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Development of Method of Matched Morphological Filtering of Biomedical Signals and Images

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Abstract—Formalized approach to the analysis of biomedical signals and images with locally concentrated features is developed on the basis of matched morphological filtering taking into account the useful signal models that allowed generalizing the existing methods of digital processing and analysis of biomedical signals and images with locally concentrated features. The proposed matched morphological filter has been adapted to solve such problems as localization of the searched structural elements on biomedical signals with locally concentrated features, estimation of the irregular background aimed at the visualization quality improving of biological objects on X-ray biomedical images, pathologic structures selection on mammogram. The efficiency of the proposed methods of matched morphological filtration of biomedical signals and images with locally concentrated features is proved by experiments.

Keywords: biomedical signal, biomedical image, locally concentrated features, matched morphologic filter, useful signal model

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1. INTRODUCTION

Introduction of computer and IT technologies led to the appearance of a wide variety of medical information systems, from simplest electronic medical records up to complicated decision support systems (DSS). Medical IT systems are most widely used within the frames of various diagnostic systems applied in instrumental patient workup systems.

Diagnostic information registered after instrumental workup mostly consists of data obtained from morphological analysis of biomedical signals and images (BMS/I) with locally concentrated features (LCF). BMS/I with LCF are signals and images having such structure where diagnostic features are concentrated at small fragments of their definition areas. The morphological analysis serves to extraction from background noise of informative fragments of BMS/I resulting in formation of diagnostic features in the form of parameters of found structural elements. The obtained diagnostic signs reflect the condition of patient bodily physiological systems under study.

Development of biomedical DSS as a part of hardware/software diagnostic complexes may improve the quality of instrumental workup of patients and reduce risks of erroneous decisions. Information processing in biomedical DSS consists of a sequence of respective stages. One important stage is pretreatment of digital BMS/I with LCF aimed to improve their quality. This stage is necessary not only under automatic analysis of BMS/I with LCF but in cases when a medical specialist takes diagnostic decisions on the basis of visual analysis of BMS/I with LCF, such as X-ray image analysis [1, 2]. Often standard digital processing methods of signals and images prove insufficient to obtain necessary BMS/I quality, as such methods do not take into consideration the peculiarities of BMS/I with LCF. For such processing, there are necessary to tailored methods based on consideration of BMS/I peculiarities bin the form of useful signal models [3–5]. A useful signal model here is a formalized description of characteristic features of a fragment or a component of BMS/I with LCF. Another critical stage of information processing in biomedical DSS is the morphological analysis of BMS/I with LCF, as errors at this stage lead to an erroneous diagnostic decision or a failure to take a decision at all. This stage also requires applying the data morphological analysis tailored method considering the peculiarities of BMS/I with LCF and their transformation methods [6, 7].

In the most generalized sense, Yu.P. Pytiev [8] determined morphological analysis as a group of methods for solving tasks of recognition, object classification, object parameter estimation, extraction of scene differences by their images (signals) based on signal shape conception. Even more generalized definition is given Yu.V. Vizilter in [9]. Morphological analysis is a scheme of data analysis in which a mandatory stage is substantiated (in certain sense optimal) construction of model description for some hypothetical (latent) preimage of observed data. The most complete theory of morphological analysis is developed for image processing and scene interpretation of a different nature [10–13], though in some works the methods of image morphological analysis are adapted for signal processing [14]. Nevertheless, in medical practice, morphological analysis of BMS/I is more often performed using various heuristic processing methods [15, 16] which operate the shape concept of signal or image as total or their particular areas on intuition level. In this case, heuristic methods of morphological analysis applied to particular BMS/I (ECG, rheogram, mammogram, fluoroscopic image, etc.) do not allow their adaptation to processing of other BMS/I types.

Thus, at present, there is not exist unified formalized approach to the problem solving of the morphological analysis of BMS/I with LCF for construction of biomedical DSS. Classic signal/image digital processing methods do not consider BMS/I peculiarities. Therefore, there exists urgent necessity in solution of development problem of theoretical foundations and decision making support tools in designing of biomedical systems based on morphological analysis of BMS/I with LCF in order to improve the quality of patient instrumental workup.

2. PURPOSE AND TASKS OF RESEARCH

The purpose of research is task formalization of matched morphological (MM) filtration of BMS/I with LCF in order to develop efficient morphological analysis methods of BMS/I with LCF to be applied in biomedical DSS.

For attainment of this purpose, the following tasks were solved:

—development of a formalized analysis approach of BMS/I with LCF based on MM-filtering with due consideration of useful signal models;

—adaptation of developed MM-filter to solution of various morphological analysis problems of BMS/I with LCF.

3. MM-FILTER DEVELOPMENT

Comparative filters based on guided contrasting are proposed in [10–13], by which a number of tasks are solved on the basis of evaluating the similarity of images by shape, in particular, one of the tasks is the detection of relative changes in the scene. Considered filters have the same structure, and different local and search coefficients of shape geometric correlation are used to calculate the response. Inherently, the comparative filters take as input two compared images (reference and test) and give as output the result, which can be interpreted as the result of filtering one (test) image.

However, such filters are unsuitable for the morphological analysis of BMS/I with LCF. For example, comparative filters cannot be adapted to the problem solution of localization of the target structural elements on BMS with LCF, since the local and search coefficients of shape geometric correlation proposed in [10, 12, 13] are not applicable to the one-dimensional case. Besides, using comparative filters, it is impossible to solve such tasks as calculating estimation of the uneven background for improving the quality of X-ray BMI with LCF and highlighting the pathological structures on mammogram, because due to the high variability of the shapes of bio-objects on X-ray images, it is impossible to set the reference image or model of the shape in an explicit form, which is necessary for the implementation of the above comparative filters. To eliminate the noted limitations, this section is devoted to formalizing the MM-filtering problem as well as to develop a generalized structure of CM-filters, in which the model of a one- or two-dimensional signal, depending on the problem being solved, can be specified both explicitly and implicitly, and specific implementations of MM-filters allow to solve these problems.

On the basis of generalized statement of morphological filtration problem as discussed in [9–13], in order to develop efficient methods for BMS/I with LCF morphological analysis let is determine the morphological matching coefficient $K_{MM}(a,b,\mathrm{M})$ of patterns $a \in \Omega$ and $b \in \Omega$ by a model M such as:

(1) $\forall a,b \in \Omega$: $K_{MM}(a,b,\mathrm{M}) \in [0;1]$ where Ω is the set (space) of patterns (signals/images), characteristic of a certain morphological system;

(2) $K_{MM}(a,b,\mathrm{M}) = 1 \Leftrightarrow \mathrm{Pr}(a,\mathrm{M}) = \mathrm{Pr}(b,\mathrm{M})$, where $\mathrm{Pr}(a,\mathrm{M})$, $\mathrm{Pr}(b,\mathrm{M})$ are the operations of projecting the patterns a and b onto the model M respectively;

(3) $K_{MM}(a,b,\mathrm{M}) = 0 \Leftrightarrow \mathrm{Pr}(a,\mathrm{M}) \cup \mathrm{Pr}(b,\mathrm{M}) = o, \mathrm{Pr}(a,\mathrm{M}) \cap \mathrm{Pr}(b,\mathrm{M}) \neq o$, where o is the simplest pattern;

(4) $\forall a,b \in \Omega_1$, $\forall c \in \Omega_2$, $\mathrm{M} \subseteq \Omega_1$: $K_{MM}(a,b,\mathrm{M}) > K_{MM}(a,c,\mathrm{M})$ where $\Omega_1 \subseteq \Omega$ is a subset of patterns passed by a morphological filter; $\Omega_2 \subseteq \Omega$ is a subset of patterns suppressed by a morphological filter.

Then MM-filter is a function of the form

$$\varphi^w_{MM}(p,a,\mathrm{M}) = o + K^w_{MM}(p,a,\mathrm{M})(a-o), \tag{1}$$

where $p \in \Omega$ is the shape standard; $K^w_{MM}(p,a,\mathrm{M})$ is the local morphological matching coefficient (the morphological matching coefficient assigned in the window w).

Depending on calculation method of the coefficient $K^w_{MM}(p,a,\mathrm{M})$ using the MM-filter (1) various tasks are solved. If $K^w_{MM}(p,a,\mathrm{M}) \in \{0;1\}$, the MM-filter (1) helps to solve pattern recognition task so that only patterns a meeting the standard p by the shape of the model M is passed by such MM-filter. If $K^w_{MM}(p,a,\mathrm{M}) \in [0;1]$, then with the help of the MM-filter (1) both tasks of similarity degree estimating of the pattern a with the standard p by the shape of the model M and noise suppression tasks.

Let us determine morphological similarity coefficient of patterns $a \in \Omega$ and $b \in \Omega$ by the shape agreed with the model M:

$$K_{MS}(a,b,\mathrm{M}) = K\left(\mathrm{Pr}(a,\mathrm{M}), \mathrm{Pr}(b,\mathrm{M})\right), \tag{2}$$

where $K(\cdot)$ is a potential function reflecting the closeness of patterns a and b by the shape agreed with the model M, with may be one of the following functions [17, 18]:

$$K\left(\mathrm{Pr}(a,\mathrm{M}), \mathrm{Pr}(b,\mathrm{M})\right) = e^{-\alpha d^2_\Omega(\mathrm{Pr}(a,\mathrm{M}),\mathrm{Pr}(b,\mathrm{M}))}; \tag{3}$$

$$K\left(\mathrm{Pr}(a,\mathrm{M}), \mathrm{Pr}(b,\mathrm{M})\right) = \frac{1}{1+\alpha d^2_\Omega\left(\mathrm{Pr}(a,\mathrm{M}), \mathrm{Pr}(b,\mathrm{M})\right)}, \tag{4}$$

where $\alpha > 0$ is a coefficient reflecting sensitivity to differences between patterns a and b by the shape agreed with the model M. In expressions (3) and (4) metrics d_Ω may be presented by various types of distances, such as ordinary or weighted Euclid distance, Minkowski distance, etc. [19]. If a morphological similarity coefficient is calculated for a signal/image fragment in assigned window w, let us call such coefficient the local morphological similarity coefficient $K^w_{MS}(a,b,\mathrm{M})$.

A morphological similarity coefficient $K_{MS}(a,b,\mathrm{M})$ (2) evidently possesses all the same properties that morphological matching coefficient $K_{MM}(a,b,\mathrm{M})$. Then in expression (1) the local morphological similarity coefficient $K^w_{MS}(a,b,\mathrm{M})$ may be used as the local morphological matching coefficient $K^w_{MM}(p,a,\mathrm{M})$.

The main task of object detection in signal is not only object classification by shape, but also its localization in the studied signal. For example, in ECG analysis all structural elements (waves and complexes) must be isolated in the signal, i.e. not only the type of the structural elements but also its temporal position must be determined. The morphological similarity coefficient (2) may be used for task solving of pattern (object) detection (localization) in signal/image as assigned by projective models.

The process of MM-filtering can be represented as the following sequence of steps:

(1) Input the initial BMS/I with LCF (in the specified format).

(2) Set the useful signal model M (if explicitly specified).

(3) Set the shape standard p (if specified explicitly).

(4) Set the type of the local morphological matching coefficient $K^w_{MM}(p,a,\mathrm{M})$.

(5) Set the parameters of the MM-filter window (aperture sizes and other parameters).

(6) Scan BMS/I by specified window.

(7) Visualization of the MM-filtering results.

It should be noted that the useful signal model and the local morphological matching coefficient determine the specific implementation of the MM-filter and allow to adapt the filter to the solution of a specific problem (some implementations of the MM-filter are discussed in Section 4). If the useful signal

model and/or the shape standard are set implicitly, then they are taken into account directly when calculating the corresponding local morphological matching coefficient. At the same time, for the task of detecting structural elements, the result of filtering is the selected fragments on the BMS/I with LCF; for the task of improving the quality of the image – a new BMI or its layer.

Thus, the essential difference between the developed MM-filter (1) and the known class of comparative filters is that it is possible to adapt the developed MM-filter to develop effective methods for the morphological analysis of BMS/I with LCF, implemented in biomedical DSS, by both explicitly and implicitly defining a useful one- or two-dimensional signal models, as well as various methods of implementing the local morphological matching coefficient. In this case, comparative filters are one of the implementations of the MM-filter.

4. MM-FILTER APPLICATION FOR SOLUTION OF VARIOUS PROBLEMS OF MORPHOLOGICAL ANALYSIS OF BMS/I WITH LCF

4.1. Morphological Analysis of BMS with LCF

Present authors in [20] developed the morphological analysis method of BMS with LCF based on MM-filtering where detection function is calculated and analyzed to localize target structural elements. Values of detection function $\tilde{y}[t]$ are determined using the local morphological similarity coefficient K_{MS}^{w} in form (2):

$$\tilde{y}[t] = K_{MS}^{w[t]}\left(\omega_p, \omega_t, \mathrm{M}_p\right), \tag{5}$$

where ω_p is standard of structural elements of the target class; ω_t is signal projection within filter aperture on the shape matched with useful one-dimensional signal model M_p of target structural element.

That is, in expression (5), the local morphological similarity coefficient K_{MS}^{w} is the morphological projector of the object ω_t on the shape of the standard ω_p, calculated in each position of the MM-filter aperture. In this case, the BMS with LCF $x[t]$ is represented as a set of objects in the parameter space defined by the useful one-dimensional signal model M_p of the target structural element: $x[t] \to \Omega = \{\omega_i \,|\, i \in \{1, 2, \ldots, n\}\}$ where ω_i is the object given by coordinates $y_{ij} = f(x[t], P)$ (i is the object number; j is the index of coordinate); P is the set of parameters; n is the cardinality of the set.

On the basis of analysis of detection function $\tilde{y}[t]$, the local morphological matching coefficient is calculated using the threshold decision rule:

$$K_{MM}^{w[t]}\left(\omega_p, \omega_t, \mathrm{M}_p\right) = \begin{cases} 1 & \forall t \in [t_{0j}; t_{0j} + T_0], \text{ if } \tilde{y}[t_{0j}] > Pd[t]; \\ 0 & \text{in other cases} \end{cases} \tag{6}$$

where $Pd[t]$ is an adaptive threshold; t_{0j} is a local maximum point of function $\tilde{y}[t]$ such that $\tilde{y}[t_{0j}] \geq \tilde{y}[t]$ $\forall t \in \dot{\mathbf{M}}(t_{0j})$; $\dot{\mathbf{M}}(t_{0j}) = \mathbf{M}(t_{0j}) \backslash \{t_{0j}\}$ is punctured neighborhood of a point t_{0j}; $\mathbf{M}(t_{0j})$ is a neighborhood of a point t_{0j}; j is an index of a local maximum.

Then according to (1) MM-filter response is calculated like this:

$$\tilde{x}[t] = x^0 + K_{MM}^{w[t]}(\omega_p, \omega_t, \mathrm{M}_p)(x[t] - x^0), \tag{7}$$

where $x[t]$ is input BMS with LCF; $x^0 = \text{const}$ is constant determining signal level which corresponds to absence of assigned type structural element in current fragment of signal (for instance, ECG baseline level).

It should be noted that each position of the MM-filter window (7) sets the current object ω_t in the parameter space, which is either simplified to the simplest pattern x^0, corresponding to the absence of a structural element of the target class, or skipped without distortion by the filter. Thus, as a result of applying the MM-filter (7) fragments containing target structural elements may be isolated in BMS.

4.2. Grayscale Morphological Filter based on Local Statistics

Present authors in [21] developed the grayscale morphological filter (GMF) based on local statistics (LS) which implicitly takes into account the model of a useful two-dimensional signal. The response of such filter is determined by the following expressions:

$$\phi_m[x, y] = q_{0.5}[x, y] + K_m\left(g^{w[x,y]}\right)(g[x, y] - q_{0.5}[x, y]); \tag{8}$$

$$K_m\left(g^{w[x,y]}\right) = \begin{cases} \dfrac{\Delta q[x, y] - \Delta q_{cp}}{\Delta q[x, y]}, & \text{if } \Delta q[x, y] > \Delta q_{cp}; \\ 0 & \text{otherwise;} \end{cases} \tag{9}$$

$$\Delta q[x, y] = q_b[x, y] - q_a[x, y]; \quad \Delta q_{cp} = \frac{1}{M_1 M_2}\sum_{x,y}\Delta q[x, y], \tag{10}$$

where $q_{0.5}[x, y]$ is local median of the image $g[x, y]$ in the window $w[x, y]$; $q_a[x, y]$, $q_b[x, y]$ are local a-quantile and b-quantile of the image $g[x, y]$ in the window $w[x, y]$, where in $a < b$; M_1, M_2 are linear dimensions of the filter aperture (i.e. dimensions of the window $w[x, y]$).

According to expression (1) in expression (8), the local morphological matching coefficient is the coefficient $K_m\left(g^{w[x,y]}\right)$ calculated using local statistics, the calculation of which does not require knowledge of the distribution law of the signal in the window, and the image median in the window is used as the simplest pattern.

GMF based on LS allows filtration of a grayscale image which does not distort object shape without need to know useful signal distribution law as well as type of noise and the way it is superimposed. This filter is used to obtain an estimate of the uneven background in the task of improving the quality of visualization of X-ray radiography BMI.

4.3. Morphological Analysis of BMI with LCF based on Fractal Dimensions Analysis

The present work proposes a mammogram morphological analysis method based on fractal dimensions analysis, wherein pathological structures are highlighted on mammogram using MM-filter of the type (1) without evident assignment of shape model of pathological structures. Studies of actual mammograms showed that the values of fractal dimensions calculated for image small sections may be used as transformation parameters of initial mammographic image in the morphological analysis task of BMI with LCF. Since pathological structures on the image are visualized as areas with low brightness values, and, at the same time, areas with pathology are characterized by a greater «smoothness» of the surface, that is, they have a smaller fractal dimension in a given window, then when comparing the brightness value of a pixel with a normalized value the fractal dimension calculated in the pixel neighborhood, the pathological structures on mammogram are highlighted. At the same time, to calculate the local morphological matching coefficient in expression (1), the useful two-dimensional signal model is implicitly defined.

In expression (1) the simplest pattern o is assumed an image with zero pixel brightness value:

$$\phi_{MM}[x, y] = K_{MM}^{w[x,y]}(g, f^{w[x,y]})g[x, y], \tag{11}$$

where $g[x, y]$ is an initial grayscale image; $f^{w[x,y]}$ is normalized value of fractal dimension in assigned window $w[x, y]$; $K_{MM}^{w[x,y]}(g, f^{w[x,y]})$ is local morphological matching coefficient considering fractal properties of image fragment in window $w[x, y]$.

The coefficient $K_{MM}^{w[x,y]}(g, f^{w[x,y]})$ is calculated by the following expression:

$$K_{MM}^{w[x,y]}(g, f^{w[x,y]}) = \frac{\max(g[x, y], mx - f^{w[x,y]}) - \min(g[x, y], mx - f^{w[x,y]})}{g[x, y]}, \tag{12}$$

where mx is maximum possible pixel brightness value.

By substituting expression (12) to (11), let us obtain MM-filter response

$$\phi_{MM}[x, y] = \max(g[x, y], mx - f^{w[x,y]}) - \min(g[x, y], mx - f^{w[x,y]}). \tag{13}$$

Thus, due to MM-filter (13) application light sections with uniform brightness are isolated in BMI which correspond to pathological structure on mammogram.

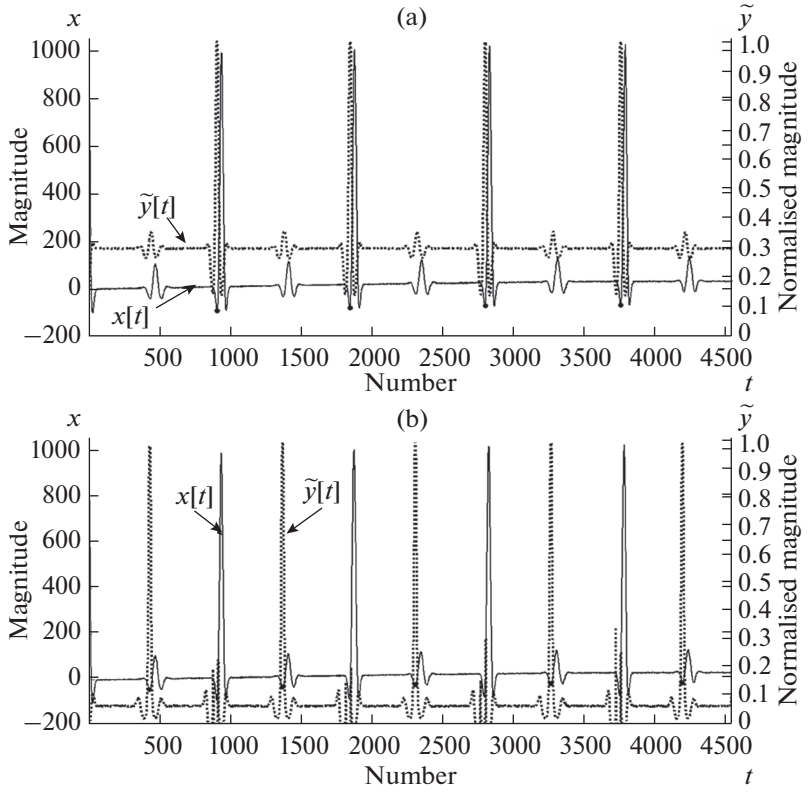

Fig. 1. Results of structural elements detection using MM-filtering (the fragment of the initial signal $x[t]$; the detection function $\tilde{y}[t]$; the initial supporting points of the detected structural elements are marked by circles; t – numbers of reference): a – type 1; b – type 2.

5. RESULTS OF MORPHOLOGICAL ANALYSIS OF BMS/I WITH LCF BASED ON MM-FILTERING

5.1. MM-filtering of a Test Signal with Locally Concentrated Features

As a test signal with locally concentrated features, there is considered the mix of two periodically repeated pulses shifted relative to each other with the repetition frequency 500 Hz, the sample rate $f_s = 500$ kHz and different amplitudes A_1 and A_2 ($A_1 > A_2$).Each pulse s_i ($i \in \{1;2\}$) is harmonic pulse modulated by a Gauss law:

$$s_i[t] = A_i e^{-a_i(\tau[t]-\tau_i)^2}\cos\left(2\pi f_c(\tau[t]-\tau_i)\right);\quad a_i = -\frac{5\left(2\pi f_c bw_i\right)^2}{bwr\ln 10},$$

where A_i is an amplitude of the i-th pulse (dimensionless quantity); a_i is duration of the i-th pulse; $\tau[t]$ is an array of time samples (t is a number of reference); f_c is carrier frequency; τ_i is an initial shift of the i-th pulse relative to the zero point in time; bw_i is a relative width of the spectrum of the i-th pulse; bwr is a level (dB) by which is used to change the width of the spectrum.

The following parameters are set for pulses: $A_1 = 1000$; $A_2 = 100$; $f_c = 5$ kHz; $bw_1 = 2$; $bw_2 = 1$; $bwr = -24$ dB. The signal mix is distorted by various interferences imitating random noises, isoline drift and quasi-periodicity (function $x[t]$ on Fig. 1). The MM-filtering results of the test signal in order to detect type 1 structural elements (standard detection signal are pulses with amplitude A_1) and type 2 structural elements (standard detection signal are pulses with amplitude A_2) are presented in Fig. 1.

In this experiment, a triangle assigned by its apices (supporting points) was chosen as the model of useful signal shape (for both type 1 and type 2 structural elements). According to (5) in each MM-filter aperture position the signal was projected onto the shape agreed with useful signal model.

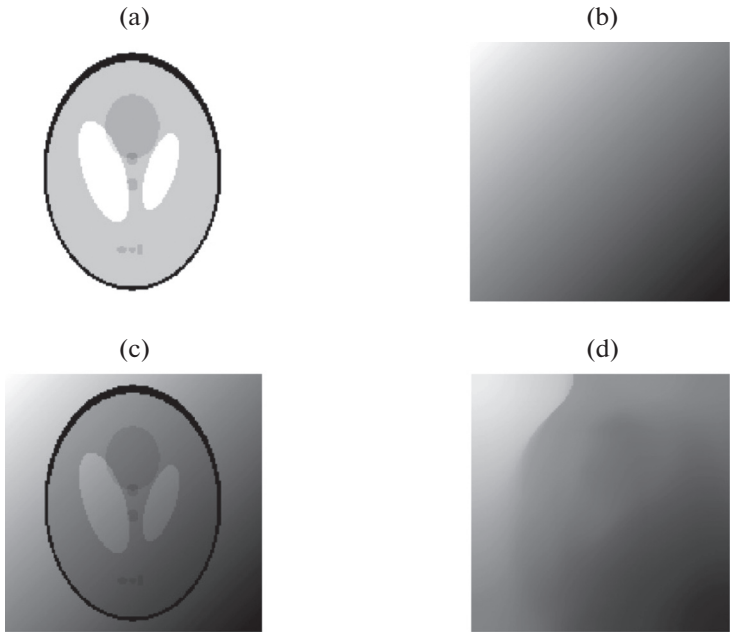

Fig. 2. The test images with size 150×150 pixels: a – the head phantom $g[x, y]$; b – the background model $f[x, y]$; c – the phantom with superimposed background $r[x, y]$; d – the background evaluation $\tilde{f}[x, y]$.

5.2. MM-filtering of a Test Image with Locally Concentrated Features

In processing of grayscale images, it is often necessary to remove an irregular background. To solve this task the irregular background evaluation must be found which is calculated using various filters [22, 23]. X-ray images are characterized by the fact that the irregular background is a multiplicative noise. As a test image $r[x, y]$ let us take the positive image of the head phantom $g[x, y]$ with superimposed gradient background $f[x, y]$: $r[x, y] = g[x, y] \cdot f[x, y]$ (Fig. 2*a*–*c*).

Because phantom image $g[x, y]$ acts as noise in the removal task of irregular background $f[x, y]$ from the image $r[x, y]$ then background evaluation $\tilde{f}[x, y]$ may be calculated using GMF based on LS (8)–(10), having large linear aperture dimensions p. Fig. 2 (*d*) presents background valuation $\tilde{f}[x, y]$ calculation results using GMF based on LS with such parameters: $a = 0,25$, $b = 0,75$, $p = 51$.

Besides, comparative analysis of calculation of background evaluation $\tilde{f}[x, y]$ was performed using the two-dimensional linear low-frequency filter (the rectangular smoothing filter) and the two-dimensional Wiener adaptive filter. For unbiased comparison of results there was used signal-to-noise ratio in dB (Table 1) which was determined by expression:

Table 1. *SNR* calculation results of the irregular background model evaluation using different filters

p (% of area $r[x, y]$)	Filter type		
	SNR, dB		
	GMF based on LS	low-pass filter	wiener adaptive filter
21 (1.96%)	15.86	14.56	12.51
31 (4.27%)	17.09	15.02	13.43
41 (7.47%)	17.18	15.26	14.20
51 (11.56%)	**17.24**	15.36	14.77
61 (16.54%)	17.14	15.35	15.16
71 (22.4%)	16.96	15.23	15.27
81 (29.16%)	16.65	15.02	15.15

(a) (b)

Fig. 3. Digital mammogram: *a* – before filtering; *b* – after MM-filtering.

$$SNR = 10\lg\frac{\sum\limits_{x}\sum\limits_{y} f^2[x,y]}{\sum\limits_{x}\sum\limits_{y}\left(f[x,y]-\tilde{f}[x,y]\right)^2}. \quad (14)$$

Comparison of results in Table 1 showed that the worst approximation was obtained in calculation of background evaluation $\tilde{f}[x,y]$ using Wiener adaptive filter, whereas GMF based on LS showed the best results.

5.3. MM-filtering of Mammograms

To check mammogram morphological analysis method the initial image will be treated as a plurality of objects, each of them being represented by a fractal set. The basic characteristic of a fractal set is its fractal dimension. To perform morphological analysis using the developed MM-filter (11) fractal dimension was calculated in given window using Differential Box Counting method.

An example of digital mammogram MM-filtering is presented in Fig. 3. For digital mammogram filtering with the size of 3072×4032 pixels there was applied the filter with aperture linear dimensions 200×200 pixels which corresponds to section area 12×12 mm.

Thus, irrespective of pathological structures dimensions and location, light sections with uniform brightness are separated after MM-filtering which corresponds to pathological structures on mammogram.

6. DISCUSSION OF MM-FILTERING OF BMS/I WITH LCF

To implement all the above MM-filters, MatLab interactive environment with a built-in high-level programming language is used. The choice of the MatLab environment and programming language is based on well-optimized algorithms for working with large matrices, which is important for increasing the computation speed when implementing the proposed MM-filtering methods. Compilation of the developed functions is performed using the MatLab compiler runtime library into an executable DLL-library, which can be connected as appropriate modules to biomedical DSS.

The studies of developed analysis methods of BMS/I with LCF based on MM-filtering showed that they help to solve various problems: detection of assigned shape signal in BMS, calculation of BMI irregular background evaluation, isolation of pathological structures on mammogram.

Analysis of the results of MM-filtering of BMS with LCF (Fig. 1) showed that under selected parameters structural elements of both type 1 and type 2 are detected unmistakably. Under these circumstances the local maxima of detection function $\tilde{y}[t]$, corresponding to initial supporting points of target structural elements (Fig. 1), are substantially higher than all other local maxima, therefore, to calculate morphological matching coefficient (6) as an adaptive threshold $Pd[t]$ it is expedient to apply the simplest case $Pd[t] = \text{const}$ (in this experiment $Pd[t] = 0,5$ in both cases).

Thus, it is shown that MM-filter may be applied to irregular background evaluation in the problem of BMI visualization quality improvement. It is seen from Table 1 that the highest value *SNR* was obtained for GMF based on LS with 51 pixels of aperture. Further aperture dimension increase leads to reduced

signal-to-noise ratio. For both low-pass filter and Wiener adaptive filter the values *SNR* turned to be less than for GMF based on LS irrespective of filter aperture linear dimensions, and with increase of LS-based GMF aperture linear dimensions from 31 to 71 the value *SNR* changes only insignificantly. Thus, unbiased *SNR* evaluation (Table 1) showed that for irregular background evaluation calculation GMF based on LS is better used with filter window area 4–10% of the area of image being filtered.

Other than this, mammograms were MM-filtered on the basis of fractal dimension values analysis. Study of actual digital mammograms showed that under total image processing differences in fractal dimension values with presence and absence of pathological structures were not found. For most mammograms values of their fractal dimensions lie within the range 2.41 to 2.46. This is due to the fact that areas of pathological sections are quite small as compared with the dimension of mammary breast image, therefore, changes in fractal dimension values are insignificant. The analysis of fractal dimension values calculated for mammogram sections with healthy and affected tissues showed that fractal dimension values for mammographic image sections containing dense tissue are lower than for mammographic image sections free from visible pathologies. Irrespective of dimensions and locations of pathological structures, after MM-filtering (13) light sections are isolated with uniform brightness, whereas under morphological analysis of normal mammograms light sections are not isolated. Thus, the fractal dimension values calculated for small image sections may be used as transformation parameters of initial mammogram for morphological analysis of BMI with LCF.

7. CONCLUSION

In the work, the MM-filtering task of biomedical signals and images with locally concentrated features is formalized, which made it possible to develop morphological filters with the use of useful signals models to solve the tasks of the recognition and localization objects of BMS/I with LCF, and the task of the visualization quality improvement of biological objects and their structural elements on X-ray images.

The performed implementations of the developed MM-filter enabled solution of such tasks as localization of target structural elements in BMS with LCF, determination of irregular background evaluation, improvement of biological objects visualization in X-ray BMI and isolation of pathological structures on mammogram.

The use of specialized methods of morphological data analysis taking into account the features of BMS with LCF and methods of their transformation helps to solve the problem of developing decision support tools in designing biomedical systems in order to improve the quality of instrumental examination of patients.

COMPLIANCE WITH ETHICAL STANDARDS

This article does not contain any studies involving human or animals participants performed by any of the authors.

CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

AUTHOR CONTRIBUTIONS

A.I. Povoroznyuk and A.E. Filatova proposed the idea of this method. A.Yu. Zakovorotniy and Kh. Shehna programmed for this method. A.I. Povoroznyuk and A.E. Filatova wrote the first draft of the manuscript. All authors edited the manuscript and approved the final version.

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