtained manually by a human expert. In this case fitness-function is a certain degree of similarity between the standard g and the processed image h (in particular, the inversion of some metric, such as Hamming relative distance):

$$f_A = 1 - \frac{1}{MN} \sum_{i=1}^N \sum_{j=1}^M |h(i, j) - g(i, j)|, \tag{8}$$

where h and g are two digital images with dimensions $M \times N$.

Obviously, the function f_A has maximum value $f_A = 1$ when two images coincide completely and minimum value $f_A = 0$ when the images do not coincide at all.

The function f_A depends on the number of coinciding images pixels only and can be applied if the maximal coincidence of images pixels is taken as the criterion of successful segmentation. However, if the number of pixels belonging to one class differs considerably from the number of pixels belonging to another class, then the use of Hamming distance as the fitness-function can lead to contradictory results.

It can be illustrated with the example of a grey image segmentation (Figure 1, a). For this purpose we will use relative Hamming distance to compare the reference image (Figure 1, b) given by a human expert with segmentation results obtained at different threshold values (Figure 1, c and Figure 1, d). In the first case the image element is not selected at all, and in the second case it is selected with wrong threshold value. Hamming distance for both cases is equal to 0.92, however it is obvious, that in the first case the result of segmentation is much worse, that in the second one.

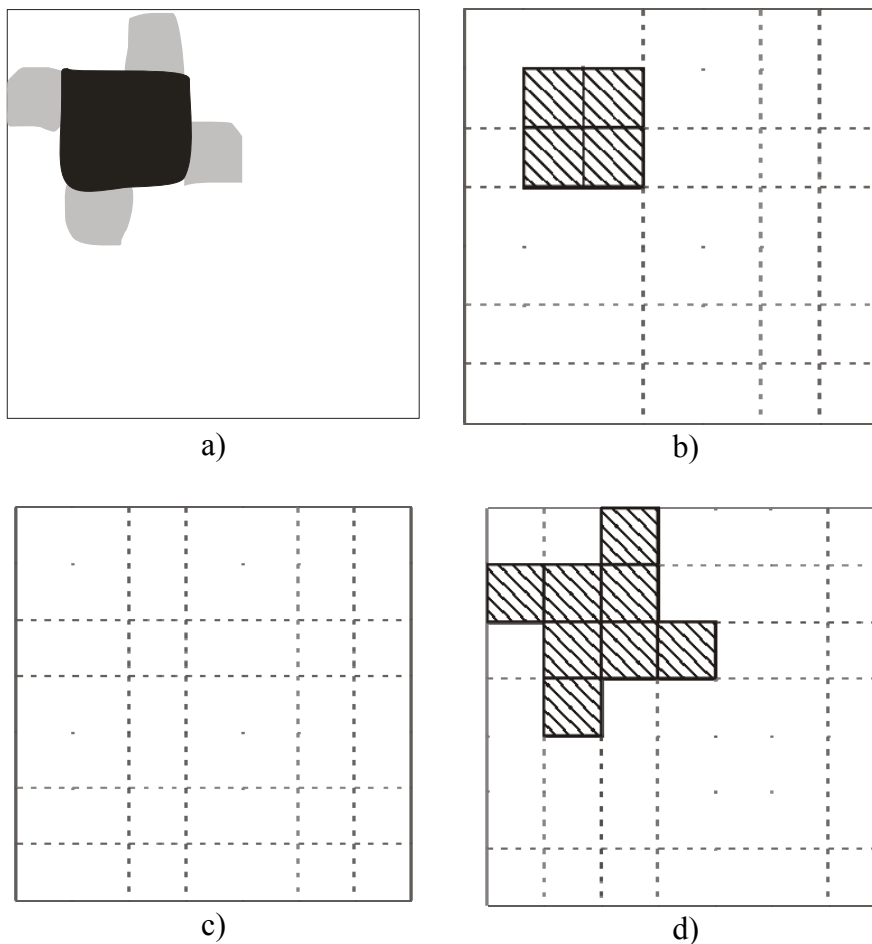


Figure 1. Example of image segmentation: a) initial image; b) reference pattern; c) result of segmentation 1; d) result of segmentation 2

So when the area of the image element differs considerably from the background area, the use of Hamming relative distance inversion as the fitness-function can lead to contradictory re-

sults. To overcome the above contradictions in such cases it is reasonable to use the fitness-function proposed in [1]:

$$f_B = 1 - \frac{\sqrt{(1-SP)^2 + (1-SV)^2}}{\sqrt{2}}, \quad (9)$$

where

$$SV = \frac{\text{card} \{ \{(i, j) | h(i, j) = 1 \ \& \ g(i, j) = 1 \} \}}{\text{card} \{ \{(i, j) | h(i, j) = 1 \} \}}, \quad (10)$$

$$SP = \frac{\text{card} \{ \{(i, j) | h(i, j) = 0 \ \& \ g(i, j) = 0 \} \}}{\text{card} \{ \{(i, j) | h(i, j) = 0 \} \}}. \quad (11)$$

Variables SV and SP are sensitivity and specificity respectively [1].

Unlike f_A the function f_B depends on the number of the correctly classified pixels, related to the background and to the image element. The optimum value $f_B=1$ when $SP=SV=1$ (the nearer SP and SV are to 1, the nearer to 1 the value of function f_B must be), otherwise $f_B=0$ when $SP=SV=0$.

In a number of cases it is reasonable to estimate two possible types of segmentation errors in different ways: These errors are: missing an element or its incorrect selection. So, if a positive cell has characteristics similar to the background it is preferable to mistakenly select this cell as a cancerous one, than to interpret a fragment as the background. Therefore it is necessary to carry out the adjustment of bias search error depending upon the values of sensitivity and specificity.

To eliminate the above drawback we suggest the following fitness-function:

$$f_C = 1 - \frac{\sqrt{(1-(SP \times (1-\alpha)))^2 + (1-(SV \times \alpha))^2}}{\sqrt{8}}, \quad (13)$$

where $\alpha \in [0;1]$ allows bias search error adjustment depending on the highest sensitiveness (high value α , close to 1) and highest specificity (low value α , close to 0).

Program tools for microsections images processing. The developed program system has a modular construction and consists of the followings basic functional units:

- image processing;
- selection of effective segmentation parameters;
- generation of effective algorithms for microsections images processing and segmentation.

The program system is implemented with object-oriented high-level language Delphi 7.0. The database (DB) is developed in the format of Paradox 7.0.

In “*Images Processing*” the images are processed depending upon the type of histological research according to the calculated parameters or a synthesized algorithm.

“*Selection of Effective Segmentation Parameters*” carries out the calculation of segmentation parameters by means of a modified genetic algorithm. Before calculations the input of training and test image sets is carried out. The form view of segmentation results for a strome micro-section image with calculated parameters is presented in Figure 2.

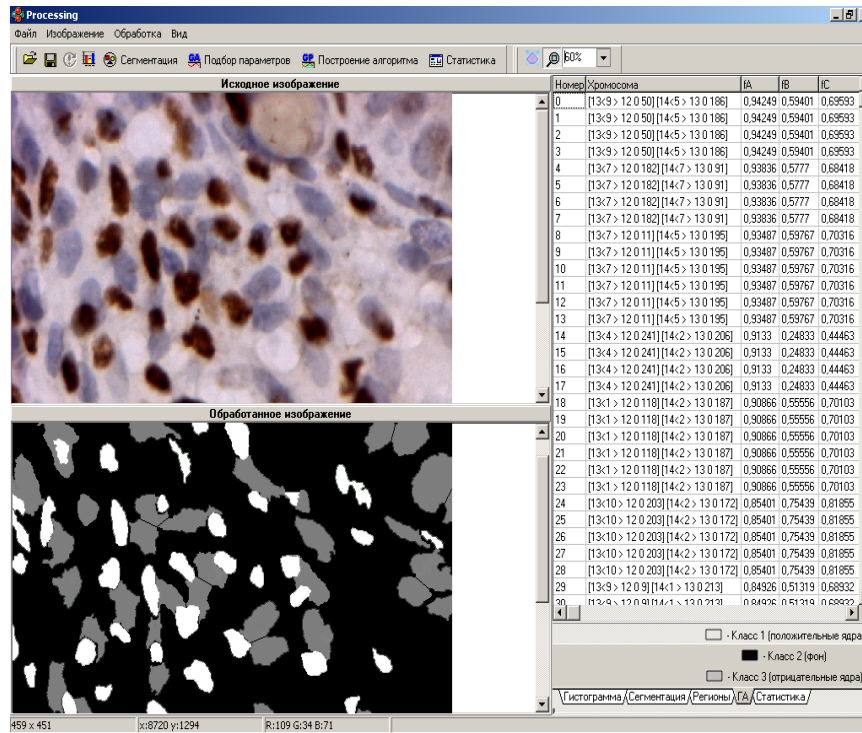


Figure 2. The results of strome microsection image segmentation

“*Generation of effective algorithms*” creates effective algorithms for microsections images processing and segmentation by means of the developed evolutionary program. The input of training and test image sets is carried out prior to evolutionary process implementation. The results of creating effective processing and segmentation algorithms for a lymphatic node microsection image are presented in Figure 3.

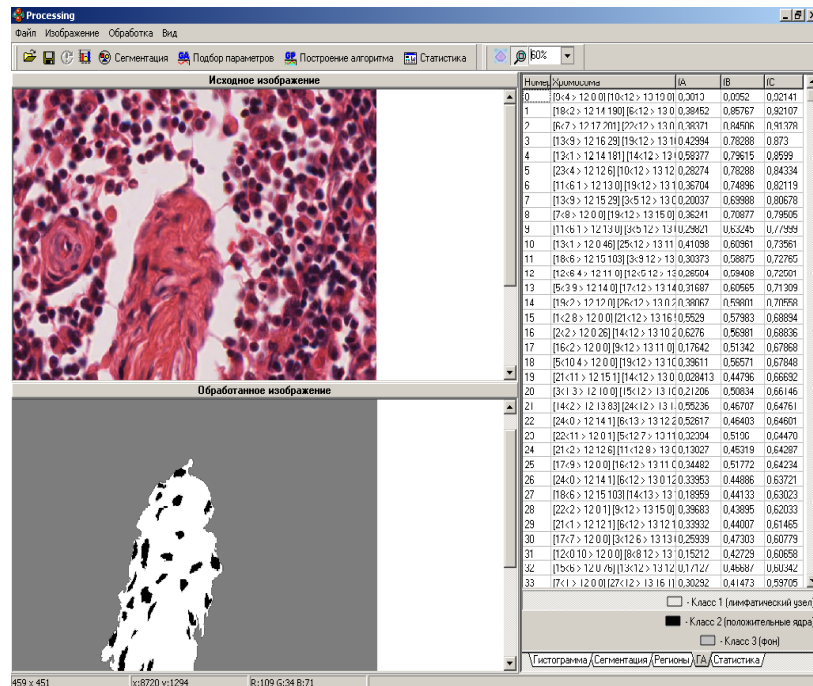


Figure 3. The results of creating effective processing and segmentation algorithms for a lymphatic node microsection image

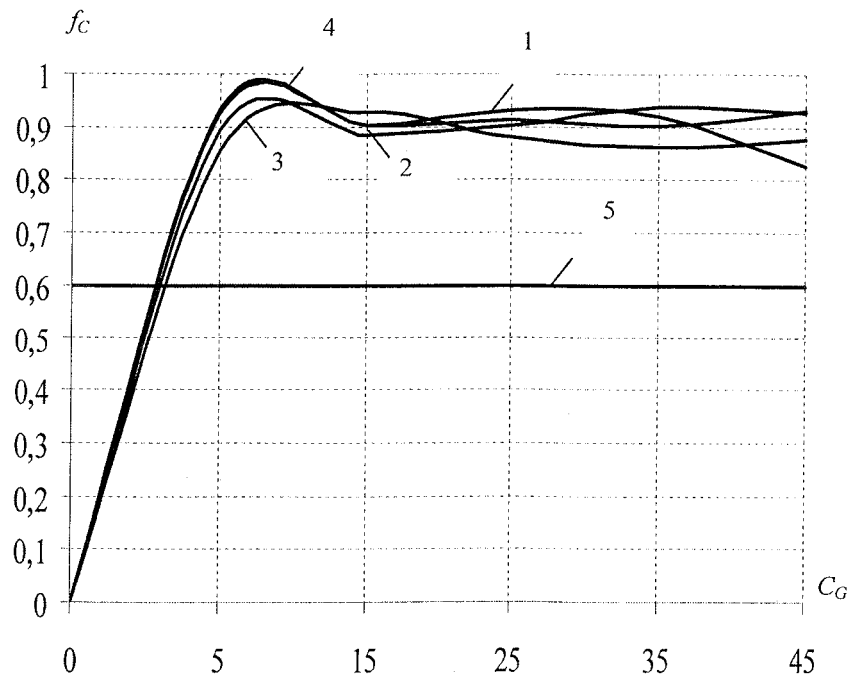


Figure 4. Dependence of fitness-function f_C on the number of generations (C_G) and power of population: 1 – for 25 chromosomes; 2 – for 50 chromosomes; 3 – for 75 chromosomes; 4 – for 100 chromosomes; 5 is a solution obtained by the k -average method

Conclusion

A new approach to image processing and segmentation on the basis of evolutionary models is proposed. Experimental researches on the example of microsections images confirmed the efficiency of the developed algorithms for image processing and segmentation.

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Received on 08.02.2010