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APPLICATION OF ENTROPY CRITERION FOR AN ESTIMATING OF QUALITY OF DNA MICROARRAY DATA NORMALIZATION

In the article the investigation on use of Shannon entropy criterion for an estimation of quality of DNA microarray data normalization is presented. The methods of linear and nonlinear normalization and contrast method were used as normalization methods. It is shown the best quality of normalization achieved by using the contrast method, that proved by a minimum value of the Shannon entropy.

Keywords: DNA microarray, data normalization, the Shannon entropy criterion.

1. Introduction.

Normalization is one of the major stages of data preprocessing in which empirical data are transformed to the same range that allow to carry out their comparative analysis. Furthermore, the character of distribution of data in the chosen range of values has been changing that defines quantity and quality of evaluating information. The character distribution of data received in the process of normalization is defined by a kind of used transfer function. Quality of data preprocessing in many respects depends on a choise of function of normalization what in turn defines quality of the preprocessing information. Questions of normalization DNA microarray data in enough detal were discussed in [1]. According to character of distribution data existing methods of normalization can be divided into two subgroups: the methods using a basic array of genes and methods using all set of investigated data. The first groups of methods are in turn subdivided into linear and nonlinear. The second groups of methods include methods of cyclic loes, contrast based method and quantile normalization [2,3]. Each of methods has advantages and disadvantages. In [2] it is shown that with other things being equal better works a method quantile normalization entering as base method in a complex data preprocessing RMA. However, it is necessary to notice that the evaluation of quality of data normalization was mainly made by visual inspection according to degree of variability of data on appropriate plots of distribution without use of any quantitative criteria. This approach is subjective, because the normalized data can contain the latten laws invisible on schedules of corresponding dependences. In

this paper it is offered to use along with the traditional methods of visual an estimation of quality normalization quantitative criterion of entropy [4,5], that will allow to raise objectivity of an estimate and to choose for current data more optimal method of normalization.

In this case as entropy we will understand a quantitative measure of ordering of structural elements in system. According to statistical definition of entropy:

$$S = k \cdot \ln W \tag{1}$$

where k - Boltzmann constant, W - probability of thermodynamic conditions defined as quantity of possible microconditions allowing to realize given macroconditions.

According to formula (1) the system in which all structural elements are ordered, has minimum entropy, but thus we have maximum information about structure of the system and configurations of its components. At increase of the level of disorder of the elements in the system (presence of noise component), entropy of the system increases because quantity of microcondition realizing given macrocondition increases, however objective information about true condition of the structural elements in the system decreases. K. Shannon proposed the formula [6] allowing to estimate information's entropy of an investigated signal:

$$H = -K \cdot \sum_{i=1}^{n} p_i \log(p_i) \tag{2}$$

where K – the positive constant entered in the equation for coordination of dimension, p_i - the probability of the i-th event. At DNA microarray analysis the event is understood as intensity of light in the given point. If to assept that s_i - the level of intensity in i-th point, the probability of realization of the given condition is connected with the function of realization of the given condition by equation [7]:

$$p_i = s_i^2 \tag{3}$$

Thus, (2) taking into account (3) it is possible to present formulay as follows:

$$H = -K \cdot \sum_{i=1}^{n} s_i \log(s_i) \tag{4}$$

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According to the received formula it is possible to draw a conclusion that in process of increases of quality of data normalization the quantity of information about a useful component of the signal increases too that agreement increases signal-noise-relative. The value of Shannon entropy criterion at the given case will seek to minimum.

The purpose of this article is to develop the system of an estimation of quality of DNA microarray data normalization on the basis of quantitative criterion of entropy.

2. Results

Suppose that array of experimental data obtained as a result of scanning of DNA microarray is presened by the matrix dimension $n \times m$:

$$I = \begin{cases} x_{11}, x_{12}, \ldots, x_{1m}; \\ x_{21}, x_{22}, \ldots, x_{2m}; \\ \ldots\ldots\ldots\ldots\ldots\ldots \\ x_{n1}, x_{n2}, \ldots, x_{nm}. \end{cases} \quad (5)$$

where n – a number of observed objects or a number of genes which expression level is necessary to be determined; m – a number of features that are characteristics of any object. Each element of the matrix (5) represents intensity of light corresponding of the given gene. For comparative analysis objects of the matrix for purpose of classification it is necessary to normalize, i.e. their value transform to the same range. Normalization of data was performed using the methods of linear and nonlinear normalization with application of the logistic transfer function and the contrast method.

Linear normalization algorithm supposed the following steps:

–from the set of vectors of matrix (5) it is selected the basis vector for which the mean value is calculated:

$$\overline{x}_{bs} = \frac{\sum_{i=1}^{m} x_{bsi}}{m} \quad (6)$$

–for each vector of array the trimmed mean is calculated herewith discarded 2% minimum and maximum values:

$$\overline{x}_k = \frac{\sum_{i=1}^{0,98m} x_{ki}}{0,98m} \quad (7)$$

–normalizing values for each vector of array are calculated accordingly equation:

$$x'_{ki} = \frac{\overline{x}_{bs}}{\overline{x}_k} x_{ki} \quad (8)$$

Nonlinear normalization was performed using logistic transfer function as follows:

–mean value of corresponding vector of array is calculated:

$$\overline{x}_k = \frac{\sum_{i=1}^{m} x_{ki}}{m} \quad (9)$$

–standard deviation is calculated for each vector of array:

$$\sigma_k = \sqrt{\frac{\sum_{i=1}^{m} (x_{ki} - \overline{x}_k)}{m \cdot (m-1)}} \quad (10)$$

–vector of arguments of the logistic function is calculated using formula:

$$a_{ki} = \frac{x_{ki} - \overline{x}_k}{\sigma_k} \quad (11)$$

–normalized values for each vector of array are calculated:

$$x'_{ki} = \frac{1}{1 + e^{-a_{ki}}} \quad (12)$$

The contrast method supposes that between vectors M and A prevail linear regression dependency. Vectors M and A represent as a set of the following values:

$$M_{ki} = \log_2\left(\frac{x_{ki}}{x_{bsi}}\right) \quad (13)$$

$$A_{ki} = \log_2(x_{ki} \cdot x_{bsi}) \quad (14)$$

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where x_k - k-th vector of investigation dataset; x_{bs} - basis vector of the given array.

Algorithm of the contrast method supposes the following steps:

–select a basis vector;

–determine parameters M and A for each investigated vector of data array accordingly equations (13) and (14);

–calculate normalizing correction for each element of the corresponding vector:

$$\delta M_{ki} = M_{ki} - \hat{M}_{ki} \tag{15}$$

where $\hat{M}_{ki}$ - value of regression function corresponding to i-th sample of k-vector;

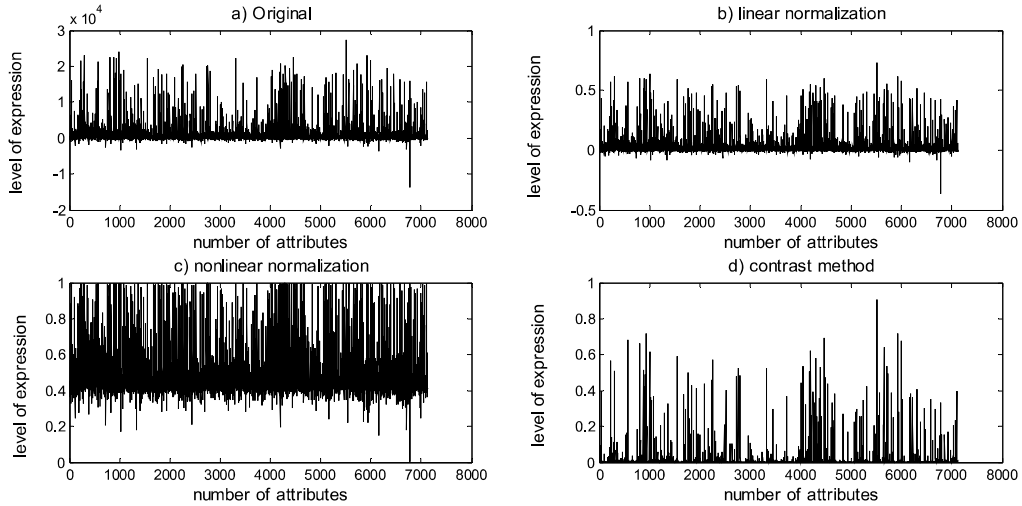
–calculate of normalizing coefficients by the formula:

$$x'_{ki} = 2^{\left(A_{ki} + \frac{\delta M_{ki}}{2}\right)}, \tag{16}$$

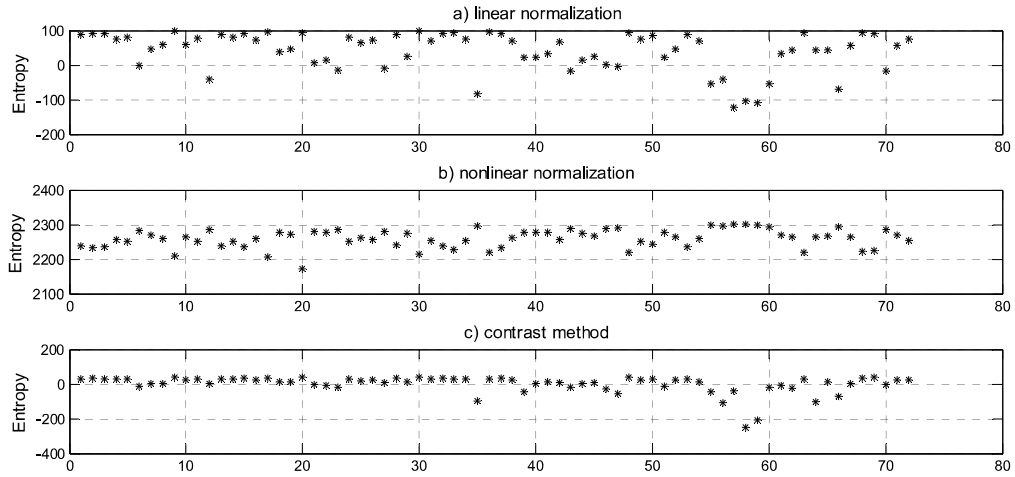
Database of leukemia patients (Golub et al, 1999) was used for research as an experimental database, represented itself array size 72×7131. Each row contains information about a level of gene expression of diseased cells of an individual human. The filtration of signals using the wavelet has been performing at the first step [8]. Necessity of the given step definice by high level of noise component in original data, arising on the stage of performing experiment and reading information from DNA microarray. As a result of wavelet signal processing it has been processing high-frequency component of the signal order to minimize the noise component. Hereinafter, each vector has been normalizing in accordance with above described algorithms. In each case for each normalized vectors was calculated the Shannon entropy in accordance with the quation (4). Plots of filtered signal of one investigated objects (Fig. 1a) and normalized signal linear normalization algorithm (Fig. 1c), nonlinear normalization (Fig. 1c) and contrast method (Fig. 1d) are showed on figure 1. Plots of entropy distribution of normalized signals depending on the method of normalization are showed in figure 2.

3. Discussion

Analysis of the graphs shown in Figures 1 and 2 allows to make a conclusion that from three methods of normalization the contrast method is more qualitative. The normalized signal shown in Figure 1d, has the least noise component than other signals. At the same time, as shown in Figure 2c, entropy of signals of investigated objects using the method of contrasts is minimal, that confirmed the assumption about effectiveness using the entropy criterion for evaluating of signal-to-noise ratio.



Picture 1 – Graphs of signals: a) original signal; b) normalized by linear normalization method; c) normalized by non-linear normalization method; d) normalized by contrast method.



Picture 2 – Graphic distribution of entropy of normalized signals investigated objects by using the method: a) linear normalization b) nonlinear normalization c) contrasts.

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Effectiveness of using of the contrast method in this case can be explained by character of data distribution in investigated signal, which supposes an existence of linear regression dependence between analyzed characteristics. The method of nonlinear normalization gives the worst quality among using normalization methods. This can be explained by linear distribution of initial data that makes more efficient use of the linear normalization method. This conclusion confirmed by the entropy distribution graphs at using corresponding methods. Value of entropy of the signal in Fig. 2c is considerably higher than in Fig. 2a. It testifies lower value of signal-to-noise ratio in case of use of the non-linear normalization method, that confirmed by visual observations. The graph of normalized signal in Fig. 1c is noisier compared with the graph shown in Fig. 1c.

4. Conclusion

The problem of DNA microarray analysis nowadays is one of the actual problems of modern bioinformatics. Its solution will allow to forecast development of many genetic and epidemiology diseases with purpose to treat them on time. Preprocessing data is an essential step in the process of data analysis, which predetermines the quality of obtained final information. Data normalization is one of the major stages of preprocessing data. Experiments showed that qualitatively executed normalization allows to transform data to range convenient for further processing, while increasing the value of signal-to-noise ratio. An efficiency of using criteria Shannon entropy for evaluating quality of data normalization is showen in the article. Improving of quality of data normalization is accompanied by simultaneous entropy decreasing, which means increasing of informativeness of secondary signal. In future the author is planing to develop a system of clustering objects DNA microarrays, where presented research will be used for selecting optimum set of data preprocessing methods.

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ON-LINE ROBUST FUZZY CLUSTERING BASED ON SIMILARITY MEASURE

Abstract. The problem of fuzzy adaptive on-line clustering of data distorted by outliers sequentially supplied to the processing when the original sample volume and the number of distorted observations are unknown is considered. The probabilistic and possibilistic clustering algorithms for such data, that are based on the similarity measure of a special kind that weakens or overwhelming outliers are proposed.

Index Terms. Computational and artificial intelligence, fuzzy neural networks, machine learning, multi-layer neural network.

Introduction

The problem of clustering data sets are often occurs in many practical problems, and its solution has been successfully used mathematical apparatus of computational intelligence [1] and first of all, artificial neural networks and soft computing methods (in the case of overlapping classes) is usually assumed that original array is specified a priori and processing is made in batch mode. Here as one of the most effective approach based on using FCM [2], which is reduced as a result to minimize the objective function with constraints of special form.

Real data often contains abnormal outliers of different nature, for example, measurement errors or distributions with "heavy tails". In this situation classic FCM is not effective because the objective function based on the Euclidean metric, only reinforces the impact of outliers. In such conditions it is advisable to use robust objective functions of special form [3], the overwhelming influence of outliers. For information processing in a sequential mode, in [4-6] adaptive procedures on-line fuzzy clustering have been proposed, which are in fact on-line modifications of FCM, where instead of the Euclidean metric robust objective functions, weaken the influence of outliers where used.

Statement of the Problem

The problem of robust on-line clustering based on objective functions is proposed using similarity measure of special form, which allows to synthesize efficient and numerically simple algorithms is proposed.

Baseline information for solving the task of clustering in a batch mode is the sample of observations, formed from N n-dimensional fea-

ture vectors $X = \{x_1, x_2, ..., x_N\} \subset R^n$, $x_k \in X$, $k = 1,2,...,N$. The result of clustering is the partition of original data set into m classes $(1 < m < N)$ with some level of membership $U_q(k)$ of k-th feature vector to the q-th cluster $(1 \le q \le m)$. Incoming data are previously centered and standardized by all features, so that all observations belong to the hypercube $[-1,1]^n$. Therefore, the data for clustering form array $\tilde{X} = \{\tilde{x}_1, ..., \tilde{x}_k, ..., \tilde{x}_N\} \subset R^n$, $\tilde{x}_k = (\tilde{x}_{k1}, ..., \tilde{x}_{ki}, ..., \tilde{x}_{kn})^T$, $-1 \le \tilde{x}_{ki} \le 1$, $1 < m < N$, $1 \le q \le m$, $1 \le i \le n$, $1 \le k \le N$ that is, all observations $\tilde{x}_{ki}$ are available for processing.

We have developed numerically simple on-line procedure for partitioning sequentially fed to the data processing $\tilde{x}_k$ on m perhaps overlapping classes, while it is not known in advance whether $\tilde{x}_k$ undistorted or contains missing values and outliers. Furthermore, it is assumed that the amount of information under processing is not known in advance and is increased with time.

Adaptive Fuzzy Robust Data Clustering Based on Similarity Measure

As already mentioned, to solve the problem of fuzzy clustering of data containing outliers the special objective functions of the form [3-6] can be used, by some means these anomalies overwhelming, and the problem itself is associated with the minimization of these functions. From a practical point of view it is more convenient to use instead of the objective functions, based on the metrics, the so-called measures of similarity (SM) [7], which are subject to more lenient conditions than metrics:

$$\begin{cases} S(\tilde{x}_k, \tilde{x}_p) \ge 0, \\ S(\tilde{x}_k, \tilde{x}_p) = S(\tilde{x}_p, \tilde{x}_k), \\ S(\tilde{x}_k, \tilde{x}_k) = 1 \ge S(\tilde{x}_k, \tilde{x}_p). \end{cases}$$

(no triangle inequality), and clustering problem can be "tied" to maximize these measures.

If the data are transformed so that $-1 \le \tilde{x}_{ki} \le 1$ the measure of similarity can be structured so as to suppress unwanted data lying at the edges of interval $[-1,1]$.

Figure 1 illustrates the use of similarity measure as the Cauchy function with different parameters width $\sigma^2 < 1$

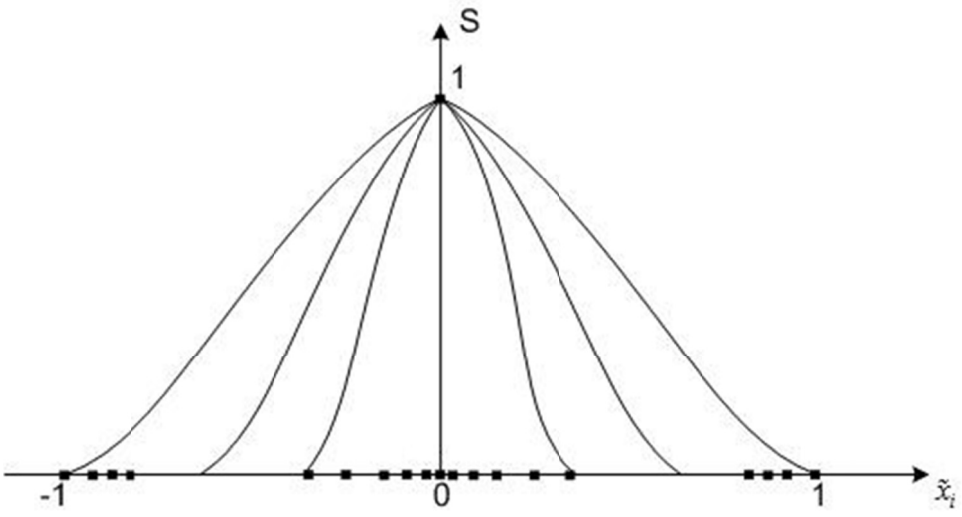

Fig. 1 Similarity measure based on the Cauchy

Picking up the width parameter σ^2 functions

$$S(\tilde{x}_k, w_q) = \frac{1}{1 + \frac{\left\|\tilde{x}_k - w_q\right\|^2}{\sigma^2}} = \frac{\sigma^2}{\sigma^2 + \left\|\tilde{x}_k - w_q\right\|^2} = \\ = \frac{\sigma^2}{\sigma^2 + D^2(\tilde{x}_k, w_q)}, \quad (1)$$

possible exclude the effect outliers, which in principle can not be done using the Euclidean metric

$$D^2(\tilde{x}_k, w_q) = \left\|\tilde{x}_k - w_q\right\|^2. \quad (2)$$

Further, by introducing the objective function based on similarity measure (1)

$$E_S(U_q(k), w_q) = \sum_{k=1}^{N}\sum_{q=1}^{m} U_q^{\beta}(k) S(\tilde{x}_k, w_q) = \\ = \sum_{k=1}^{N}\sum_{q=1}^{m} \frac{U_q^{\beta}(k)\sigma^2}{\sigma^2 + \left\|\tilde{x}_k - w_q\right\|^2},$$

probabilistic constraints

$$\sum_{q=1}^{m} U_q(k) = 1,$$

Lagrange function

$$L_S(U_q(k), w_q, \lambda(k)) = \sum_{k=1}^{N}\sum_{q=1}^{m}\frac{U_q^{\beta}(k)\sigma^2}{\sigma^2 + \left\|\tilde{x}_k - w_q\right\|^2} + \\ + \sum_{k=1}^{N}\lambda(k)(\sum_{q=1}^{m}U_q(k) - 1) \quad (3)$$

(here $\lambda(k)$ - indefinite Lagrange multipliers) and solving the system of Karush-Kuhn-Tucker equations, we arrive at the solution

$$\begin{cases} U_q(k) = \dfrac{(S(\tilde{x}_k, w_q))^{\frac{1}{1-\beta}}}{\sum\limits_{l=1}^{m}(S(\tilde{x}_k, w_l))^{\frac{1}{1-\beta}}}, \\ \lambda(k) = -(\sum\limits_{l=1}^{m}(\beta S(\tilde{x}_k, w_l))^{\frac{1}{1-\beta}})^{1-\beta}, \\ \nabla_{w_q} L_S(U_q(k), w_q, \lambda(k)) = \sum\limits_{k=1}^{N} U_q^{\beta}(k) * \\ \quad * \dfrac{\tilde{x}_k - w_q}{(\sigma^2 + \left\|\tilde{x}_k - w_q\right\|^2)^2} = \vec{0}. \end{cases} \quad (4)$$

The last equation (4) has no analytic solution, so to find a saddle point of the Lagrangian (3) we can use the procedure of Arrow-Hurwitz-Uzawa, as a result of which we obtain the algorithm

$$\begin{cases} U_q(k+1) = \dfrac{(S(\tilde{x}_{k+1}, w_q))^{\frac{1}{1-\beta}}}{\sum\limits_{l=1}^{m}(S(\tilde{x}_{k+1}, w_l))^{\frac{1}{1-\beta}}}, \\ w_q(k+1) = w_q(k) + \eta(k+1)U_q^{\beta}(k+1) *, \\ \quad * \dfrac{\tilde{x}_{k+1} - w_q}{(\sigma^2 + \left\|\tilde{x}_{k+1} - w_q\right\|^2)^2} = \\ = w_q(k) + \eta(k+1)\varphi_q(k+1)(\tilde{x}_{k+1} - w_q) \end{cases} \quad (5)$$

where

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$$\varphi_q(k+1)=\frac{\tilde{x}_{k+1}-w_q}{(\sigma^2+\left\|\tilde{x}_{k+1}-w_q\right\|^2)^2}$$

neighbourhood robust functions of WTM-self-learning rule.

Assuming the value fazzifier as $\beta=2$, we arrive at a robust variant of FCM:

$$\begin{cases} U_q(k+1)=\dfrac{(S(\tilde{x}_{k+1},w_q))}{\sum\limits_{l=1}^{m}(S(\tilde{x}_{k+1},w_l))}, \\ w_q(k+1)=w_q(k)+\eta(k+1)\dfrac{U_q^2(k+1)}{(\sigma^2+\left\|\tilde{x}_{k+1}-w_q\right\|^2)^2}. \end{cases}$$

Further, using the concept of accelerated time, it's possible to introduce robust adaptive probabilistic fuzzy clustering procedure in the form

$$\begin{cases} U_q^{(\tau+1)}(k)=\dfrac{(S(\tilde{x}_k,w_q^{(\tau)}(k)))^{\frac{1}{1-\beta}}}{\sum\limits_{l=1}^{m}(S(\tilde{x}_k,w_l^{(\tau)}))^{\frac{1}{1-\beta}}}, \\ w_q^{(Q)}(k)=w_q^{(0)}(k+1), \\ w_q^{(\tau+1)}(k+1)=w_q^{(\tau)}(k+1)+\eta(k+1)* \\ \quad *\dfrac{(U_q^{(Q)}(k))^{\beta}}{(\sigma^2+\left\|\tilde{x}_{k+1}-w_q^{(\tau)}(k+1)\right\|^2)^2}* \\ \quad *(\tilde{x}_{k+1}-w_q^{(\tau)}(k+1)). \end{cases} \qquad (6)$$

Similarly, it's possible to synthesize a robust adaptive algorithm for possibilistic [8] fuzzy clustering using criterion

$$E_S(U_q(k),w_q,\mu_q)=\sum_{k=1}^{N}\sum_{q=1}^{m}U_q^{\beta}(k)S(\tilde{x}_k,w_q)+$$

$$+\sum_{q=1}^{m}\mu_q\sum_{k=1}^{N}(1-U_q(k))^{\beta}.$$

Solving the problem of optimization, we obtain the solution:

$$\begin{cases} U_q(k+1) = \left(1 + \left(\dfrac{S(\tilde{x}_{k+1}, w_q(k))}{\mu_q(k)}\right)\right)^{-1}, \\ w_q(k+1) = w_q(k) + \eta(k+1) U_q^{\beta}(k+1) * \\ \quad * \dfrac{\tilde{x}_{k+1} - w_q(k)}{(\sigma^2 + \left\|\tilde{x}_{k+1} - w_q(k)\right\|^2)^2}, \\ \mu_q(k+1) = \dfrac{\sum\limits_{p=1}^{k+1} U_q^{\beta}(p) S(\tilde{x}_p, w_q(k+1))}{\sum\limits_{p=1}^{k+1} U_q^{\beta}(p)}, \end{cases} \tag{7}$$

receiving at $\beta = 2$ the form

$$\begin{cases} U_q(k+1) = \dfrac{1}{1 + \dfrac{S(\tilde{x}_{k+1}, w_q(k))}{\mu_q(k)}}, \\ w_q(k+1) = w_q(k) + \eta(k+1) \dfrac{U_q^2(k+1)}{(\sigma^2 + \left\|\tilde{x}_{k+1} - w_q(k)\right\|^2)^2} * \\ \quad * (\tilde{x}_{k+1} - w_q(k)), \\ \mu_q(k+1) = \dfrac{\sum\limits_{p=1}^{k+1} U_q^2(p) S(\tilde{x}_p, w_q(k+1))}{\sum\limits_{p=1}^{k+1} U_q^2(p)}. \end{cases}$$

And, finally, introducing the accelerated time we obtain the procedure

$$U_q^{(\tau+1)}(k) = \frac{1}{1 + \left(\dfrac{S(\tilde{x}_k, w_q^{(\tau)}(k))}{\mu_q^{(\tau)}(k)}\right)^{\frac{1}{\beta-1}}}, \tag{8a}$$

$$w_q^{(Q)}(k) = w_q^{(0)}(k+1), \tag{8b}$$

$$w_q^{(\tau+1)}(k+1) = w_q^{(\tau)}(k+1) + \eta(k+1) \frac{(U_q^{(Q)}(k))^{\beta}}{(\sigma^2 + \left\|\tilde{x}_{k+1} - w_q^{(\tau)}(k+1)\right\|^2)^2} (\tilde{x}_{k+1} - w_q^{(\tau)}(k+1)), \tag{8c}$$

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$$\mu_q^{(\tau+1)}(k) = \frac{\sum_{p=1}^{k} (U_q^{(\tau+1)}(p))^{\beta} S(\tilde{x}_p, w_q^{(\tau+1)}(k))}{\sum_{p=1}^{k} (U_q^{(\tau+1)}(p))^{\beta}}. \quad (8d)$$

Experimental Research

Experimental research conducted on samples of data such as Iris UCI repository.

Iris. This is perhaps the best known database to be found in the pattern recognition literature. Fisher's paper is a classic in the field and is referenced frequently to this day. The data set contains 3 classes of 50 instances each, where each class refers to a type of iris plant. One class is linearly separable from the other 2; the latter are NOT linearly separable from each other. Predicted attribute: class of iris plant. This is an exceedingly simple domain. Number of Instances: 150 (50 in each of three classes). Number of Attributes: 4 numeric, predictive attributes (sepal length in cm, sepal width in cm, petal length in cm, petal width in cm) and the 3 classes: Iris Setosa, Versicolour, Virginica.

To estimate the quality of the algorithm we used quality criteria partitioning into clusters such as: Partition Coefficient (PC), Classification Entropy (CE), Partition Index (SC), Separation Index (S), Xie and Beni's Index (XB), Dunn's Index (DI).

Partition Coefficient (PC): measures the amount of "overlapping" between clusters.

Classification Entropy (CE): it measures the fuzzyness of the cluster partition only, which is similar to the Partition Coefficient.

Partition Index (SC): is the ratio of the sum of compactness and separation of the clusters. It is a sum of individual cluster validity measures normalized through division by the fuzzy cardinality of each cluster. SC is useful when comparing different partitions having equal number of clusters. A lower value of SC indicates a better partition.

Separation Index (S): on the contrary of partition index (SC), the separation index uses a minimum-distance separation for partition validity.

Xie and Beni's Index (XB): it aims to quantify the ratio of the total variation within clusters and the separation of clusters. The optimal number of clusters should minimize the value of the index.

Dunn's Index (DI): this index is originally proposed to use at the identification of "compact and well separated clusters". So the result of the clustering has to be recalculated as it was a hard partition algorithm.

The experimental results are presented in the table 1.

We also compared the results of our proposed algorithm with other more well-known such as Fuzzy C-means (FCM) clustering algorithm.

Table I

Results of Experiments

Algorithms	Iris UCI repository					
	PC	CE	SC	S	XB	DI
Adaptive fuzzy robust clustering data based on similarity measure	0,0199	0,0122	-2439807	0,0022	0,0015	1
FCM	0,8011	0,3410	0,2567	0,0030	7,1965	0,0080

Fig. 2 shows the work of data clustering algorithm that is not corrupted by abnormal outliers.

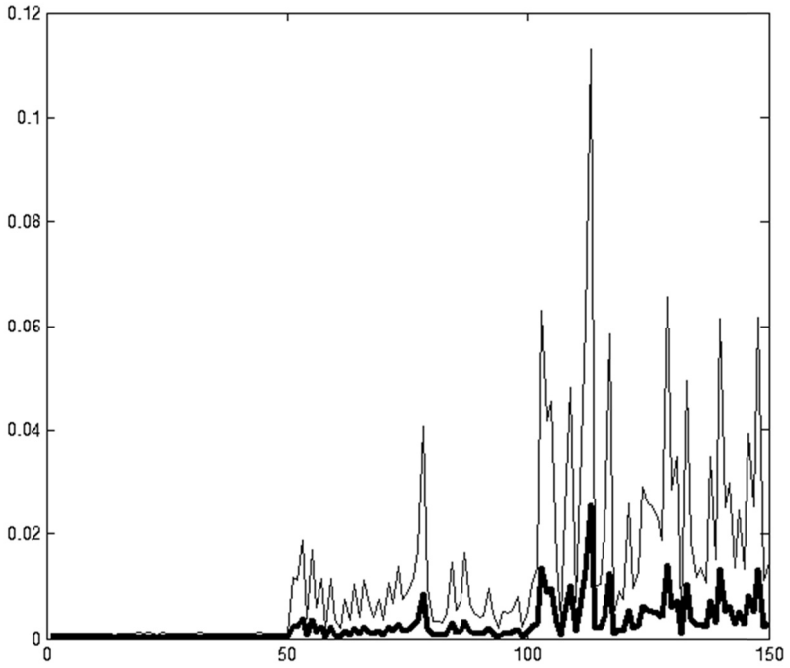

Fig. 2. Data clustering that is not corrupted by abnormal outliers, where solid line is membership level; bold line is function of similarity measure.

The outliers were added manually. Next figure (fig. 3) shows sensitivity to outliers in the data set Iris.

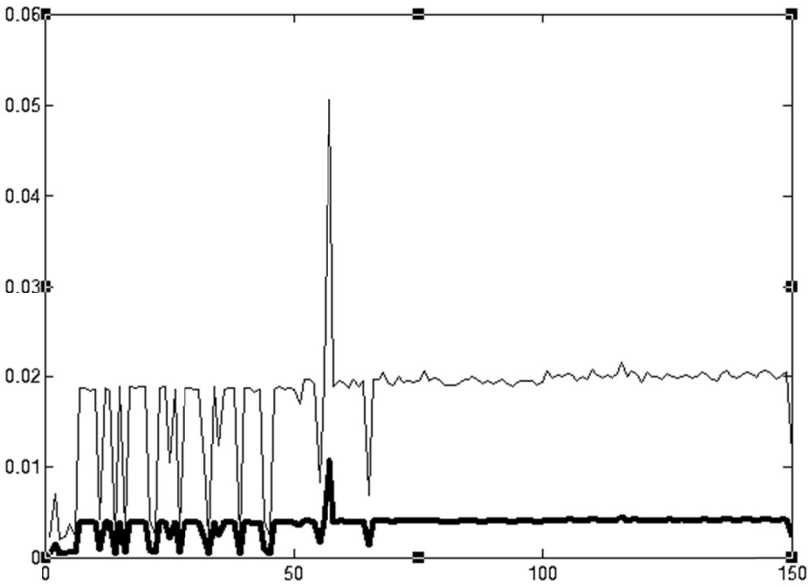

Fig. 3. Sensitivity to outliers in the data set Iris, where solid line is membership level; bold line is function of similarity measure.

Conclusions

There is a group of robust adaptive fuzzy clustering algorithms introduced, allowing in on-line mode to process distorted data containing outliers. The basis of the proposed algorithms is using of classical procedures as fuzzy c-means of J. Bezdek, T. Kohonen self-learning, as well as specially introduced similarity measure allowing to work with distorted information. The algorithms are simple in numerical implementation, being essentially gradient optimization procedures for objective functions of special form.

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MATHEMATICAL ASPECTS OF BIBLIOMETRICAL ANALYSIS OF INVESTIGATIONS CARRIED OUT ON NEUROPHYSIOLOGICAL OBJECTS OF DIFFERENT KINDS (MEDLINE-INTERNET)

Introduction

Abstract. Bibliometrical data on neurophysiological published works carried out on different objects (the brain, the cortex, neurons, nerves) are presented. Quantitative characteristics of published works of choose subdivisions during 35-year time interval (1966-2000) be considered. Dynamics of number of published works of these trends is analyzed. Conclusion about prospects of neurophysiological investigations, in particularly on neuronal levels done.

Keywords. Published work, non-ionized radiation, neurophysiological, bibliometrical indices, nervous system.

Neurophysiology is one of the most intensively developing parts of biology. Its achievements can enable to understand organization and control of functions of organism and even mentality [1, 2, 5, 15]. Neurophysiological investigations are extremely in touch with electrophysiological approaches [1].

Purposeful investigation of electrical processes in the brain arose in the late XIX-th century. Formation of Russian neurophysiology and electrophysiology is undoubtedly relates to M.N. Livanov who created whole school of excellent specialists of mentioned trend - I.N. Kondratyeva, T.A. Korolkova, G.I. Shulgina and etc. [10]. The author of the present work began to work in laboratory by M.N. Livanov.

Bibliometrical investigation of published material on neurophysiology and electrophysiology was not carried out up to now. The present work is devoted just to this material. Some results of our bibliometrical investigations on this problem partly were presented in our published works [3, 4, 6].

Materials and methods

Quantitative characteristics of published works in trend of neurophysiology in world during 35-year interval in second half of the XX century (1966-2000) were considered. Investigations were carried out by means of mainly the database "Medline" accessible through Internet.

Bibliometrical data concerned published works performed in different neurophysiological objects were studied: the brain, the cortex, neurons, nerves. The numbers of published works of observed trends were determined for every analyzed years with the aid of corresponding key words.

At statistical analysis of the received bibliometrical data usual Student *t*-test for comparison of mean values, another Student *t*-test and Wilcoxon test for conjugate pairs were used. Besides the comparison of the parts of the numbers of publications carried out on different neurophysiological objects in general totality and the comparison of the numbers of publications in different time periods were performed as the comparison of two selective sampling fractions of variants.

Results

In considered 35-yaer interval the total number of published works carried out in different neurophysiological objects reached almost 1.5 millionth.

General characteristics of received totalities are presented in table 1. Sampling fractions of obtained data on different neurophysiological objects from their total sum are shown in table 2. Statistical comparison of mean quantities, conjugate pairs of corresponding values, and indicated sampling fractions is reflected in table 3. Dynamics of the numbers of published neurophysiological works of different kinds is show in table 4. Dynamics of the considered sampling fractions (%) are demonstrated in tables 5 and 6. All kinds of dynamics are in base of indices for different five-year intervals.

Table 1 shows that among published neurophysiological works carried out in different neurophysiological objects the predominance of works carried out in the whole brain took place in investigated time interval

Table 2 demonstrates that sampling fraction (%) from total data in published neurophysiological works completely prevailed in works carried out in the whole brain. The least sampling fraction (%) is observed at works on the cortex.

Data of statistical analysis represented in table 3 proved significance of distinctions between mean quantities of the numbers of indicated of published works, conjugate pairs of corresponding values, and indicated sampling fractions. The letter is most pronounced.

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Table 1

General data on the number of published neurophysiological works carried out upon different objects during 35-year interval

Objects	Characteristics of totalities			
	Total number of papers in 35 years	Sampling variance	Average number of papers in 1 year	Standard deviation
1	705259	58408316.37	20150.26	1291.82
2	180602	3266247.76	5160.06	305.49
3	237160	19665941.47	6776.00	749.59
4	278279	10921755.50	7950.83	558.61
5	1401300	293697907.7	40037.14	2896.79

Application: 1 - the brain, 2 - the cortex, 3 - neurons, 4 - nerves, 5- sum.

Table 2

Sampling fractions (%) of published neurophysiological works carried out upon different objects from their sum during 35-year interval

Objects	Sampling fractions from total number of neurophysiological works (%)
1	50.33
2	12.89
3	16.92
4	19.86
5	100.00

Application: as in table 1.

Dynamics of the observed bibliometrical indices during 35-year period is presented in tables 4-6.

Table 4 gave dynamics of the concrete numbers of published neurophysiological works carried out carried out in different neurophysiological objects during 35-year interval. In this table one can see the gradually development of the considerable increase of the numbers of published neurophysiological works of all kinds during 35-year interval.

Table 5 reflects dynamics of the sampling fractions (%) of published neurophysiological works of different kinds from them number during 35-year interval. Essential increase of these values is observed. The most distinct progressive increase was observed at work on neuronal

level. Comparison of indices with average quantity of sampling fractions shows its statistical significance in all cases.

Table 3

Comparison of quantitative indices of published neurophysiological works of different kinds

Objects	Comparison of received data			
	Student test for comparison of mean quantities (*t*)	Student *t*-test for conjugate pairs	Wilcoxon test for conjugate pairs (*U*)	Comparison of sampling fractions of totality (*U*)
1 - 2	**11.29**	**15.16**	**5.15**	**705.63**
1 - 3	**8.95**	**23.74**	**5.15**	**611.05**
1 - 4	**8.67**	**16.61**	**5.15**	**546.59**
2 - 3	**2.00**	**3.57**	**2.78**	**94.59**
2 - 4	**4.38**	**10.82**	**5.15**	**159.04**
3 - 4	**1.26**	**5.42**	**3.93**	**64.45**

Application: statistically significant distinctions between distributions are underlined (U>2.58 corresponds to p<0.01); the other designations as in table 1.

Table 4

Dynamics of the number of published neurophysiological works carried out upon different objects during 35-year interval

Objects	Indices for different five-year intervals						
	1966-70	1971-75	1976-80	1981-85	1986-90	1991-95	1996-2000
1	47198	66047	79531	95671	119201	143246	154365
2	13629	17837	21071	23911	28873	35417	39864
3	7436	13723	19356	28933	41574	58503	67635
4	16895	24918	29804	37964	47548	58285	62865
5	85158	122525	149762	186479	237196	295451	324729

Application: as in table 1.

Table 6 demonstrates dynamics of the sampling fractions (%) of neurophysiological published works of different kinds in single five-year periods from their total number. Predominance of the sampling fractions (%) of works on the whole brain takes place. Therefor gradual increase of sampling fractions (%) of works on neurons is observed. Found arrangements (except works on nerves and the cortex in some periods) are statistical significance.

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Table 5

Dynamics of the sampling fractions (%) of published neurophysiological works carried out upon different objects from them number during 35-year interval

Objects	Indices for different five-years periods						
	1966-70	1971-75	1976-80	1981-85	1986-90	1991-95	1996-2000
Sampling fractions from total number of these works (%)							
1	6.69	9.36	11.28	13.57	16.90	20.31	21.89
2	7.54	9.88	11.67	13.24	15.99	19.61	22.07
3	3.14	5.79	8.16	12.20	17.53	24.67	28.52
4	6.07	8.95	10.71	13.64	17.09	20.94	22.59
5	6.08	8.74	10.69	13.31	16.93	21.08	23.17
Comparison of indices with average quantity of sampling fractions (U)							
1	149.64	91.45	54.04	13.06	42.16	94.42	117.58
2	66.41	40.87	23.74	9.32	14.12	42.37	60.70
3	144.63	100.21	67.84	21.35	30.30	90.57	97.45
4	103.70	62.67	41.03	7.46	28.72	65.28	80.20
5	232.70	147.32	92.08	24.27	80.27	148.99	190.85

Application: average quantity of sampling fractions of published works for five-year interval was 14.29% (100%:7); the other designations as in table 3.

Conclusion

The results of the present bibliometrical investigations makes it possible to analyze quantitative characteristics of neurophysiological published works carried out in different objects (the brain, the cortex, neurons, nerves) during 35-year interval of second half of XX century (1966-2000 years). The numbers of these published works were found for every observed year. Dynamics of the numbers of published works was studied.

It was established that the total number of published works on neurophysiological objects was almost 1.5 millionth. The predominance of works performed in the whole brain took place in investigated period, which is conditioned by relatively simplicity of research approaches.

Positive dynamics of the number of neurophysiological published works of all indicated kinds during 35-year interval was observed. But dynamics of the sampling fractions (%) of neurophysiological published works carried out in different objects were complex and unequal. The most considerable increase was observed at work on neuronal level.

Table 6

Dynamics of the sampling fractions (%) of published neurophysiological works carried out upon different objects in single five-year periods from their total number

Objects	Indices for different five-year intervals						
	1966-70	1971-75	1976-80	1981-85	1986-90	1991-95	1996-2000
Sampling fractions from total number of these works (%)							
1	55.42	53.91	53.10	51.30	50.25	48.48	47.54
2	16.00	14.56	14.07	12.82	12.17	11.99	12.28
3	8.73	11.20	12.92	15.51	17.53	19.80	20.82
4	19.84	20.34	19.90	20.36	20.05	19.73	19.36
Comparison of indices with average quantity of sampling fractions (U)							
1	24.69	19.57	16.10	5.90	0.66	12.73	19.71
2	21.51	12.96	9.95	0.93	7.25	9.67	6.69
3	60.62	45.77	32.78	12.12	4.94	25.56	35.19
4	0.24	3.31	0.29	3.73	1.32	1.38	4.57

Application: average quantities of sampling fractions of published works in five-year interval were 1 - 50.33%; 2 - 12.89%; 3 - 16.92%; 4 - 19.86%; the other designations as in table 3.

Unfortunately neurophysiological researches will have further development in XXI century that is necessary for understanding of function of nervous system. The most development is expected at investigations on neurons level.

At present it is recognized that fundamental science is need for our civilization itself and humanity even [2, 7, 8, 11, 13, 14]. Only on the base of fundamental science applied investigation in part technology and medicine [9, 15]. Consequently society (and government) must support fundamental science [12].

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SPECTRAL PROPERTIES OF DISCRETE NEURAL FUNCTIONS OVER A GALOIS FIELD

Abstract. The paper deals with the discrete functions over a Galois field. We give the necessary and sufficient condition of discrete functions decomposition in group characters. The notion of neural element over a Galois field is introduced and the criterion of discrete functions realizability on a single neuron is proved in the paper. We also propose a spectral synthesis method over a finite field.

Keywords: neuron, spectral coefficient, structure vector, group character.

Introduction

Finite fields and groups are widely spread in the automata theory and logic [1-3]. They are particularly important in the coding theory [1]. It is shown in [4] that any finite automaton is isomorphic to the linear one over some finite field. Analysis and synthesis of linear automata over an arbitrary finite field are carried out by the traditional spectral analysis. It is shown in the paper that the basic methods of spectral analysis can be successfully used for the verification of discrete functions realizability by one neural element over a Galois field.

1. Spectral analysis of discrete functions over a Galois field

Let $F = GF\left(p^m\right)$ be the Galois field containing cyclic groups

$$H_{k_1} = \langle a_1 \mid a_1^{k_1} = 1\rangle, \quad H_{k_2} = \langle a_2 \mid a_2^{k_2} = 1\rangle, \quad \ldots \quad , H_{k_n} = \langle a_n \mid a_n^{k_n} = 1\rangle$$

and $G_n = H_{k_1} \otimes H_{k_2} \otimes \ldots \otimes H_{k_n}$ be the direct product of cyclic groups H_{k_i}.

Let $F = GF\left(p^m\right)$ be the Galois field containing cyclic groups

$$H_{k_1} = \langle a_1 \mid a_1^{k_1} = 1\rangle, \; H_{k_2} = \langle a_2 \mid a_2^{k_2} = 1\rangle, \ldots, \; H_{k_n} = \langle a_n \mid a_n^{k_n} = 1\rangle$$

and $G_n = H_{k_1} \otimes H_{k_2} \otimes \ldots \otimes H_{k_n}$ be the direct product of cyclic groups H_{k_i}.

A mapping $f : G_n \to F$ is a discrete n-variable function.

It should be noted that the spectral analysis of discrete functions

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$f: G_n \to C$ over complex field is always possible because complex field contains the primitive k-th root of unity, where k is the least common multiple of $k_1, k_2, \ldots, k_n$.

If $F = GF\left(p^m\right)$, then the spectral analysis of discrete functions $f: G_n \to C$ isn't always possible. It is possible when the dimension of vector space $V_F^n = \left\{ f \mid f: G_n \to GF\left(p^m\right) \right\}$ and the order of character group $X(G_n)$ over fields F are equal.

We consider the task of function $f: G_n \to F$ decomposition in characters of the G_n group over F field. If $k_1 = k_2 = \ldots = k_n = 2$ and F is the field of real numbers R, then the characters group $X\left(G_n\right)$ of the group G_n over field R is equal to Hadamard-Walsh functions system and the spectral analysis is possible.

If $k_1 = k_2 = \ldots = k_n = k\left(k > 2\right)$ and the field F is the complex field C, then the characters group $X\left(G_n\right)$ of the group G_n over field C is equal to Vilenkin-Krestenson functions system and the spectral analysis of discrete function is also possible.

Let $k = \mathrm{lcm}\left(k_1, k_2, \ldots, k_n\right)$. It's easy to show that if the field $F = GF(p^m)$ contains the primitive k-th root of unity, then $u = p^m - 1$ is multiple of k. Suppose that the field with the primitive element $\square$ contains the primitive k-root $\square$. Then the cyclic group $H_k = \left\langle \sigma \mid \sigma^k = 1 \right\rangle$ is the subgroup of field cyclic subgroup. Using the Lagrange theorem [5], we obtain that k is the divisor of number u. Let's consider $\sigma = \varepsilon^{u/k}$ and prove that $\square$ is the primitive root of unity. Since $\square$ is the primitive in F, we have [6-8] that for all $i, j, r \in \left\{1, 2, \ldots, k-1\right\}$ $\sigma^i \neq \sigma^j$, if $i \neq j$ and $\sigma^r \neq 1$. Therefore k is the least natural number that $\sigma^k = 1$. So we can conclude that the spectral analysis of discrete function $f: G_n \to F$ is possible then and only then when u is multiple of k.

Let's find the analytic view of group G_n characters over the field $F = GF\left(p^m\right)$. Let $k = \mathrm{lcm}\left(k_1, k_2, \ldots, k_n\right)$, $\square$ be the primitive element of field $F = GF\left(p^m\right)$, $H_k = \left\langle a \mid a^k = 1 \right\rangle$ is the cyclic group of the order k, and k is

the divisor of the number u. Then for all $h_i \in H_{k_i}$ exists number $j_{k_i} \in \{0,1,\ldots,k_i-1\}$ such that $h_i = a_i^{j_{k_i}}$, where $a_i = a^{k/k_i}$ is the generating element of group $H_{k_i}\,(i=1,2,\ldots,n)$. The characters χ_{r_i} of the group H_{k_i} over the field $F = GF(p^m)$ may be written as

$$\chi_{r_i}(h_i) = \sigma_i^{r_i j_{k_i}}, \tag{1}$$

where $\sigma_i = \varepsilon^{u/k_i}$, $r_i \in \{0,1,\ldots,k_i-1\}$.

Since the group G_n is the direct product of cyclic groups $H_{k_1},\ldots,H_{k_n}$, for all $\mathbf{g} \in G_n$ there exist numbers $j_i \in \{0,1,\ldots,k_i-1\}, i=1,2,\ldots,n$ such that $\mathbf{g} = \left(a_1^{j_1},\ldots,a_n^{j_n}\right) = \left(a^{kj_1/k_1},\ldots,a^{kj_n/k_n}\right)$.

The next formula follows from the multiplicative property of characters [6] and (1) concerning the general form of characters:

$$\chi_{(r_1,\ldots,r_n)}(\mathbf{g}) = \sigma^{t_1 r_1 j_1 + \ldots + t_n r_n j_n}, \tag{2}$$

where $\sigma = \varepsilon^{u/k}$, $t_i = \dfrac{k}{k_i}$, $r_i \in \{0,1,\ldots,k_i-1\}$, $i=1,2,\ldots,n$. It's possible to define the character product on the group G_n as follows:

$$\forall \mathbf{g} \in G_n \quad \chi_{(r_1,\ldots,r_n)}(\mathbf{g}) \cdot \chi_{(q_1,\ldots,q_n)}(\mathbf{g}) = \chi_{(r_1 \oplus_1 q_1,\ldots,r_n \oplus_n q_n)}(\mathbf{g}),$$

where $\oplus_i$ is the k_i-addition. Thus we obtain the multiplicative character group $X(G_n)$. We have the next consequence from (2): the number of different characters of group G_n over the field F is equal to the order of group G_n. Then from the orthogonality of characters [6, 9] and from $\left|X(G_n)\right| = \dim_F V_F^n = k_1 k_2 \ldots k_n$ we obtain that $X(G_n)$ is the orthogonal basis of the space V_F^n. Thus, an arbitrary $f \in V_F^n$ can be uniquely written as follows:

$$f(\mathbf{g}) = \sum_{r_1=0}^{k_1-1} \ldots \sum_{r_n=0}^{k_n-1} s_{(r_1,\ldots r_n)} \chi_{(r_1,\ldots,r_n)}(\mathbf{g}), \tag{3}$$

where addition and multiplication are considering in the field F.

The decomposition (3) is called the spectral decomposition of discrete function $f: G_n \to F$ in characters of G_n over the field F.

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Multiplying the both sides of (3) in $\chi^{-1}_{(q_1,\ldots,q_n)}$ and summarizing by all elements of G_n, we obtain the following equality

$$\sum_{\mathbf{g}\in G_n} f(\mathbf{g})\chi^{-1}_{(q_1,\ldots,q_n)}(\mathbf{g}) = \sum_{\mathbf{g}\in G_n}\left(\sum_{r_1=0}^{k_1-1}\cdots\sum_{r_n=0}^{k_n-1} s_{(r_1,\ldots,r_n)}\chi_{(r_1,\ldots,r_n)}(\mathbf{g})\right)\chi^{-1}_{(q_1,\ldots,q_n)}(\mathbf{g}).$$

Subject to the orthogonality of characters the right side of last equality can be written as follows:

$$\sum_{\mathbf{g}\in G_n}\left(\sum_{r_1=0}^{k_1-1}\cdots\sum_{r_n=0}^{k_n-1} s_{(r_1,\ldots,r_n)}\chi_{(r_1,\ldots,r_n)}(\mathbf{g})\right)\chi^{-1}_{(q_1,\ldots,q_n)}(\mathbf{g}) =$$

$$= \sum_{r_1=0}^{k_1-1}\cdots\sum_{r_n=0}^{k_n-1} s_{(r_1,\ldots,r_n)}\left(\sum_{\mathbf{g}\in G_n}\chi_{(r_1,\ldots,r_n)}(\mathbf{g})\chi^{-1}_{(q_1,\ldots,q_n)}(\mathbf{g})\right) = s_{(q_1,\ldots,q_n)}|G_n|.$$

Therefore, the spectral coefficients of the function can be obtained with following formula

$$s_{(q_1,\ldots,q_n)} = |G_n|^{-1}\sum_{\mathbf{g}\in G_n} f(\mathbf{g})\chi^{-1}_{(q_1,\ldots,q_n)}(\mathbf{g}), \qquad (4)$$

where $q_i \in \{0,1,\ldots,k_i-1\}$ $(i\in\{1,2,\ldots,n\})$.

Note. The calculation of spectral coefficients $s_{(r_1,\ldots r_n)}$ of discrete function $f\in V_F^n$ can be done by using the quick algorithms issuing from matrices factorization method [10] and the well-known theorem of the theory of representations [9]: if $G_n = H_{k_1}\otimes H_{k_2}\otimes\ldots\otimes H_{k_n}$ and $|G_n|$ is the divisor of p^m-1, then $X(G_n) = X(H_{k_1})\otimes X(H_{k_2})\otimes\ldots\otimes X(H_{k_n})$ over $GF(p^m)$ field.

2. Discrete neural functions over a Galois field

In this section we introduce the notion of neuron over field $GF(p^m)$ and give the criterion of discrete functions realizability by single neuron over a Galois field.

Let $k_1,k_2,\ldots,k_n,q$ be natural numbers $(k_i\geq 2, i=1,\ldots\ldots,n, q\geq 2)$ and $k=\mathrm{lcm}(k_1,k_2,\ldots,k_n,q)$. We consider only finite fields $F=GF(p^m)$ satisfy-

ing the following condition: $p^m - 1$ is exactly divided by k. It means that field $F = GF\left(p^m\right)$ contains cyclic groups H_{k_i}, H_q with respective group generators $\sigma_i = \varepsilon^{u/k_i}$ $\left(i = 1,2,\ldots,n\right)$, $\sigma = \varepsilon^{u/q}$, where ε is the primitive element of field F, $u = p^m - 1$.

Define the function $\mathrm{Fsign}\xi$ on $F \setminus \{0\}$ as follows:

$$\forall \xi \in F \setminus \{0\} \quad \mathrm{Fsign}\xi = \sigma^j, \text{ if } \frac{ju}{q} \le \deg \xi < \frac{(j+1)u}{q},$$

where $\deg \xi$ is the degree of element $\xi\left(\xi = \varepsilon^{\deg \xi}\right)$, $j \in \{0,1,\ldots,q-1\}$.

A neuron over field $F = GF\left(p^m\right)$ is a logical unit with $n+1$ inputs $x_1,\ldots,x_n; x_0$ $\left(n \ge 1\right)$ taking values respectively from cycling group H_{k_i} $(i = 1,\ldots,n)$ and $H_0 = \{1\}$, and a single output taking value from the group H_q. Weights ω_i from the field F correspond to respective inputs x_i. The output of unit is obtained as the result of sign-function $\mathrm{Fsign}\xi$ on "weighted sum" $\omega_1 x_1 + \ldots + \omega_n x_n + \omega_0$ of inputs as Fig. 1 illustrates.

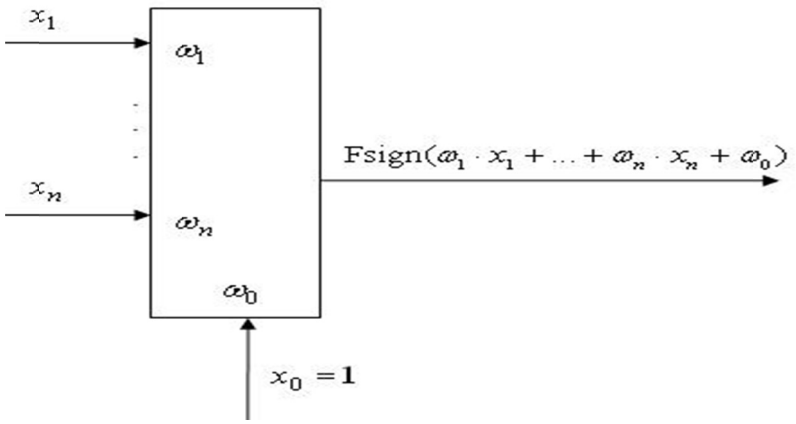

Fig. 1. A representation of neuron over a Galois field

The vector $\mathbf{w} = \left(\omega_1,\ldots,\omega_n;\omega_0\right)$ is called the structure vector of neuron over a Galois field $\left(\omega_i \in GF\left(p^m\right)\right)$.

Let $G_n = H_{k_1} \otimes H_{k_2} \otimes \ldots \otimes H_{k_n}$ be a direct product of cyclic groups H_{k_i}. A discrete function $f : G_n \to H_q$ is realizable by a single neuron over field $F = GF\left(p^m\right)$ if exists $(n+1)$-dimensional vector $\mathbf{w} = \left(\omega_1,\ldots,\omega_n;\omega_0\right)$

such that for all $\mathbf{g}=(\gamma_1,\ldots,\gamma_n)\in G_n$ $f(\mathbf{g})=\mathrm{Fsign}\,\mathrm{w}(\mathbf{g})$, where $\mathrm{w}(\mathbf{g})=\omega_1\gamma_1+\ldots+\omega_n\gamma_n+\omega_0$. A discrete function $f:G_n\to H_q$ realizable on a single neuron over field F is called a neural function over F.

Let $f:G_n\to H_q$ be an arbitrary discrete function. The question arises about realizability of f by a single neuron over filed $F=GF(p^m)$ and synthesis of structure vector $\mathbf{w}=(\omega_1,\ldots,\omega_n;\omega_0)$ of a corresponding neuron.

Let $X^*(G_n)=\left\{\chi_{(0,0,\ldots,0,0)},\chi_{(1,0,\ldots,0,0)},\chi_{(0,1,\ldots,0,0)},\ldots,\chi_{(0,0,\ldots,1,0)},\chi_{(0,0,\ldots,0,1)}\right\}$.

Theorem 1. *A discrete function $f:G_n\to H_q$ is realizable by a single neuron over field $F=GF(p^m)$ with the structure vector $\mathbf{w}=(\omega_1,\ldots,\omega_n;\omega_0)$ if and only if there exists $r:G_n\to F\setminus\{0\}$ such that*

$$0\le\deg r(\mathbf{x})<\frac{u}{q}, \tag{5}$$

and

$$\left(r(\mathbf{x})f(\mathbf{x}),\chi^{-1}(\mathbf{x})\right)=0, \tag{6}$$

for all $\chi\in X(G_n)\setminus X^*(G_n)$, where $(\mathbf{a},\mathbf{b})$ is the standard inner product of vectors **a** *and* **b**.

Proof. At first we shall prove the necessity of the conditions. A discrete function $f:G_n\to H_q$ is realizable over F by a single neuron with the structure $\mathbf{w}=(\omega_1,\ldots,\omega_n;\omega_0)$. That is

$$\forall\mathbf{g}\in G_n\quad f(\mathbf{g})=\mathrm{Fsign}\,\mathrm{w}(\mathbf{g}). \tag{7}$$

Construct the function $r(\mathbf{g})$ in the following way: for all $\mathbf{g}\in G_n$ assume

$$\deg r(\mathbf{g})=\deg \mathrm{w}(\mathbf{g})-\deg f(\mathbf{g}). \tag{8}$$

Then $\deg \mathrm{w}(\mathbf{g})=\deg r(\mathbf{g})+\deg f(\mathbf{g})$ and for an arbitrary $\mathbf{g}\in G_n$

$$f(\mathbf{g})r(\mathbf{g})=\omega_0+\omega_1x_1(\mathbf{g})+\cdots+\omega_nx_n(\mathbf{g}). \tag{9}$$

Suppose that the value of f on an arbitrary fixed element $\mathbf{g} \in G_n$ is σ^j. Then from (7) follows

$$\frac{ju}{q} \le \deg \mathrm{w}(\mathbf{g}) < \frac{(j+1)u}{q}. \tag{10}$$

The inequality (10) can be written as follows:

$$\frac{ju}{q} - \deg f(\mathbf{g}) \le \deg \mathrm{w}(\mathbf{g}) - \deg f(\mathbf{g}) < \frac{(j+1)u}{q} - \deg f(\mathbf{g}).$$

From the last inequality, (8) and

$$\deg f(\mathbf{g}) = \frac{ju}{q},$$

$\left(f(\mathbf{g}) = \sigma^j = \varepsilon^{ju/q}\right)$ follows $0 \le \deg r(\mathbf{g}) < \frac{u}{q}$.

Now we give the proof of the sufficiency of the theorem condition. Let us assume that for $f: G_n \to H_q$ exists a function $r: G_n \to F \setminus \{0\}$ satisfying conditions (5) and (6). We can expand the function $r(\mathbf{x}) f(\mathbf{x}) \in V_F^n$ in characters of group G_n over field F. In consideration of (6) and $\forall \chi \in \chi(G_n) \setminus \chi^*(G_n)$ $s_\chi = =|G_n|^{-1} \left(r(\mathbf{x}) f(\mathbf{x}), \chi^{-1}(\mathbf{x})\right)$ we have $s_\chi = 0$. It means

$$r(\mathbf{x}) f(\mathbf{x}) = \sum_{\chi \in \chi^*(G_n)} s_\chi \chi(\mathbf{x}). \tag{11}$$

The equality (11) can be written as follows:

$$r(\mathbf{x}) f(\mathbf{x}) = s_{(0,\cdots,0)} \chi_{(0,\cdots,0)}(\mathbf{x}) + s_{(1,\cdots,0)} \chi_{(1,\cdots,0)}(\mathbf{x}) + \cdots + s_{(0,\cdots,1)} \chi_{(0,\cdots,1)}(\mathbf{x}),$$

or

$$r(\mathbf{x}) f(\mathbf{x}) = \omega_0 + \omega_1 \chi_{(1,\cdots,0)}(\mathbf{x}) + \cdots + \omega_n \chi_{(0,\cdots,1)}(\mathbf{x}). \tag{12}$$

According to our definition $\chi_{(1,\cdots,0)}(\mathbf{x}) = x_1(\mathbf{x}), \cdots, \chi_{(0,\cdots,1)}(\mathbf{x}) = x_n(\mathbf{x})$. Thus,

$$r(\mathbf{x}) f(\mathbf{x}) = w(\mathbf{x}). \tag{13}$$

The direct consequence from (13) is the fact that for all $\mathbf{g} \in G_n$

$$\deg r(\mathbf{g}) = \deg \mathrm{w}(\mathbf{g}) - \deg f(\mathbf{g}).$$

Condition (5) implies that

$$0 \le \deg \mathrm{w}(\mathbf{g}) - \deg f(\mathbf{g}) < \frac{u}{q}. \qquad (14)$$

Let $\mathbf{g}$ is an arbitrary element in G_n and $f(\mathbf{g}) = \sigma^j$. Then

$$\deg f(\mathbf{g}) = \frac{uj}{q}$$

and from (14) follows

$$\frac{uj}{q} \le \deg \mathrm{w}(\mathbf{g}) < \frac{u(j+1)}{q}.$$

So, for all $\mathbf{g}$ in G_n $f(\mathbf{g}) = \mathrm{Fsign}\,\mathrm{w}(\mathbf{g})$, that proves the sufficiency of theorem conditions.

If a discrete function $f: G_n \to H_q$ satisfies all conditions of theorem 1, then the coordinates of the structure vector $\mathbf{w} = (\omega_1, \ldots, \omega_m; \omega_0)$ of the neuron, realizing f over field F, can be found as follows:

$$\omega_0 = |G_n|^{-1} \left(r(\mathbf{x}) f(\mathbf{x}), \chi^{-1}_{(0,\ldots,0)}(\mathbf{x}) \right),$$

$$\omega_1 = |G_n|^{-1} \left(r(\mathbf{x}) f(\mathbf{x}), \chi^{-1}_{(1,0,\ldots,0)}(\mathbf{x}) \right), \qquad (15)$$

$$\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots$$

$$\omega_n = |G_n|^{-1} \left(r(\mathbf{x}) f(\mathbf{x}), \chi^{-1}_{(0,\ldots,0,1)}(\mathbf{x}) \right).$$

Example. Let $n = 2, k_1 = 2, k_2 = q = 3$ i $G_2 = H_2 \otimes H_3$. Then $k = \mathrm{lcm}(2,3,3)$. So, we can use $GF(13)$ as F with 2 as the primitive element of F, that is $GF(13) \setminus \{0\} = \{2^j \mid j = 0,1,\ldots,11\}$. The group generators of groups H_2, H_3 over F are correspondently $\sigma_1 = 2^{12/2} = 12$ and $\sigma_2 = 2^{12/3} = 3$, and the range of values of function $f: G_n \to H_q$ is the set $\{1,3,9\}$. Table 1 can be used for value assignment of functions $f: G_n \to H_q$, $r: G_n \to F \setminus \{0\}$ and the character group $X(G_2)$ of group G_2 over F:

Table 1.

Values of f, r and characters from $\chi(G_2)$

x_1	x_2	f	r	$\chi_{(0,0)}$	$\chi_{(0,1)}$	$\chi_{(0,2)}$	$\chi_{(1,0)}$	$\chi_{(1,1)}$	$\chi_{(1,2)}$
1	1	1	r_0	1	1	1	1	1	1
1	3	1	r_1	1	3	9	1	3	9
1	9	3	r_2	1	9	3	1	9	3
12	1	3	r_3	1	1	1	12	12	12
12	3	9	r_4	1	3	9	12	10	4
12	9	9	r_5	1	9	3	12	4	10

On the basis of theorem 1 and table 1 we can write the following linear equation system over F:

$$\begin{cases} r_0 + 3r_1 + r_2 + 3r_3 + r_4 + 3r_5 = 0, \\ r_0 + 9r_1 + 9r_2 + 10r_3 + 10r_4 + 12r_5 = 0, \\ r_0 + 3r_1 + r_2 + 10r_3 + 12r_4 + 10r_5 = 0, \end{cases}$$

$r_0, r_1, r_2, r_3, r_4, r_5 \in \{1,2,4,8\}$. The last system has several solutions, one of these is $(1,8,1,1,4,2)$. This system solution may be use for finding the structure vector of the neuron, realizing the function f:

$$\omega_0 = 11 \cdot (1 + 8 + 3 + 3 + 36 + 18) = 11 \cdot 4 = 5,$$
$$\omega_1 = 11 \cdot (1 + 8 + 3 + 3 \cdot 12 + 36 \cdot 12 + 18 \cdot 12) = 11 \cdot 7 = 12,$$
$$\omega_2 = 11 \cdot (1 + 72 + 9 + 3 + 9 \cdot 9 \cdot 4 + 9 \cdot 3 \cdot 2) = 11 \cdot 8 = 10.$$

Therefore, $f(x_1, x_2) = \text{Fsign}(12x_1 + 10x_2 + 5)$.

The design of neuron synthesis methods for partially specific discrete functions is very important in practice, because this task often arises in many applications, such as pattern recognition, diagnostics and talk synthesis

Let a discrete function $f : G_n \to H_q$ be not fully defined on group G_n. We shall denote $D_n \subset G_n$ the set of elements, in which the value of the function f is well defined and let $D'_n = G_n \setminus D_n$ be the set of elements in which the function f is undefined.

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The partially defined discrete function $f: G_n \to H_q$ is realizable on a single neuron over the field F if exists $(n+1)$-dimensional vector $\mathbf{w} = (\omega_1, \ldots, \omega_n; \omega_0)$ such that for all $\mathbf{g} \in D_n$ $f(\mathbf{g}) = \mathrm{Fsign}\, \mathrm{w}(\mathbf{g})$.

Theorem 2. *A partially defined discrete function* $f: G_n \to H_q$ *is realizable on a single neuron over field* $F = GF(p^m)$ *with the structure vector* $\mathbf{w}$ *if such well defined functions* $r: G_n \to F \setminus \{0\}$, $h: G_n \to H_q$ *exist, that the restriction of* h *on* D_n *coincides with* f *and for all* $\mathbf{x}$ *in* D_n *the following conditions are satisfied*

$$0 \le \deg r(\mathbf{x}) < \frac{u}{q},$$

$$\left(r(\mathbf{x}) f(\mathbf{x}), \chi^{-1}(\mathbf{x})\right) = 0,$$

where $\chi \in X(G_n) \setminus X^*(G_n)$.

The proof results from theorem 1.

The class of discrete functions realizable on a single neuron depends on selected Galois field. The computer modeling of synthesis neurons over a finite field F proves that increasing of the cardinality of the field F implies that the cardinality of the class of neural functions does not decrease. The following example confirms the last claim. Let $n = 2, k_1 = k_2 = q = 2$ i $F = GF(3)$. The number u is multiple of $k = \mathrm{lcm}(k_1, k_2, q)$, thus the spectral analysis of Boolean functions over F is possible. It is evident that $\varepsilon = 2$ is the primitive element of the field F. All Boolean neural functions of two variables over F are given in the following table.

Table 2

Neural functions over $GF(3)$

x_1	x_2	g_0	g_1	g_2	g_3	g_4	g_5
1	1	1	1	1	2	2	2
1	2	1	1	2	2	2	1
2	1	1	2	1	2	1	2
2	2	1	2	2	2	1	1

The respective structure vectors are $\mathbf{w}_{g_0} = (0,0;1)$, $\mathbf{w}_{g_1} = (1,0;0)$, $\mathbf{w}_{g_2} = (0,1;0)$, $\mathbf{w}_{g_3} = (0,0;2)$, $\mathbf{w}_{g_4} = (2,0;0)$ and $\mathbf{w}_{g_5} = (0,2;0)$. Thus, the class of Boolean neural functions of two variables over $GF(3)$ contains six functions $g_0, g_1, g_2, g_3, g_4, g_5$.

Let us consider the field $F = GF(5)$. It is possible to take $\varepsilon = 2$ as a primitive element Then $\sigma = \varepsilon^{\frac{5-1}{2}} = 4$. The Boolean neural functions of two variables over $GF(5)$ are given in Table 3.

Table 3

Neural functions over $GF(5)$

x_1	x_2	f_0	f_1	f_2	f_3	f_4	f_5	f_6	f_7	f_8	f_9	f_{10}	f_{11}	f_{12}	f_{13}	f_{14}	f_{15}
1	1	1	1	1	1	1	1	1	1	4	4	4	4	4	4	4	4
1	4	1	1	1	1	4	4	4	4	1	1	1	1	4	4	4	4
4	1	1	1	4	4	1	1	4	4	1	1	4	4	1	1	4	4
4	4	1	4	1	4	1	4	1	4	1	4	1	4	1	4	1	4

The respective structure vectors are

$\mathbf{w}_{f_0} = (0,0;1), \mathbf{w}_{f_1} = (2,2;2), \mathbf{w}_{f_2} = (2,3;2), \mathbf{w}_{f_3} = (1,0;0), \mathbf{w}_{f_4} = (3,2;2), \mathbf{w}_{f_5} = (0,1;0),$
$\mathbf{w}_{f_6} = (1,1;4), \mathbf{w}_{f_7} = (2,2;3), \mathbf{w}_{f_8} = (3,3;2), \mathbf{w}_{f_9} = (4,4;1), \mathbf{w}_{f_{10}} = (0,4;0), \mathbf{w}_{f_{11}} = (2,3;3),$
$\mathbf{w}_{f_{12}} = (4,0;0), \mathbf{w}_{f_{13}} = (3,2;3), \mathbf{w}_{f_{14}} = (3,3;3), \mathbf{w}_{f_{15}} = (0,0;4)$.

We see that all two variable Boolean function are realizable over $GF(5)$. The field $GF(5)$ is the minimal Galois field (by cardinality) having the mentioned property.

Let $k = \text{lcm}(k_1, \ldots, k_n, q) (k_i \geq 2, q \geq 2)$ and $G_n = H_{k_1} \otimes \ldots \otimes H_{k_n}$.

Hypothesis. For any k and n there exists minimal Galois field $F_{\min}$ such that all functions $f : G_n \to H_q$ are realizable on single neuron over which.

Conclusions

The effective synthesis method of many valued neurons over a Galois field is designed on the basis of spectral analysis of discrete functions. This method can be used for solving practical problems, such as information encoding, data compression, data communication, classification, pattern recognition, etc.

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COMPUTER SIMULATION OF THE ACOUSTIC COHERENT IMAGES FORMING AND PROCESSING

Abstract. The approach to increasing the acoustic coherent images space contrast on the base of the using of the proposed methods of multiplicative weighted processing of their space spectra in the receiving plane and effectiveness confirmation of the developed methods by computer simulation of all stages of considered images formation and processing.

Keywords. Methods of image processing, computer simulation.

Introduction. The main purpose of non-destructive testing of power equipment is the detection of latent defects in metal constructions and their space localization and classification with probing of different nature fields. Acoustic waves have a high penetrating power, which enables to study not only the constructions surfaces, but their internal structure. Field, reflected from the investigated object, forms on the receiving aperture its acoustic image. The main feature of these images is their coherent nature, which displays itself in the so-called “speckle pattern”, that impede of their visualization and interpretation. Known mathematical models of objects acoustic fields at the receiving point, that are described in the literature [1,2], are mainly qualitative nature and do not take into account the features of all stages of acoustic coherent images (ACI) formation, namely the creation of a given probe field, its propagation in an inhomogeneous medium, dispersion on a complex surface of the probing object, conditions of backpropagation, processing in receiving equipment [3]. In order to ensure the required ACI space contrast it is necessary to create the receiving apparatus, having a high space resolution in both the longitudinal and broadside directions. The main part of modern receivers are the phased arrays (PA), signal processing in which can be carried out by different methods. Application of classical methods of image processing is based on the theory of linear space-time filtering [2], but they does not give the desired results. It is necessary to use such methods of ACI processing in received arrays, which the most would fit with the characteristics of imades space and time structures. In [4] was proposed the method of weighted multiplicative processing of signals (WMPS), allowing to increase the PA resolution in the breadside direction relative to the resolution of the additive

PA, having the same aperture dimensions, that improves the obtained ACI contrast.

In view of the fundamental differences ACI from their optical analogs there is the need for more in-depth researching and development of methods of improving of these images space contrast on the basis of mathematical models taking into account all stages of their formation and processing.

The purpose of the paper is to justify the possibility of increasing the acoustic coherent images space contrast on the base of the using of the proposed methods of multiplicative weighted processing of space spectra and confirmation of their effectiveness by computer simulation of all stages of considered images formation and processing.

Main part. Creation of adequate ACI mathematical models of the investigated objects in the receiving plane is not possible without simulation of all stages of their formation [3]. Mechanisms of acoustic and optical fields dispersion on the objects surfaces have fundamental differences. Optical fields are inherently incoherent and this leads to the destruction of the phase relations between the signals, reflected from the object surface roughness and to the appearance of the visible image contours.

In the most acoustics applications the space coherence range of the field is comparable or greater than the object dimensions, so the reflected acoustic waves are mostly coherent and the phase information is stored in the received space-time signal. Its preservation is a fundamental difference of optical and acoustic images, that lie to presence in ACI the interference phenomena such as the image spotting. Image spotting is caused by intensity changing of signals, reflected from the character parts of the object surface. This is due to the phase amplification or phase attenuation of the coherent space components of wave fields, receiving on the image plane. In the acoustic image there are interference fringes, arising due to acoustic waves reflection from the sharp corners, cracks on the object surface. Coherent space wave components, taking part in image formation, interfere with each other, that appears in the speckle pattern of images. Acoustic images spotting carries useful information about the object, but the nature of this information is unfamiliar to the observer, so it is difficult to interpret of the object acoustic images.

In view of the difference of space-time scales of the formed secondary acoustic and optical wave fields of investigated objects the interaction of the probe acoustic field with the object surface describes in the literature by the dispersion models, that are significantly different from the incoherent optical dispersion models [5].

For the most problems of secondary field formation of objects complex surfaces by means of ultrasonic probing the description of the wave fields dispersion is based on the Kirchhoff approximation [2,5,6]. Under the conditions, when the Kirchhoff approximation is fulfilment, the object ACI is formed by finite set of local areas of reflection – the first Fresnel zone surrounding area points of stationary phase [5,7], in which the normal to the surface is directed to the receiving point.

Kirchhoff approximation allows sufficiently accurate description of the secondary acoustic fields of objects with complex surfaces, for such its areas, for which the wavelength of the emitted signals are significantly smaller, than the character irregularities of the investigated surfaces. In this case, the complex amplitude of the wave field is described by the equation:

$$w(x,y,z_0)=\frac{e^{jkz_0}}{j\lambda z_0}\cdot\exp\left(jk\frac{x^2+y^2}{2z_0}\right)\cdot(2\pi)^2\cdot F(k_x,k_y), \qquad (1)$$

where x,y – the Cartesian coordinates in the aperture plane, z_0 – the distance between the investigated object and the plane of the receiving aperture, $\square$ – wavelength, k – wave number, $k_x=kx/z_0, k_y=ky/z_0$ – angular frequency, $F(k_x,k_y)$ – angular (space) spectrum of the dispersion function (DF) of the surface relatively to the object plane, defined as follows:

$$F(k_x,k_y)=\frac{1}{(2\pi)^2}\cdot\int_{-\infty}^{\infty}\int_{-\infty}^{\infty}\dot{u}(\xi,\zeta)\exp[-j(k_x\xi+k_y\zeta)]d\xi d\zeta, \qquad (2)$$

where ξ,ζ – the current coordinates, $\dot{u}(\xi,\zeta)$ – the function of the acoustic field distribution on the object surface. As in (1), (2) the scattering surface form is not taking into account, the mathematical description of the indicated distribution is necessary to extend, for example, on the base of the approach, which developed in [8]. Equation for the angular spectrum object DF will look like:

$$F(k_x,k_y)=\frac{1}{(2\pi)^2}\cdot\int_{-\infty}^{\infty}\int_{-\infty}^{\infty}\dot{u}(\xi,\zeta)\exp[-j(k_x\xi+k_y\zeta+k_z\gamma(\xi,\zeta)]d\xi d\zeta, \qquad (3)$$

where $\gamma(\xi,\zeta)$ – equation of the dispersion surface relatively to z_0, $k_z=2k\cos\theta$,

θ – the incidence angle of the primary wave (the angle between the normal to the surface and the normal to the wavefront of the probe field). In contrast to [8] the angular spectrum (3) contains under the integral sign the function of the field distribution on the surface $\dot{u}(\xi,\zeta)$, which depends, in particular, on the type of probing field, so the equation (3) generalize the results and the models, proposed in [6, 8]. On the basis of the Kirchhoff approximation angular spectrum (3) can be represented as:

$$F(k_x,k_y)=\frac{1}{(2\pi)^2}\cdot\int_{-\infty}^{\infty}\int_{-\infty}^{\infty}U(\xi,\zeta)\cdot V(\xi,\zeta)d\xi d\zeta, \qquad (4)$$

and $V(\xi,\zeta)=\exp\left[-jk_z\gamma(\xi,\zeta)\right]$ – is a rapidly oscillating function .

In accordance with the concept of ACI formation as a multistep process, that takes into account the specificity of the interaction of coherent acoustic field with the investigated reflected surfaces, the appropriate models and software package blocks for their implementation, describing all stages of ACI formation and processing, were working out [9]. Developed software using Symbolic Math Toolbox MATLAB permits the machine-assisted realization of the mathematical models for a given configurations of the reflection surfaces and also for the acoustic field distribution on these surfaces. The numerical implementation consist of substituting in the obtained numerical equation the concrete numerical values of the input variables and in the subsequent formation of numerical data arrays of the space distribution of the acoustic field for further operations of its transformation. ACI visualization also carried out with the using of the Symbolic Math Toolbox MATLAB application. This allows on the each step of simulation verify the correctness of the proposed approach for objects with surfaces of a simple configurations (limited plate, disk). Complex surfaces can be approximated by a combinations of simple constructions with phase relationships.

Numerical implementation of ACI space models is fulfilled for the combinations of standard models of reflection surface and verified by experimental data. The illustrations show the angular spectra of the

most important types of objects for the solved problem, for example, figure 1 shows the angular spectrum of the superposition of three interfering objects.

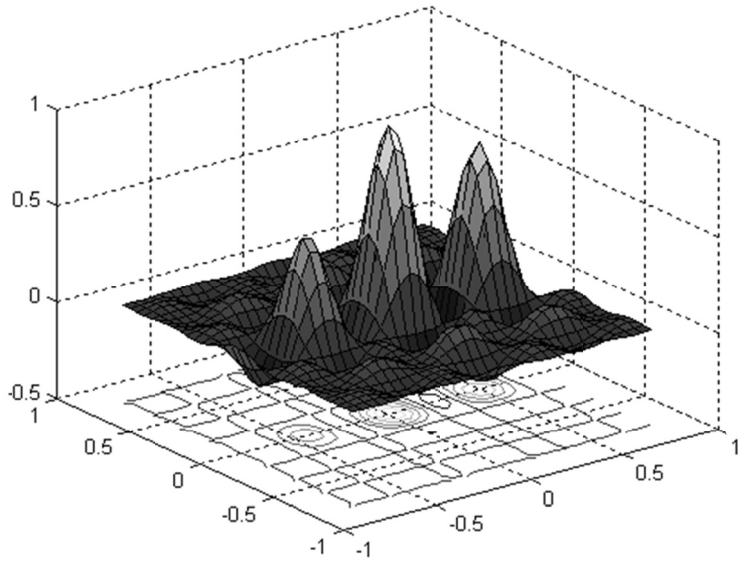

Fig. 1. Angular spectrum of three interfering objects superposition

Carried out the numerical implementation of ACI space models can demonstrate the most important features of the investigated images, namely: the interference of highlight field in the aperture plane at the presence of several local sources in the object plane; the speckle structure of secondary field in the aperture plane at the presence of the noise field in the object plane. As mentioned above, the quality of the received ACI depends on the methods of space-time processing in the received PA therefore for proving of their application effectiveness with the purpose of ACI space contrast improvement the numerical implementation of models of space data processing and visualization was carried out. Its include the following stages:

– Transformation of the object field in the received aperture plane with taking into account the phase relations between space spectra;

– Additive processing of the received field in the aperture plane;

– Weighted multiplicative processing of the object field in the aperture plane according to the theoretically justified algorithms and algorithms for the direct implementation of the multiplicative convolution;

– Beam forming processing of the object field;

– Visualization and comparing of the processing results.

In figure 2 there are the application results of the proposed weighted multiplicative processing and additive processing of the object

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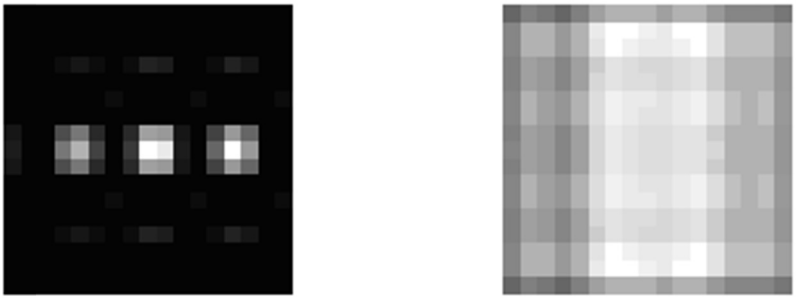
field in the PA plane of the stated aperture. As we can see from figure 2, weighted multiplicative processing permits to improvement the ACI space contrast relative to using of the additive processing.



a) b)

Fig. 1. Results of the space processing of interfering sources group: a) result of WMPS; b) result of additive processing.

Conclusion. It is established, that the high coherentness of the secondary acoustic field permits using of the effective methods of space contrast improving, in particular, the using of the methods of weighted multiplicative processing.

The proposed generalized mathematical models of the acoustic coherent images formation and processing taking into account the equation of the reflection surface permit the simulation of the secondary acoustic field distribution on the objects surfaces in the receiving aperture plane in order to illustration of the effectiveness of well-known and developed algorithms for recognizing the nature of investigated surfaces, that is the subject for further researches.

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V.I. Lytvynenko

APPLICATION OF CLONAL SELECTION ALGORITHM FOR SOLVING THE PROBLEM OF IMAGE SEGMENTATION CELLS

У статті пропонується підхід до рішення задачі сегментації зображень кліток при високому рівні шуму. Для цієї мети використовується методика динамічного об'єднання в кластери та алгоритм клонального відбору. Запропонований метод припускає наявність апріорних відомостей про форму клітини. Для опису границь клітки використовується модель побудови контуру клітки.

Ключові слова: *клітина, модель, кластеризація, клональний відбір, сегментація*

Introduction

There are three central tasks in the analysis of images: detection, segmentation and classification of object images. Detection of localization of objects as well as their boundaries of segmentation is the first step in many image analysis problems, especially in problems of quantitative analysis of objects.

For example, in medical imaging, detection and segmentation of cells, organs, etc. play an important role for the diagnosis and prognosis. Unfortunately, even with the help of image analysis software, traditional manual analysis is tedious and time consuming, especially in cases which should be determined by a large number of objects [1]. Thus, the development of effective and sustainable methods for automatic and rapid detection and accurate segmentation of their boundary is a very important goal.

Image Segmentation - is the most important and difficult stage of the analysis of medical images. This process is a natural and logical extension of functionalities of the digital image processing because it allows for visual analysis of objects and their yaskravistnyh geometrical characteristics [2]. Segmentation divides an image into its constituent area and facilities. That level of detail, which proves this division depends on the problem being solved. Image segmentation is not trivial, is one of the most complex image processing tasks.

The quality of segmentation depends on the accuracy of morphological calculation characteristics of biological objects and

therefore the accuracy of the classification and diagnosis.

Detection and segmentation of the object does not mean its identification. Many applications of image analysis require that the object was classified. For example, in [3] presented an algorithm that allows to extract outlines five types of vehicles moving. They are also segment the contours of the vehicle using their templates to further classify the vehicle in question. In this and other studies [4,5], segmentation is used to obtain information about the form [6,7,8].

In [4] the segmentation of cells images of the thyroid gland is used with a genetic algorithm. In [5] the same author used Tabu-search. In our work for the first time to solve the problem of segmentation of gray-scale images of blood cells used the immune clonal selection algorithm [10].

The suggested method consists of the following components: a) obtaining a gray-scale images; b) use gray-scale images to obtain of points that perhaps belong to the cell boundaries; c) application of Clonal algorithm to tune the ellipsoid model parameters to establish compliance its boundaries with the boundaries of the real cell.

1. Statement of the problem

Pathologists often make diagnostic decisions according to the results observation of individual cells, including their geometrical parameters such as area, radius, circumference, perimeter of cage, its compact size, the bump coefficients, Fourier descriptors and others [9].

However, to perform an accurate segmentation it is necessary the shape facilities modeling. Over recent years, has been developed a set of methods for image segmentation of cells [11-16]. As examples of such methods are methods based on regions, different boundary methods and so on. Methods based on the regions to perform image segmentation use the real increasing of region, its division and fusion. Boundary methods - they are a simple methods based on the classification of individual pixels. According to such methods with each pixel is associated with any property, such as brightness level; this property is compared with a threshold and the pixel is classified as part of the object or image, or as a body. The limiting conversion can be considered as a transaction in which the comparison is made with the function T that has the form [1]:

$$T = T(x, y, p(x, y), f), \quad (1)$$

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where f - is an image and $p(x,y)$ indicates a some local characteristics of image points (x,y) ; for example, the average brightness in the vicinity of the center at this point. The image $g(x,y)$, obtained as a result of limit transformation, defined as follows:

$$g(x,y)=\begin{cases} 1, if\ f(\mathrm{x},\mathrm{y})>T \\ 0, if\ f(x,y)\le T \end{cases} \quad (2)$$

Thus, the pixels which appropriated the value 1 correspond to objects and pixels with value 0 corresponds to the background. If the value T depends only on f, that is the same for all image points, then the threshold is called global. If the threshold T depends on the spatial coordinates x and y, that it is called local or dynamic. If the threshold is depends on $p(x,y)$, such threshold is called adaptive. Thus, the main difficulty in this method consist in determining of threshold. The most simple method - a selection of the threshold based on the principal value in the histogram [1]. More sophisticated version of this approach is given in [18, 19]. The problem of these methods is that they use only local information (for individual pixels) and do not use any information about the shape of the object as a whole, although such knowledge can greatly improve segmentation especially in the presence of noise and other image distortions that lead to fuzzy distinction between object and background. Images of cells are characterized by the following features.

1. **Feeble** contrast, that is, objects (cells) in their brightness levels can be similar to the background.

2. **Multiple overlay of objects** on the considered area of the image. Multiple overlay makes segmentation very difficult.

3. **Poor quality.** The staining methods of cell preparations make a lot of irregularities in the image and lead to the fact that not all parts of the investigated object are equally colored.

In the presence of noise, interference, and overlays, the image segmentation the cell is a difficult problem to be solved [19]. Therefore, for the solution of such problems, are used constraints imposed a priori knowledge. This means that the efficiency of segmentation can be greatly improved by using a priori knowledge of the shape of cells. In fact, one of the most common problems in medical image segmentation is an extension of traditional approaches to segmentation and classification of objects with inclusion of information about the form,

and not only about the intensity of objects. In this paper, for accurate image segmentation the cell is not only used the information about the border, but also information about its shape.

For image segmentation of cell, we propose to use the immune clonal selection algorithm [10,23].

The proposed method consists of the following three parts:

1) identification of possible boundaries of cells;

2) an approximate determination of the location of the cells and the detection of image points that are most probably are belong to boundaries of cells;

3) creation a model the cell circuit, characterized by five parameters that accurately allocate circuit the cell and eliminate the noise impact.

By setting the parameters of the model it is possible to accurately describe the contour of cells in the image. Thus, the problem of image segmentation is transformed into optimization problem.

2. Contoured model of cell picture

The most cells of the human body are generally of ellipsoid shape as shown in fig. 1a and fig. 2a. It can be seen that although the cells themselves brightness is lower than the brightness of body, image contrast remains quite low. In addition, there is the presence of noise and overlapping cells in the image. As mentioned earlier, this type of problem can be solved by overlay restrictions on the parameters in the form of a priori information. The approach based on modeling of the cell contour, can be represented as a problem of parameters optimization. If the contour of the cell model defined, you can restore the segmented image for the necessary values of the geometrical parameters. To describe the contour of the cell will use the equation of an ellipse:

$$\frac{x^2}{a^2}+\frac{y^2}{b^2}=1 \qquad (3)$$

where a and b – respectively with the length of the major and minor axis.

Given the possible movements and rotation, equation (3) can be written as:

$$\frac{\left[(x-x_0)\cos\theta+(y-y_0)\sin\theta\right]^2}{a^2}+\frac{\left[(x-x_0)\sin\theta+(y-y_0)\cos\theta\right]^2}{b^2}=1 \quad , \qquad (4)$$

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where x_0, y_0 - the center of the ellipse, θ indicates its orientation.

Thus, we obtain the five parameters: x_0, y_0, a, b and θ that describe the model.

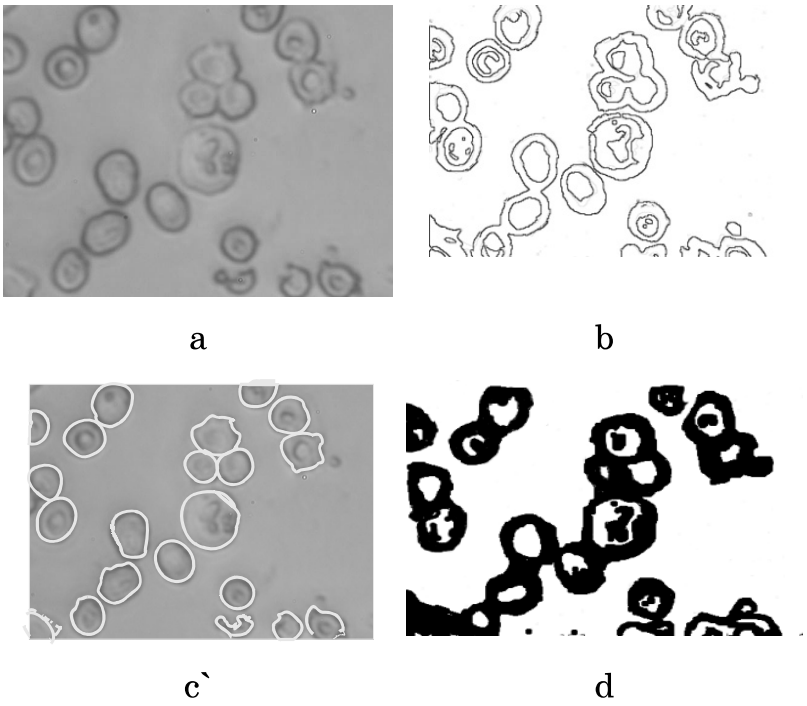
3. Approach to identify image points in the cell

3.1. Location of cells

Certainly, segmentation based on the boundary definition is divided into two stages: identifying of boundaries and merging of boundaries. In [20] the selection of boundary is considered as the several independent tasks, where each task has its own input information, the method of processing and output information. However, this approach can lead to incorrect results because of possible error propagation. In the present scheme at first are determined the dots of images that have a high probability of belonging the cell that is used to determine the approximate location of the cell. This process can be seen as the transformation of local information into global.

Based on the approximate location and model of the cell, we can re-evaluate the correctness of the assumptions about belonging of pixel to boundaries of the cell. For the detection of boundaries, we use the method of the boundaries determining of Cannes [21].

Essence of the method consists in finding of local areas with differences in brightness. Differences in brightness are sought by filtering on each axis one-dimensional filter lapsyan-haussyan. In the method of Cannes for the classification differences to "weak" and "strong" used two thresholds: “bottom” and “top”. "Weak" boundaries observed in the resulting image, if they are connected to the "strong" differences. Due to the influence of noise, there is a set of false directions in gray-scale image (see Fig. 1b). Many points of adjacent boundaries are connected. In the original image of blood cells (see Fig.1a), we can see a great variation in brightness levels at the boundaries of the cell. So, created boundaries, due to the influence of noise, contain a small amount of connected of image points. Thus, we can use the threshold value to determine whether the contour direction correctly indicates the border of the cell. Otherwise, we remove the contour appeared as a result of noise. Threshold values can be determined experimentally.



a b

c` d

Fig. 1. Results of image segmentation of blood cells: (a) the original image; (b) the image of boundary; (c) the proposed approach by us. (d) the method based on the histogram.

3.2. Detecting of image points in the cell by means of a dynamic clustering

After determining the approximate location of cells, use the method of dynamic clustering for finding points of the image possibly belonging to cells.

According to this method initially defined kernel k_j, which is a cluster. The kernel can be either a function or set of image points or other models.

To determine the belonging considered point to the cluster, enter a value $\Delta(y,k_j)$ that describes the similarity between the examined point y and cluster k_j. The method is implemented using the following actions:

1. Determine the initial core for each cluster.

2. For all considered points, perform the following rules for their classification: if $\Delta\left(y,k_j\right)\le t$, then $y\in\gamma_j$, where y indicates the considered point, t - the threshold value, and γ_j represents the j-th cluster.

3. Refresh core k_j. If thus to is no change kernels then stop execution, otherwise return to step 2.

Because the cell is ellipsoidal boundary, we use as kernel Gauss function that can be represented as:

$$K_j(y) = \frac{1}{2\pi\left\|\Omega_j\right\|}\exp -\frac{1}{2}\left(y-m_j\right)\Omega_j^{-1}\left(y-m_j\right)^T \quad (5)$$

where m_j - the average value of samples and Ω_j - covariance matrix.

The similarity between the examined point y and the cluster j is determined as follows:

$$\Delta\left(y,k_j\right) = \frac{1}{2}\left(y-m_j\right)\Omega_j^{-1}\left(y-m_j\right)^T + \frac{1}{2}log\left\|\Omega_j\right\| \quad (6)$$

Using the above method, we can find the points of the image, with a high probability of belonging to the cells. After detection of such points, we can search the ellipse in best possible way corresponding of contour cells in a relatively small area.

4. Using of clonal selection algorithm for the selection of the body boundary

4.1. Clonal selection algorithm

Clonal algorithm - is one form of evolutionary algorithms based on the use of the mechanisms of the immune system of vertebrates and humans. Studies have shown that clonal algorithm demonstrated to be very effective in solving optimization problems. Managing a population of individuals, it conducts the search for optimal solutions by means of mechanisms of reproduction, genetic variability and selection. Clonal selection principle used by the immune system to describe the basic characteristics of the immune response in antigenic stimulation. It is based on that fact that only the cells that able to recognize the foreign antigens can be selected and spread. The selected cells are subjected to mutation process to improve their affinity to selected antigens. Formally algorithm of clonal selection can be represented as [23,24,25]:

$$\text{CLONALG} = (P^l, G^k, l, k, m_{Ab}, \delta, f, I, \tau, AG, AB, S, C, M, n, d), \quad (7)$$

where P^l is space of search (space of forms); G^k is space representation; l is the length of vector of attributes (dimension of space of search); k is the length of antibody receptor; m_{Ab} is dimension of population of antibodies; δ is the expression function; f is the affinity function; I is the function of initialization of the initial

population of antibodies; τ is the condition of completion of algorithm work; AG is the subset of antigenes; AB is population of antibodies; S is the operator of selection; C is the operator of cloning; M is the mutation operator; n is the number of the best antibodies selected for cloning; d is the number of the worst antibodies subjected to substitution for new ones.

The process of converting a population of antibodies by clonal selection algorithm can be represented as a sequence of the following statements:

$$\mathrm{AB}_t \xrightarrow{\text{Selection (S)}} \mathrm{G}_S \xrightarrow{\text{Cloning (C)}} \mathrm{G}_C \xrightarrow{\text{Mutation (M)}}$$

$$\mathrm{G}_M \xrightarrow{\text{Repeat mutation (S)}} \mathrm{G}_S \xrightarrow{\text{Replacemen t(d)}} \mathrm{AB}_{t+1},$$

Whe.re t - is the number of generation, AB - is the population of antibodies (detectors), G_S - the subset of selected best antibodies, G_C - is the subset of clones, G_M - is the subset of clones after mutation.

Let us show the generalized stepwise description of the algorithm.

1. *Initialization.* Creation (usually by random generation) of the initial poulation of antibodies AB.

2. *Determination of affinity.* For every antibody AB_j, $AB_j \in AB$ determine its affinity relative to every antigen Ag_i, $Ag_i \in AG$. Write the result into the matrix of affinities $D: D = \left[\left|AG\right| \times m_{Ab}\right]$, and $d_{ij} = f\left(Ab_j, Ag_i\right), d_{ij} \in D$.

3. *Clonal selection and propagation.* Select from population n of each the best antibodies for every row of the matrix D and place them into separate population of clones $AB_C, \left|AB_C\right| = n \cdot \left|AG\right|$. It is necessary to generate clones of elements of the population AB_C proportionally to their affinity, i.e., the greater it is, the greater number of clones is generated and vice versa.

4. *Affinity maturation.* Subject to mutation all the clones of population AB_C with probability inversely proportional to affinities, i.e., probability of mutation is the greater, the lower is its affinity. Determine new affinity of every antibody AB_j, $AB_j \in AB_C$ similar to item 2 and obtain the matrix of affinities D_C. Select n antibodies from the population AB_C, for which the corresponding vector-column of the

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matrix D_C gives the best generalized result of affinity, and transfer them into population of cells of memory M_R.

5. *Meta-dynamics.* Substitute the worst d antibodies of the population AB by new random individuals.

Substitute n antibodies of the population AB by cells of memory from M_R and pass to item 2 until the stoppage criterion is reached.

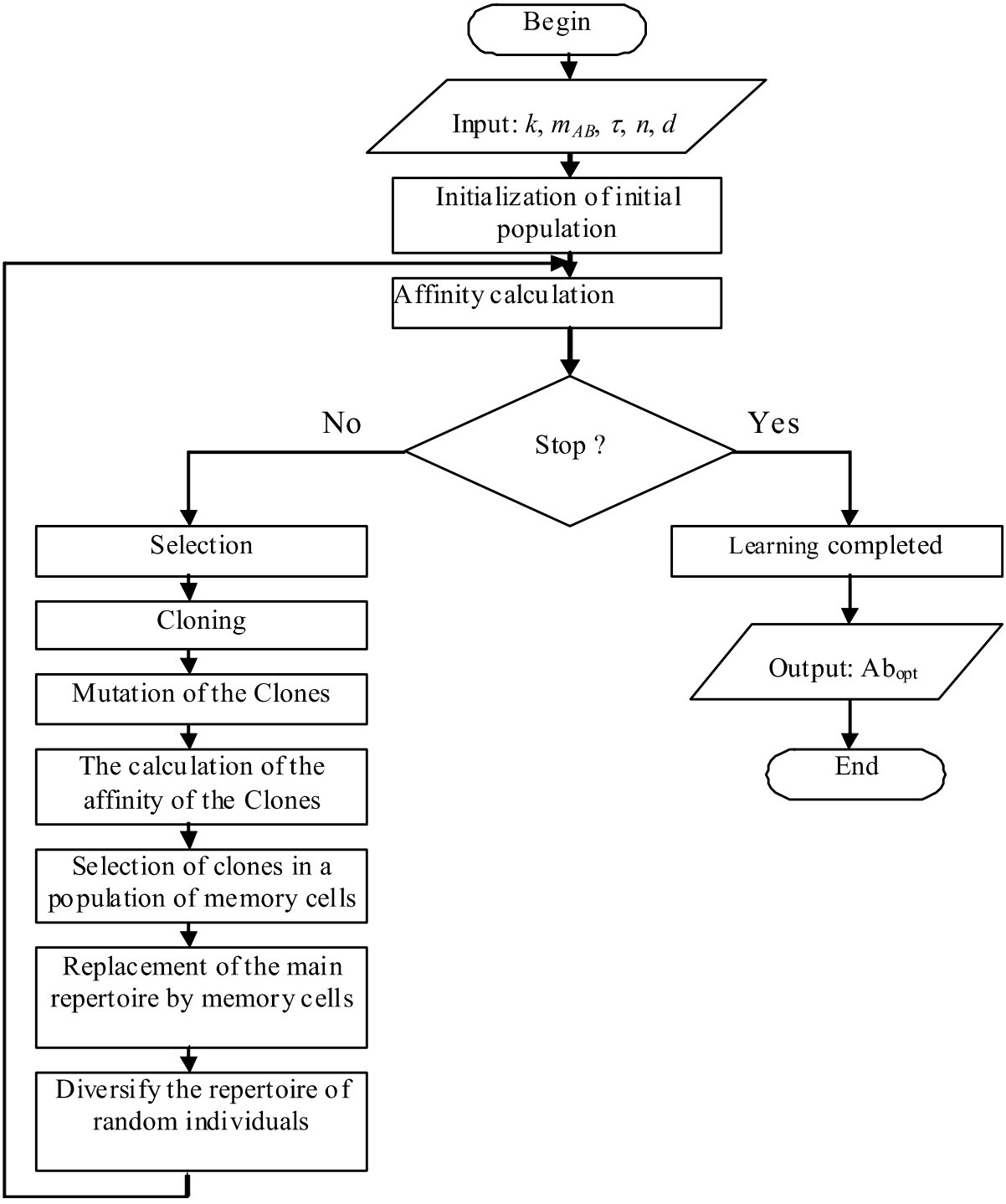

Fig. 2. Block-diagram of clonal selection algorithm.

4.2. Setting algorithm for task of allocation boundaries of cells

The input data for the solution of the problem are N possible points that are on the contour line of the cell. Each of these pixel has a unique number from 1 to N. To determine the ellipse we need to know only five of them. Let the vector $I = (I_1, I_2, ..., I_5)$ indices the five selected points. Assume that $I_i < I_j$ at $i < j, i, j = 1, ..., 5$. Affinity function in this case will be:

$$f(I) = \sum s(r_{I_i}^2) \quad (9)$$

where s - step function; s = 1 at r_j greater than or equal to the width of the template and s = 0 otherwise. This function counts the quantity of points that are within a certain distance of the ellipse. We denote by P the population of M antibodies $I_1, I_2, ..., I_M$. Let L - population size and GEN - number of generations. n_1 - the quantity of antibodies selected for cloning, and n_2 - the quantity of antibody clones elected from the population to restore the repertoire. In this case, the basic step by step description of the algorithm for the solution of the problem would look like this.

Step 1. **Initialization.** To initialize antibodies randomly to generate the five integers in the range from 1 to N inclusive. These numbers are the five points of index image. To initialize the entire population must repeat this process L times.

Step 2. **Selection and cloning.** When using affinity function, to assess of individuals of populations and to choose the best n_1 of them. Cloning involves the creation of copies selected individuals in proportion to their affinity.

Step 3. **Mutation and substitution.** For all newly created clones based on the likelihood of mutation and inversely proportional to their affinity, to conduct the operation being accidentally changed. For this task mutation operator is described as follows. Originally are generated two integers m and n (m ranging from 1 to 5, and n in the range from 1 to N). Next, the gene selected for mutation antibody with an index of m is replaced by the value of n. From population altered by mutation of clones are selected n_2 antibodies and replace the same number in the basic population to restore repertoire.

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Step 4. **Replacing the worst antibodies.** To increase the diversity of the repertoire from the main population to reselect the antibody with lowest value of affinity and replace them with new randomly generated individuals.

Step 5. **Repeat** steps 2-4 until you reach stopping criterion.

5. Results of conducted experiments

In this section, we present results of experimental investigations of image segmentation with blood cells and give a comparison of methods based on histograms. The method is based on histogram is described as follows:

(1) obtain a histogram of the segmented image;

(2) according to the histogram to obtain the corresponding threshold of the segmented image;

(3) if the brightness level of a pixel is less than or equal to the threshold, the pixel belongs to the cluster object, otherwise it will be classified as background.

The threshold can be determined using the method of minimum error or the method of maximum entropy [18,19]. In our experiment, we set population size L= 200; meaning the number of antibodies selected, n_1= 70% of the population; hyper mutation probability P_m = 0.8; number of generations GEN = 100; and the number of the worst antibodies are replaced, n_2 = 30% of the population; cloning factor β = 0.8.

Fig. 1c shows the results of segmenting images experiments of blood cells. Image of contours obtained by the method of determining the boundaries by Cannes [22] method options below:

- upper threshold - 0.85;
- lower threshold - 0.79;
- covariance - 1.75.

Experimental results with boundary methods are shown in Fig. 1d. From Fig.1, are seen the benefits of our proposed method compared with the methods based on the histogram. The proposed approach is immune to noise. If the brightness near the boundaries of cells have insignificant scatter, the proposed method can allocates the border of cells and correctly to solve the problem of segmentation.

When two cells are very close to each other, simple methods based on histograms can not to distinguish them, while our method successfully identifies these cells. Thus, the proposed approach has the ability to work successfully with the imposition of boundaries cells.

The time spent on finding a pixel-owned cell, is about 20 sec to 1.6 GHz processor. The time spent on setup of contour model parameters is about 20 seconds.

6. Conclusion and further research

This paper proposes an approach to image segmentation of cells under significant noise effects, this method is based on a combination of dynamic clustering algorithm and clonal selection. In our algorithm, we use not only information about the circuit, but also the boundary cell model, assuming that the cell has an elliptical shape. Using prior knowledge about boundary cells, our method has a high resistance to noise.

Points of the image, which possibly belong to cells are determined by the method of dynamic clustering thus reducing the search space and time is spent on the optimization objective function by clonal algorithm. The obtained results suggest a possible direction for future research in the field of segmentation automation, which is especially important in the design of biomedical systems. Experimental studies have shown that the proposed approach is able to handle the partial overlapping of objects in images, but to improve of such ability the further studies are needed.

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CLUSTERING ALGORITHM CLONAL SELECTION

Clustering algorithm based on clonal selection principle named clonal selection clustering algorithm (CSCA) is proposed in this paper. The new proposed algorithm is data driven and self-adaptive, it adjusts its parameters to the data to make the classification operation as fast as possible. The performance of CSCA is evaluated by comparing it with the well known K-means, EM, Cobweb DBSCAN algorithms using several real-life data sets. The experiments show that the proposed CSCA algorithm is more reliable and has high clustering precision comparing to traditional clustering methods such as K-means, EM, Cobweb DBSCAN.

Keywords: clonal selection algorithm, clustering, Optimization.

1. Introduction

Clustering technique is an effective tool for exploring the underlying structure of a given data set. Its main objective is to partition a given data set into homogeneous groups (called clusters) in such a way that patterns within a cluster are more similar to each other than patterns belonging to different clusters [1]. Clustering technique have been applied in a wide variety of engineering and scientific disciplines such as medicine, psychology, biology, sociology, pattern recognition, and image processing [2]. Many types of clustering algorithms have been developed. Among them, k-means is perhaps the most popular one, because it can be implemented easily and efficiently. This algorithm and its variant [3] have been successfully employed in many practical clustering problems. However, it easily converges to arbitrary local optima and is unable to deal with non-spherical shaped clusters. Recently, evolutionary algorithm (EA) inspired by biological evolution provides a new idea for clustering analysis, and a series of clustering algorithms based on evolutionary computation have been proposed [4]. Most of the available clustering algorithms are prone to get in local optima and cannot find the proper clustering partition. As an artificial immune system algorithm, CSA has been successfully applied to the study of cluster analysis [5–8]. In order to improve the performance of clustering algorithms based on CSA for clustering multi-class data sets, a modified clustering algorithm based on CSA is proposed in this paper.

2. Optimization approach to clustering

In accordance to [11] an optimization problem consists in maximiza-

tion or minimization of some function (objective function) $f: S \to \Re$ in a set $S \subseteq \Re^n$. The feasible set S can be either finite or infinite, and can be described with the help of a finite or infinite number of equalities and inequalities or in the form of some topological structure in $\Re^n$. In case global maxima or minima (global extreme) are looked for, we have a global optimization problems, otherwise the problem is of local optimization. When the function f is continuous or piece-wise continuous and the set S is described with the help of functions (constraint functions) that have the same continuity property, we obtain a continuous optimization problem. The methods for solution of certain optimization problem depend mainly on the properties of the objective function and the feasible set. Thus, when we are looking for extrema of a linear function regarded on some polyhedral set, then the methods of linear programming can be applied; when f is a convex function and S is a convex set, we apply methods of convex programming; if the feasible set S is described with the help of an infinite number of equalities or inequalities, the methods of semi-infinite programming should be used, etc.. Let us describe the clustering problem formally. Assume that X is the given a finite set in the $n-$ dimensional space $\Re^n$: $X = \{x^1, x^2, \ldots, x^M\}$, where $x^i \in \Re^n, i = 1,2,\ldots,M$. Let us call the elements of the set X patterns. The aim of cluster analysis is to partition X into a finite number of clusters based on similarity between patterns. As a measure of similarity we use any distance function. Here for the sake of simplicity we consider Euclidean distance $\| \cdot \|_2$ Given a number $q \in N$, we are looking for q subsets C^i, $i = 1,2,\ldots,q$, such that the medium distance between the elements in each subset is minimal and the following conditions are satisfied:

$$C^i \neq 0, i = 1,2,\ldots,q, \tag{2.1}$$

$$X = \bigcup_{i=1}^{q} C^i \tag{2.2}$$

The set C^i, $i = 1,2,\ldots,q$ introduced above are called clusters and the problem of determination of clusters is the clustering problem. When the clusters can overlap, the clustering problem is fuzzy. If we request additionally

$$C^i \bigcap C^j = 0 \text{ if } i \neq j; \quad i, j = 1,2,\ldots,q \tag{2.3}$$

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then we obtain a hard clustering problem. Let us assume that each cluster C^i, $i=1,2,\ldots,q$, can be

identified by its center or centroid, defined as [12] $c^i = \frac{1}{\left|C^i\right|}\sum_{x\in C^i} x$,

where $\left|C^i\right|$ denotes a cardinality of the cluster C^i. Then the clustering problem can be reduced to the following optimization problem, which is known as a minimum sum of squares clustering [13]:

$$\min \frac{1}{M}\sum_{i=1}^{q}\sum_{x\in C^i}\left\|c^i - x\right\|_2^2, \qquad (2.4)$$

such that $C=\{C^1,C^2,\ldots,C^q\}\in\overline{C}$.

Here, $\overline{C}$ is a set of all possible q — partitions of set X, $c=\left(c^1,c^2,\ldots,c^q\right)\in\Re^{n\times q}$

According to [14], clustering algorithms differ each from other depending on the input data representation, e.g., pattern-matrix or similarity matrix, or data type, e.g., numerical, categorical, or special data structures, such a rank data, strings, graphs, etc.;

- the output representation, e.g., a partition or hierarchy of partitions;
- optimization method chosen for solution of optimization model;
- clustering direction, e.g., agglomerative or divisive.

3. A Clonal Selection Algorithm for Clustering

3.1. Clonal Selection Theory

The clonal selection theory was originally proposed by Burnet, in order to explain the reinforcement learning of the immune system of mammals [15]. The theory of clonal selection [16], suggests that B and T lymphocytes that are able to recognize the antigen, will start to proliferate by cloning upon recognition of such antigen. When a B cell is activated by binding an antigen (and a second signal is received from T lymphocytes), many clones are produced in response, via a process called *clonal expansion*. The resulting cells can undergo *somatic hypermutation*, creating offspring B cells with mutated receptors. The higher the affinity of a B cell to the available antigens, the more likely it will clone. This results in a Darwinian process of variation and selection, called *affinity maturation*. The increase in size of these populations

couples with the production of cells with longer than expected *lifetimes*, assuring the organism a higher specific responsiveness to that antigenic attack in the future. This gives rise to *immunological memory* which is demonstrated by the fact that, when the host is first exposed to the antigen, a *primary* response is initiated; in this phase the antigen is recognized and immune memory is developed. When the same antigen is encountered in the future, a *secondary* immune response is initiated. This results from the stimulation of cells already specialized and present as memory cells: a rapid and more abundant production of antibodies is observed. The secondary response can be elicited from any antigen that is similar, although not identical, to the original one that established the memory. This is known as cross-reactivity.

The main property of the clonal selection theory can be summarized as follows [17]: 1) *Negative selection:* elimination of self-antigens; 2) *Clonal expansion:* proliferation and differentiation; 3) *Monospecificity:* phenotypic restriction; 4) *Somatic hypermutation:* new random genetic changes; 5) *Autoimmunity*.

3.2. Clonal Selection Algorithm

The clonal selection algorithm, CSA, was first proposed by de Castro and Von Zuben in [18] and was later enhanced in their 2001 paper [19] and named CLONALG. The algorithm takes a population of antibodies and by repeated exposure to antigens, over a number of generations, develops a population more sensitive to the antigenic stimulus [20].

The artificial immune systems (including clonal selection algorithm) is composed of the following basic elements [9, 10]: (1) a representation for the components of the system; (2) a set of mechanisms to evaluate the interaction of individuals with the environment and each other. The environment usually simulated by a set of input stimuli or patterns, one or more fitness function(s) or other means; and (3) procedures of adaptation that govern the dynamics and metadynamics of the system, i.e. how its behavior varies over time. Under the affinity [17] we could understand the interaction measure (or the power connection) of the complementary areas of antigen and antibodies or of two antibodies, which formally can be represented as one of the metrics (e.g. Euclidean distance). This measure indicates the degree of similarity or differences between the appropriative attributes of lines such as $S^P \times S^P \to \Re^+$.Often

the type of attributes is defined by the subject area of AIS and is an important point in the degree of affinity determination.

Generalized function of affinity can be represented as the following expression [21]:

$$c_{ij} = f\left(x_i, x_j\right), \tag{3.1}$$

where c_{ij} – is the affinity between molecules *i* and *j*; x_i and x_j – vectors that represent molecules in space forms, f – corresponding affinity function.

In optimization problems, the generalized form of antibodies is a vector of arguments $Ab = (x_1, x_2, ..., x_l)$, and as antigens used optimality criteria y_j, expressed as functions $Ag = f(x_1, x_2, ..., x_l)$. Affinity values g_j calculated on the basis of criteria values y_j reflected in the set of nonnegative numbers such as:

$$f : X \to \Re, \quad F : \Re \to \Re^+ \tag{3.2}$$

Thus, there is some affinity function $g = F\left(f(x_1, x_2, ..., x_n)\right)$, that determines that determines the degree of conformity of individuals to each other. In such problems, we can not to operate the notion of distance, so that the best value criteria is previously unknown, and, therefore, we do not know the maximum possible extent to which individuals. Thus, the control dynamics of AIS is performed by the relative affinity values or by rank individuals set. This approach is very close to the concept of suitability (fitness) used in evolutionary algorithms that have some earlier theory of artificial immune systems.

Formally algorithm of clonal selection can be represented as [22]:

$$CLONALG = (P^l, G^k, l, k, m_{Ab}, \delta, f, I, \tau, AG, AB, S, C, M, n, d), \tag{3.3}$$

where P^l is space of search (space of forms); G^k is space representation; l is the length of vector of attributes (dimension of space of search); k is the length of antibody receptor; m_{Ab} is dimension of population of antibodies; δ is the expression function; f is the affinity function; I is the function of initialization of the initial population of antibodies; τ is the condition of completion of algorithm work; AG is the subset of antigenes; AB is population of antibodies; S is the operator of selection; C is the operator of cloning; M is the mutation operator; n is

the number of the best antibodies selected for cloning; d is the number of the worst antibodies subjected to substitution for new ones.

Consider the shape- space $\left(P^l\right)$ phenotypes and their space images as antibodies $\left(G^k\right)$ or genotype space [22].

3.3. Clustering Algorithm Based on Clonal Selection

Traditional clustering algorithms find the data distribution in such a way that the cluster centers are placed in more or less the middle of the data subset, that constitutes the cluster. When used for classification, these cluster centers are sometimes not the best ones, especially when the number of clusters is too small [23]. In our study, we investigated the possibility of using clonal selection algorithm as stochastic optimization methods for clustering. This clustering algorithm based on clonal selection principle is proposed. The clonal selection clustering algorithm (CSCA) is data driven and self-adaptive, it adjusts its parameters to the data to make the classification operation as fast as possible. The proposed approach has been tested on several data sets and its performance is compared with the *K*-means algorithm. Experiments show that clonal selection clustering algorithm is more reliable and has high classification precision comparing to traditional classification methods such as *K*-means [24]. In this CSCA, clustering problem is considered as optimization problem and the objective is to find the optimal partitions of data where the resulting clusters tend to be compact as possible. A simple criterion which is the within cluster spread is used in CSCA, this criterion needs to be minimized for good clustering [24]. In difference from *K*-means which uses the square-error criterion to measure the within cluster spread, CSCA uses the sum of the Euclidean Distances of the points from their respective cluster centroids as clustering metric and uses clonal selection algorithm as clustering algorithm which warrants finding the global optima when most of others algorithms such as *K*-means stuck into local optima [24]. Clonal selection algorithm and a mathematical description of his basic steps are described in detail to our section 3.2. Figure 3.1. shows the basic structure for the CSCA.

Each antibody in P forms a string of real numbers representing the K cluster centers. For *d*-dimensional space, the length of the string is $d * K$ number, where the coordinates of the centers are localized in sequence[24].

$$p = [Ab_1, Ab_2, \ldots, Ab_n] \quad (3.4)$$

$$Ab_1 = [m_{11}, m_{12}, \ldots, m_{1d}, m_{21}, \ldots, m_{Kd}], l = 1, \ldots, n \quad (3.5)$$

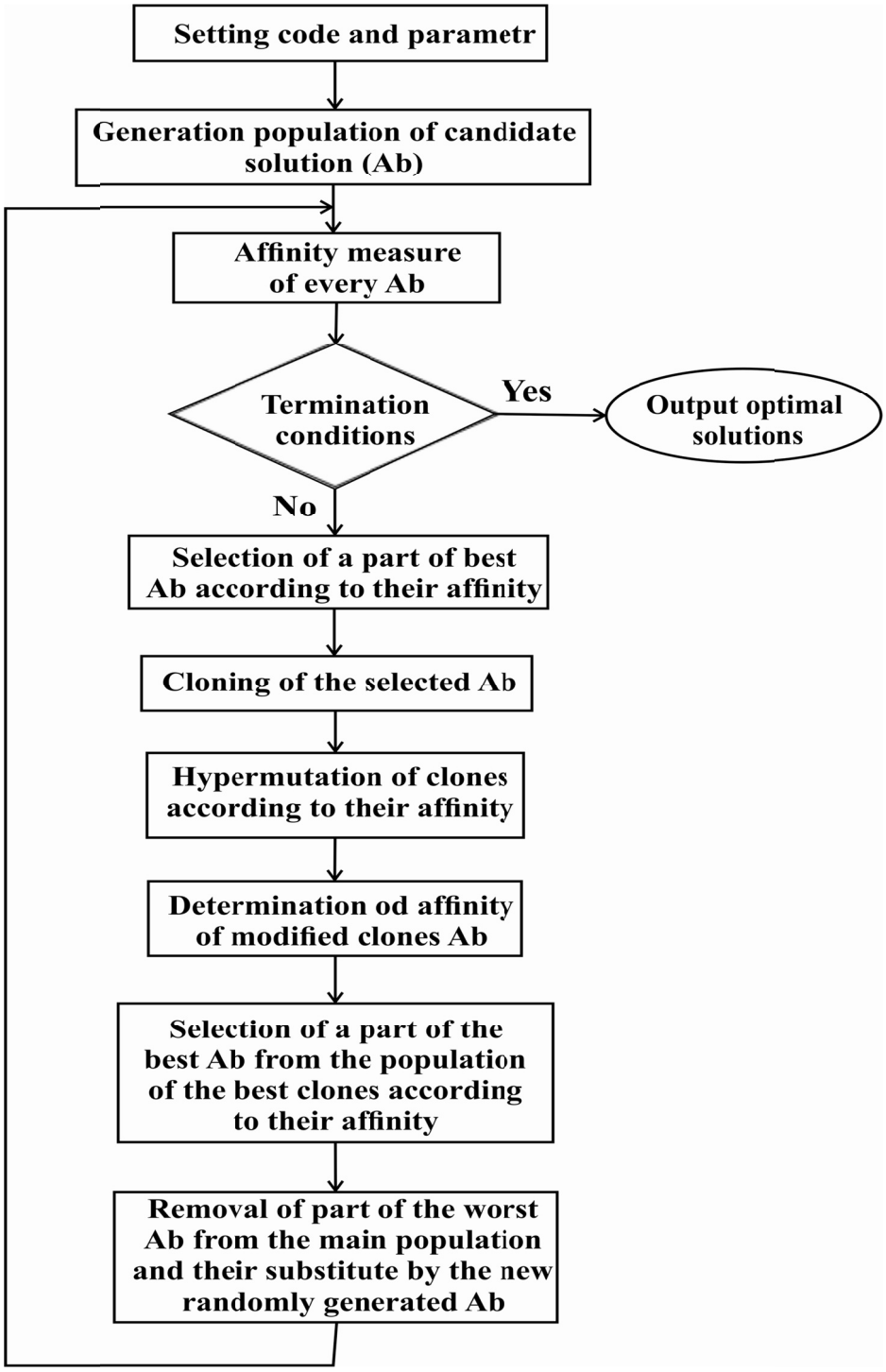

Fig. 3.1 Diagram of clonal selection clustering algorithm

The first d numbers represent the d dimensions of the first cluster center; the next d positions represent those of the second cluster center, and so on.

The number of clusters K is supposed to be known and the appropriate cluster centers $m_1, m_2, \ldots, m_k$ have to be found such that the clustering metric J is minimized. Mathematically, the clustering metric J for the K clusters $C = \{C_1, C_2, \ldots, C_K\}$ is given by the following equation:

$$J(\Gamma, M) = \sum_{i}^{K} \sum_{j}^{N} \gamma_{ij} \left\| x_j - m_i \right\| \tag{3.6}$$

where $x_j \in \Re^d, j = 1, \ldots, N$ are data points, $\Gamma = \{\gamma_{ij}\}$ is a partition matrix witch given by the eq. (2.4) , M is centroid matrix witch given by the eq. (2.5) and $m_i \in \Re^d, i = 1, \ldots, K$ is the mean for the C_i cluster with N_i data points.

$$\gamma_{ij} = \begin{cases} 1 \; if \; x_j \in C_i \; with \sum_{i=1}^{K} \gamma_{ij} = 1 \; \forall j \\ 0 \qquad\qquad\quad \text{otherwise} \end{cases} \tag{3.7}$$

$$M = [m_1, m_2, \ldots, m_K] \; where \; m_i = \frac{1}{N_i} \sum_{j=1}^{N} \gamma_{ij} x_j, \; i = 1, \ldots, K \tag{3.8}$$

In general, the task of clonal selection algorithm is to search for the appropriate cluster centers wherefore J is minimized. Based on clustering criterion, CSCA is supposed to give right results if the clusters are compact and hyperspherical in shape. To measure the affinity of an antibody, the clusters are formed according to the centers encoded in the antibody under consideration, this is done by assigning each point $x_j \in \Re^d, j = 1, \ldots, N$ to one of the clusters C_i whose center are the closest to the point. After the clustering is done, the new cluster centroids are calculated by finding the mean points of the respective clusters, then clustering criterion J is calculated by eq. (3.6). The affinity is defined as:

$$affinity = \frac{1}{J} \tag{3.9}$$

The maximum value of the affinity standing for the minimum value of J . Zero is assigned to the affinity if any cluster becomes empty. Antibodies will be cloned proportionally to their affinities, the higher the affinity the higher the number of clones generated for the antibody. The antibodies were sorted in descending order according to their affinity and then the amount of clones generated for the antibodies was given by:

$$nc = round(\beta \cdot n) \quad (3.22)$$

where nc is number of clones and β is clonal factor, n is the total amount of antibodies and $round(\cdot)$ is the operator that round its argument towards the closed integer.

Every antibody in *PC* is submitted to a mutation that is inversely proportional to the affinity and this is done according to the following equations: $Ab' = Ab + \alpha N(0,1)$, where $N(0,1)$ is Gaussian number generated by Gaussian function given as $f_{\text{Gaussian}}(x) = \frac{1}{\sqrt{2\pi}} e^{-\frac{x^2}{2}}$ and α control the learning imposed on the antibodies.

4. Experiments

The CSCA was tested using several artificial and real-life data sets, then compared with the well-known *K*-means, EM, Cobweb DBSCAN, [25]. **K-means clustering algorithm.** In data mining, *k*-means clustering [26] is a method of cluster analysis which aims to partition *n* observations into *k* clusters in which each observation belongs to the cluster with the nearest mean. The procedure follows a simple and easy way to classify a given data set through a certain number of clusters (assume k clusters) fixed a priori. The main idea is to define k centroids, one for each cluster.

EM algorithm. EM algorithm [27] is also an important algorithm of data mining. We used this algorithm when we are satisfied the result of k-means methods. An expectation– maximization (EM) algorithm is an iterative method for finding maximum likelihood or maximum a posteriori estimates of parameters in statistical models, where the model depends on unobserved latent variables.

COBWEB algorithm. The COBWEB algorithm yields a clustering dendrogram called classification tree that characterizes each cluster with a probabilistic description. Cobweb generates hierarchical clustering [29], where clusters are described probabilistically. COBWEB uses a heuristic evaluation measure called category utility to guide construction of the tree. **DBSCAN** is a data clustering algorithm for density-based spatial clustering of applications with noise. It is a density-based clustering algorithm because it finds a number of clusters starting from the estimated density distribution of corresponding nodes [30]. The key idea of density-based clustering is that for each instance of a cluster the

neighborhood of a given radius (Eps) has to contain at least a minimum number of instances (MinPts).

3.1 Artificial Data Sets

The experimental results comparing the clonal clustering algorithm with the *K*-means, EM, COBWEB and DBSCAN algorithms are provided for three real-life data sets (*Vowel*, *Iris* and *Crude Oil*), respectively. The data sets are described below:

• *Vowel data*: This data consists of 871 Indian Telugu vowel sounds [31]. These were uttered in a consonant-vowel-consonant context by three male speakers in the age group of 30-35 years. The data set has three features F_1, F_2 and F_3, corresponding to the first, second and third vowel formant frequencies, and six overlapping classes $\{\delta, a, i, u, e, o\}$. The value of K is therefore chosen to be 6 for this data.

• *Iris data*: This data represents different categories of irises having four feature values. The four feature values represent the sepal length, sepal width, petal length and the petal width in centimeters [32]. It has three classes (with some overlap between classes 2 and 3) with 50 samples per class. The value of *K* is therefore chosen to be 3 for this data.

• *Crude oil data*: This overlapping data [33] has 56 data points, 5 features and 3 classes. Hence the value of *K* is chosen to be 3 for this data set.

The was tested with the following parameters of CSCA algorithm: n=70,

m_{AB}=100; d =30 and number of generations *gen*=100. For testing the algorithms K-means, EM, COBWEB and DBSCAN was used WEKA. For *K*-means algorithm [34] 100 as a maximum number of iterations was used in case it does not terminate normally. For EM algorithm: the number of folds to use when cross-validating to find the best number of clusters — 10; the minimum improvement in log likelihood required to perform another iteration of the E and M steps — 0.000001; the number of folds to use when cross-validating to find the best number of clusters — 10; number of iterations was used-100. For COBWEB algorithm: the random number seed to be used— 42; set the category utility threshold by which to prune nodes— 0.00282; set the minimum standard deviation for numeric attributes — 0.7. For DBSCAN algorithm: minimun number of DataObjects required in an epsilon-range-query — 6; radius of the ep-

silon-range-queries— 0.9. At every experiment the algorithms were run for 100 times with different random initial configurations To provide statistical evaluation of the performance.

The experiments show that the proposed CSCA algorithm is more reliable because it finds the best solution all the time unlike *K*-means, EM, COBWEB and DBSCAN which got stuck at sub-optimal solutions.

Table 1

Classification result for dataset

Dataset	CSCA	K-means	EM algorithm	COBWEB	DBSCAN
Vowel data	91%	82%	85%	87%	88%
Iris data	98%	86%	85%	88%	91%
Crude oil data	98%	88%	83%	95%	96%

CSCA algorithm has high classification precision comparing to *K*-means, EM, COBWEB and DBSCAN algorithms. The clonal algorithm is data driven and self-adaptive, it adjusts its parameters to the data to make the classification operation as fast as possible.

5. Conclusion

In this work, clustering algorithm based on clonal selection principle is designed to find the optimal partition between the data. This algorithm uses within cluster spread criterion as a clustering criterion. The criterion is based on Euclidean distance between the data in the clusters. CSCA is data driven and self-adaptive, it adjusts its parameters to the data to make the clustering operation as fast as possible. CSCA is tested on several data sets and its performance is compared with the well known *K*-means, EM, COBWEB and DBSCAN algorithms. The experiments show that CSCA algorithm has classification precision higher than *K*-means, EM, COBWEB and DBSCAN algorithms which got stuck at sub-optimal solutions even for simple data sets. Developed by us CSCA gives good results if the clusters are compact and hyperspherical in shape

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TECHNIQUE FOR ACCELERATION OF XML DOCUMENTS VALIDATING AGAINST XSD SCHEMA

Abstract. This work deals with researching of techniques of validation XML-files against XSD-schemes and proposes a new technique based on performing ordinary and partial validations. Suggested technique of XML validation lies in the fact that file is valid. The next step is to perform partial validation on every change of XML-file instead of full.

Keywords: XML, XSD, validation

Introductory

As for the last decade, the complexity of software has grown in many times in comparison with the beginning of 2000. If twenty years ago web sites were kind of static pages with the text decorated with bunch of tags, nowadays every web site is a web application with complicated structure, lots of multimedia content and non-trivial design. Most of businesses solutions are based on using of modern web technologies, as web solutions are platform independent. This means much less money and time consuming process of development for wide variety of target platforms. After appearance of smartphones and tablets amount of target platforms and even screen resolutions became even greater and thus making many pros of web applications.

As known, XML is an extensible markup language, which is basically a plain text document which syntax has to correspond some rules [1]. Since the invention of XML, developers found a huge amount of different use cases, like:

- data storage;
- usage within web translations and services;
- platform independent application settings;
- large amount of XML extensions such as electronic books (fb2, epub, XHTML), RSS news, etc;
- UI declarations.

Web services are almost mandatory part of every web application for server-client solutions. Functioning of web service is based on exchanging of XML messages, mostly by SOAP protocol. Confidence that received XML message conforms some specific rules makes developer

able to perform some processing and transformations with assurance as shown on fig. 1. Thus, one of the main tasks appears.

The point is finding out whether XML document conforms specified rules or not, and if it is not then why.

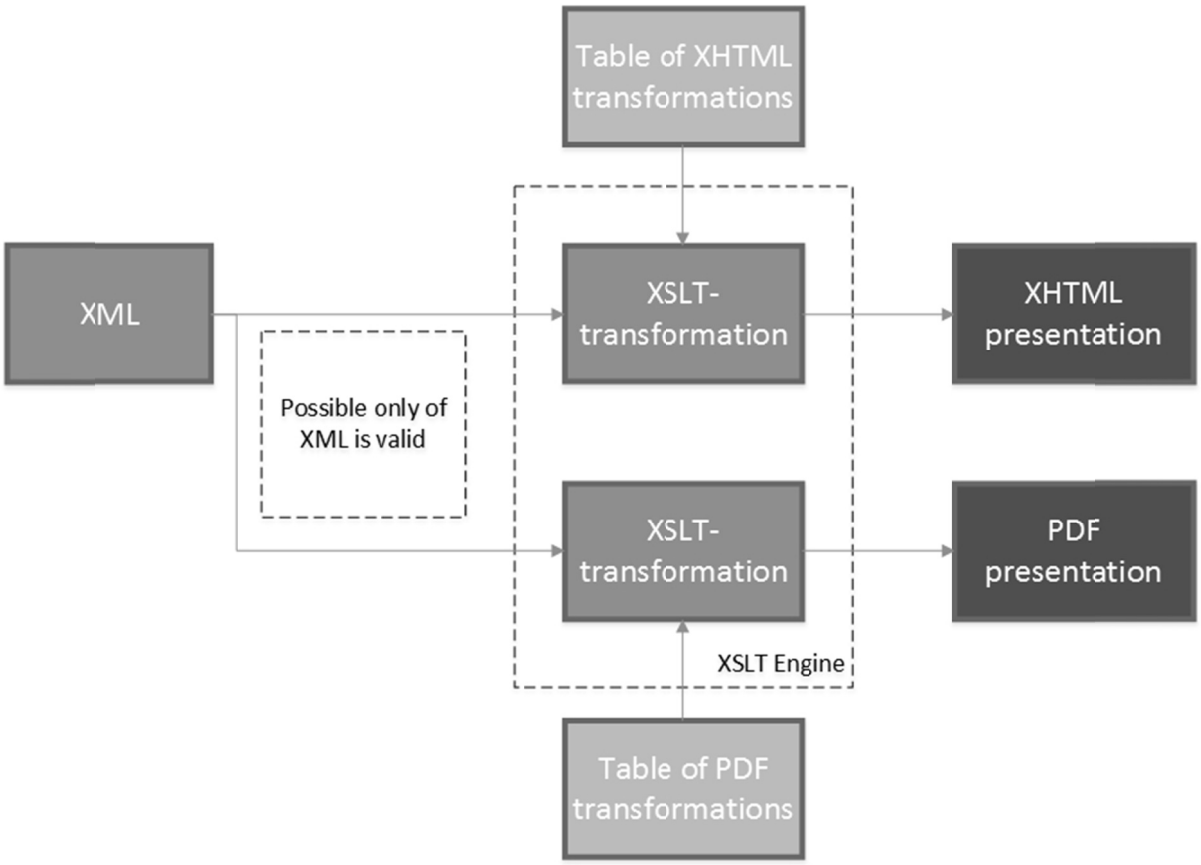

Fig 1 – XML transformations

Aims

Most of documents is not just plain text, but has some semantics. XML solves syntax presentation problem, whereas schema partially solves the problem of semantic meaning.

Software systems that perform some operations upon XML require performing lots of documents validation, which means that this process must be optimized and fast.

Talking about existing techniques, the vast majority of them are aimed to solve the problem of full validation, such as incremental validating or even splitting the document into chunks and checking simultaneously several chunks in different threads. Validating small files is a simple task for any of numerous algorithms. However, when the file is big (more than 5 Mb), it may be a problem. Moreover, there are situations when it is required to make several sequential actions on XML and

not to break document correctness [2, 3, 4]. It can be some automatic changes (adding information into document by web agents) or making manual changes in some visual editors. This may dramatically increase duration of XML validation.

Thus, the main purpose of this work is considered to be a research of techniques and algorithms of XML validation against XSD schemas [5]. In addition, a new validation technique is proposed. It is based on this research and has lesser algorithm complexity in case of sequential validation of the same XML after some changes.

Research description

Basically, before the process of XML validation against XSD schema, it is required to make two steps: firstly, perform syntax analysis of a document and secondly, perform syntax analysis of its schema.

There are two main techniques of XML processing:

- DOM (Document Object Model);
- SAX (Simple API for XML).

The first technique is parsing and building of full element tree of the document. The majority of XML applications works with documents using DOM. Data types of DOM nodes are abstract; every implementation has its own programming language dependent data types. The main disadvantage of DOM is extensive use of memory, because before any operation upon DOM requires XML to be fully loaded, processed and transformed to the object tree (fig 2).

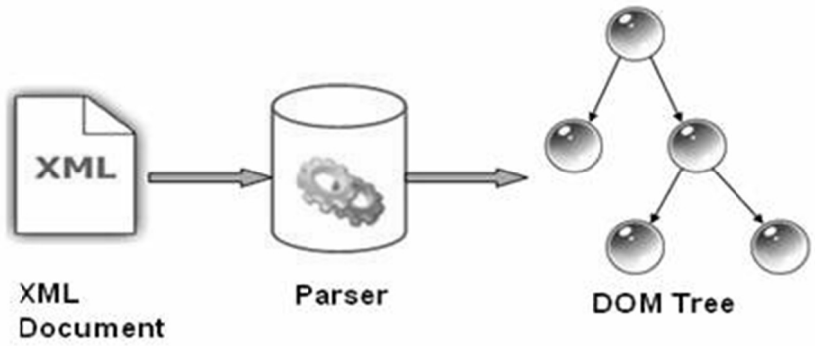

Fig 2 – Parsing XML into DOM

DOM model is very useful for data manipulating due to loading the whole document into memory. However, this can cause excessive use of memory.

SAX solves the problem of memory overuse by scanning the document from the beginning till the end and notifying the application about such events (fig 3) as “start of element” and “end of the element”. This approach allows reducing the use of memory considerably. However, this also means that manipulating the document will be impossible due to absence of elements tree as with DOM.

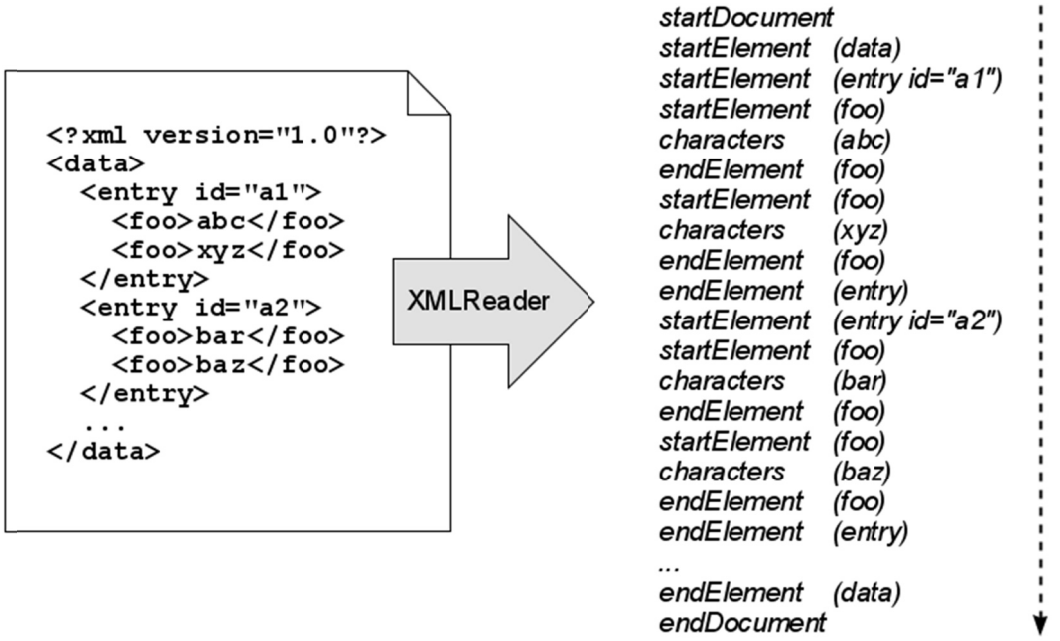

Fig 3 – SAX XML processing

Finally, let us look through the main opportunities of XML schema:

- strong controlling of data typing document nodes and attributes;
- defining sequence of nodes appearing, observe for the presence of mandatory nodes and attributes;
- demanding the element uniqueness in specified context;
- creating optional nodes that require presence of one or another node, depending on the context;
- fulfilling the requirements of specific predicate on the group of nodes and attributes.

Schema features

XSD describes a document schema by declaring set of definitions (parameters, elements and attributes), which describe its class in terms of syntax restrictions for this document. XSD is developed from DTD (Document Type Definition – previous W3C recommendation for XML schema). Thus, it has common features such as set of regular expres-

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sions that can be performed upon atomic terms or elements. However, XML schema also extends functionality of DTD by:

- patterns (any, anyType, anyAttribute) that make possible usage of any element from specified namespace;
- substitution group that defines the group of types that can be used instead of specific one;
- amount of occurrences and opportunity of specifying of minimal and maximal amounts for any element.

Speaking about algorithmic complexity, it should be mentioned that validation upon XML schema is heavier than validation upon DTD. However, the latest XML specification simplifies this process significantly.

Building a validator

As it was said at the beginning of the article, the main use case for this validator is when it is already known that XML is valid and required to be validated again after some small changes.

For the beginning, let us specify the list of simple structure changes that will be checked for correctness:

- Add: creating of new sub-element with the type X on the position N;
- Remove: removing of sub-element from the position N;
- Move: element carrying from the position N to the position M (even if this action reduces to element remove and add, but intermediate state may be inconsistent).

The basis of validating algorithm is in converting XSD model to finite state machine (FSM) which consists of two parts: one is for particles and another is for terms.

To translate a particle to an FSM ending at the state S [6]:

1. Set the start state n to S;
2. If the particles MaxOccurs is infinity:
   2.1. Add a new intermediate state t; which is got as a result of translating term to an FSM;
   2.2. Add lambda (also known as epsilon, or empty) edges from t to n and from n to S (fig 4).
3. If MaxOccurs is numeric:

Build a chain of (MaxOccurs-MinOccurs) copies of the term translation of backwards from S, with lambda transitions from intermediate state on each step to S;

For example, for min=2 and max=4 (fig 5)

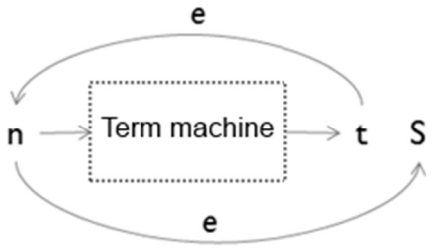

Fig 4 – Particle FSM first step

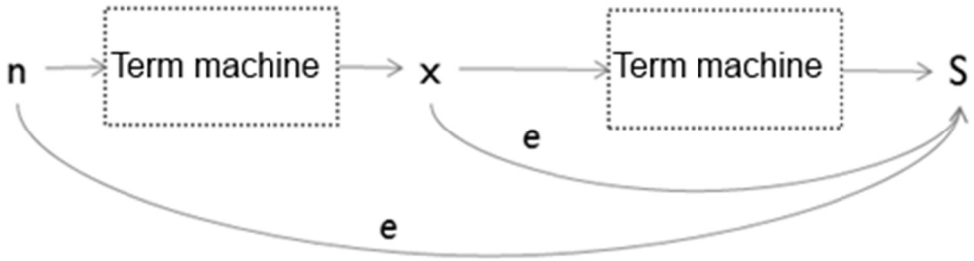

Fig 5 – Particle FSM for min/max values

4. Build a chain of MinOccurs copies of the translation of term from start state n, and as the result of previous steps.

As for the second step, building of FSM with specified final state S for concrete term:

1. If the term is a pattern (any):
   1.1. Create new state b and connect it with edge S, which is labeled with the term type.
   1.2. Return b;
2. If the term is element definition:
   2.1. Create new state b and for each element of the substitution group create edge from b to S, labeled with the type of the element.
   2.2. Return b;
3. If the term is a choice:
   3.1. Create new state b, for every choice element create machine (first step) and connect it with lambda edges with state b and S.
   3.2. Return b;
4. If the term is a sequence:
   4.1. For every sequence element create machine (first step) and connect them in reverse order, starting from the state S.

4.2. Return the first state in received chain.

After applying of proposed algorithm to every type in schema, accordance of type and the validating FSM is received in outcome. In addition, the last task would be selecting of proper FSM for validating of changed node of the document. This could be achieved by use of PSVI (Post Schema Validation Infoset) which is generated by almost every full validator. For every tree node, it points to according schema type. Finally, if there was an element X and it was added a new sub-element B, validation would be performed by FSM of X element (fig 6).

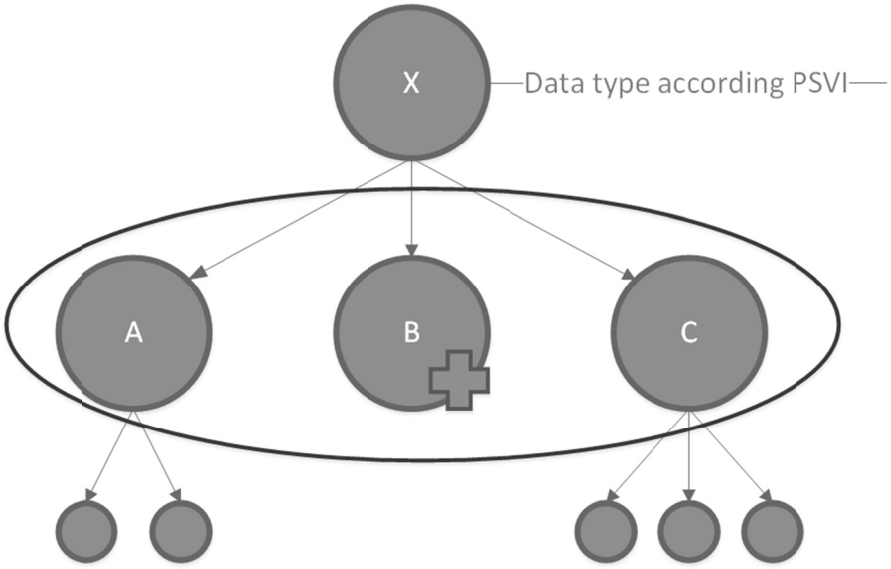

Fig 6 – Validation of X element after B was added

Conclusions

The results of performed tests are below:

Table 1

Validation time tests

Amount of element structure	Nesting level	Amount of types	Average validation time by Xerses	Implementation of algorithm average time
32	4	16	10 ms	<1 ms
32	4	40	17 ms	<1 ms
12000	4	16	47 ms	<2 ms
12000	4	40	56 ms	<2 ms
12000	32	16	2460 ms	<5 ms
12000	32	40	2650 ms	<6 ms

As it can be seen from the table, proposed validation technique shows great performance increase, thus making this algorithm suitable for use in visual editors and for validation of batch operations upon XML documents.

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TO THE QUESTION OF CODE GENERATION FOR TEMPLATES OF MODELING LANGUAGES

Abstract. The research covers translation of modeling language templates to constructs of object-oriented programming languages. The main feature of modeling language templates is ability to define signature constraints on type parameter. Type constraints on template parameter in a target language are taken into account if present. The paper provides a brief overview of general techniques of templates translation and illustrates features of their implementation for translation of templates with signature constraints. Comparative analysis of the techniques was made and cases, when using each of the techniques is reasonable, are presented.

Keywords: template, modeling language, signature constraint, type constrain, object-oriented language.

Introduction

Nowadays, construction of complicated software is often based on Model-Driven Development (MDD) approach. The first stage of the approach is creation of a model that addresses the problem, the second stage is the model verification and the third one is code generation to a High-Level General-Purpose Programming Language (HLGPPL), usually to an Object-Oriented Language (OOL) [1]. As a rule the primary model description is implemented in modeling languages. Those languages have high expressive power and usually provide high-level abstract Template Data Types (TDTs) with specific features that are not common in HLGPPLs.

The experience in development of HLGPPL compilers gives us different techniques of templates translation. These techniques are well studied and show good results. Some of them could be adopted in order to translate modeling language TDTs.

Reworking the techniques, we should take into account some new criteria for evaluating the translation process that were not important in development of HLGPPL compilers. These criteria are code readability and maintainability (simplicity of further support).

Customers set often requirements to the developed according to MDD models to be supported both in the source modeling language and in the target HLGPPL. Thus, readability and maintainability play an important role in modern approaches of software development.

Analysis of recent achievements

Translation process of TDTs is well described for OOLs. The focus of the previous research is put on two main approaches of code generation for templates. The first approach implies OOL to OOL transformations that removes templates from the code. Such approach is used in some compilers of C++ programming language [2]. The other approach is based on translation from OOL to an intermediate language. Such approach is used in Java programming language compilers [3]. The slightly different idea of the second approach involves usage of type objects that are used to keep type information in run-time. This idea is implemented in most modern compilers of C# programming language [4].

During the past few decades, the concept of readability [5] and maintainability [6] measurements was developed and is suitable for evaluation of TDTs translation for modeling languages.

Purpose of the research

Research of the paper has the several objectives described below.

1. Analyzing the existing techniques of OOL templates translation. Adopting the techniques to generate OOL code for modeling language templates. The main feature of modeling language templates is ability to define signature constraints on a type parameter.

2. Developing combined techniques of translation that will allow to translate certain TDT of modeling language more efficiently.

3. Comparative analysis of the techniques and determination of the cases when using each of the technique is reasonable.

Main part

During the research, templates translation techniques of OOL were analyzed and 3 techniques for templates transformation of modeling languages are proposed. These techniques are:

1) full substitution of templates;

2) direct translation of templates;

3) combined translation of templates.

Before going into details of the techniques some characteristics of modeling language templates should be illustrated.

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Signature constraints

A distinctive feature of modeling languages used in the research is ability to define signature constrains on a template parameter. The semantics of signature constraints is described below.

If signature constraint *C* is defined on a formal type parameter *T* of template *class TC <template T :? C>* then each actual type parameter of *TC* should contain a method with the prototype corresponding to *C*, otherwise it will be a compile error.

Figure 1 illustrates the semantics described above.

Signature constraints do not influence on the logic of the model. They used in order to perform automatic model verification and should be preserved in an OOL after translation if possible.

```
SIG_CONSTRAINT C = f2(int)-> double
CLASS TC <TEMPLATE T :? C> {
    v1 : T;
    m1 () -> double {
      return v1.f2(10);
    }
}
CLASS UT1 {
        f2(int i)-> double {
            return i*9.81;
        }
}
CLASS UT2 {
}
...
var1 : TC <UT1>;    <--- OK
var2 : TC <UT2>;    <--- ERROR
```

Fig. 1 – Semantics of signature constraints

Full substitution of templates

The idea of the technique is the following: if a translator encounters specialization of the template with actual parameter then new non-template data type is created. Each usage of a formal type parameter is replaced by an actual type parameter in all places where the formal type parameter was used. Thus, the transformation is performed on the modeling language layer.

Signature constrains on a type parameter are omitted after the transformation. They are only used for TDTs verification.

We might say that the model containing TDTs are replaced by equivalent model without TDTs. Figure 2 illustrates this technique.

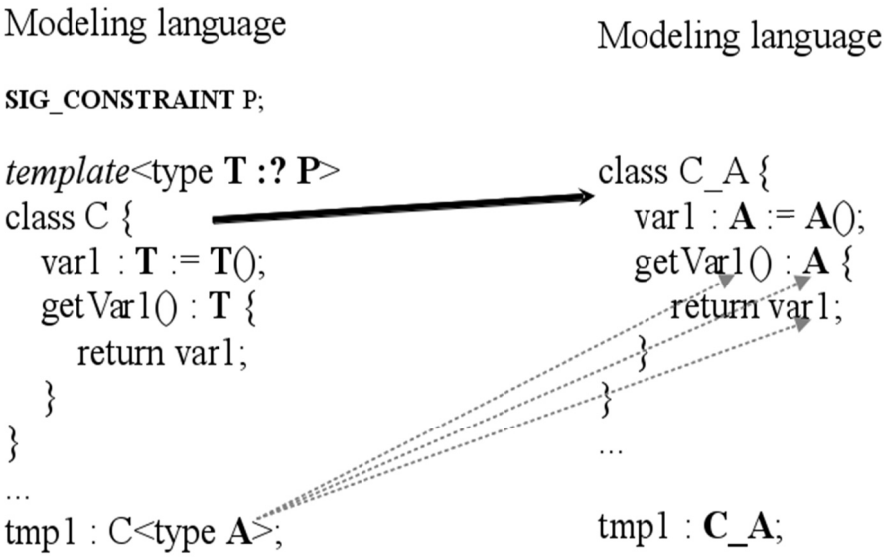

Fig. 2 – Full substitution of templates

This translation technique is faster than the others but leads to code blow-up. Consequently future modifications of the generated code is more difficult and compilation takes more time.

The technique is independent from a target language. This is useful in cases when one modeling language is translated into several target languages.

Direct translation of templates

According to this technique, all TDTs of a modeling language are translated into TDTs of an OOL with preservation of their semantics. Suchwise, semantics of the modeling language templates is implemented by means of OOL templates and other constructions presented in the OOL. Figure 3 illustrates the technique for translation from a modeling language to the OOL Java.

In order to implement semantics of the modeling language the signature constraints are translated into an interface that contains methods defined by the signature. Each class that is used as an actual template parameter implements the interface. Type constraint is put on a formal template parameter. Thus, semantics of templates of the modeling language is implemented for translation into Java.

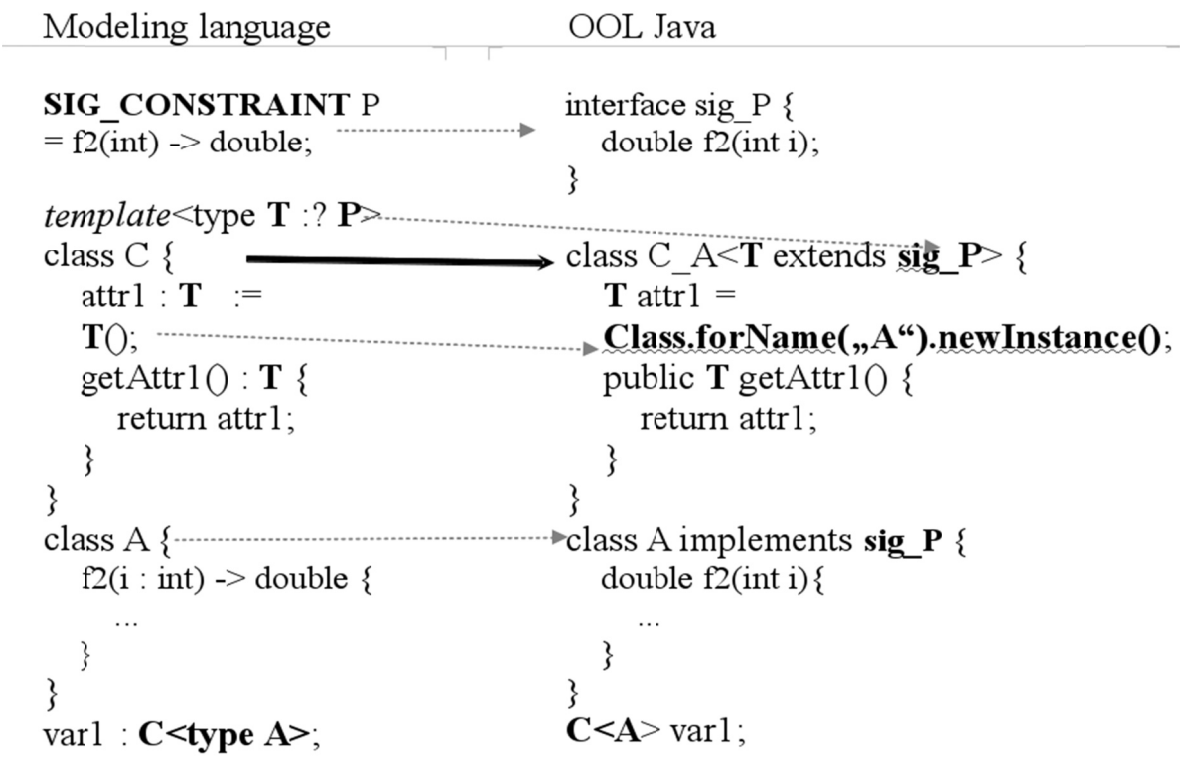

Fig. 3 – Direct translation

In most cases the technique is slower than previously discussed one, but allows generating less code with usage of constructs that are widely-used among programmers in a certain target language. This feature of the technique increases readability of the generated code and simplifies its further support.

Combined translation of templates

Combined techniques of templates translation are based on the idea that some templates are translated according to the technique of full submission and the others are translated according to the technique of direct translation. Thus, partial substitution of the modeling language templates is performed. The key point of the combined translation is determination of translation technique (substitution or direct translation) for certain TDT of a modeling language.

In order to determine translation of an arbitrary TDT of a modeling language the following combined technique is proposed:

1) if an actual template type parameter is a primitive type (int, double, char, etc.) it is reasonable to use full substitution of templates;

2) if an actual template type parameter is a heap-allocated data type, it is reasonable to use direct translation of templates;

3) if signature constraints are defined on a formal template type parameter then any of the techniques (full substitution and direct translation) can be used because they show practically the same results.

Comparative analysis of the translation techniques

In order to compare the transformation techniques the following evaluating critera were taken into account:

1) productivity;
2) compilation time;
3) size of generated code;
4) readability and maintainability.

Tab. 1

Results of comparative analysis of the translation techniques

Translation technique	**Productivity**	**Compilation time**	**Size of generated code**	**Readability and maintainability**
Full substitution	high	long	large	low
Direct translation	low	short	small	high
Combined translation	middle	middle	middle	Middle

As it can be noticed in the table 1, the first two techniques are opposite to each other. As it happens often, in this case «low of the lever» is applied: the more we gain in productivity the less we gain in other characteristics and otherwise. The proposed combined approach has middle values between the two others for all characteristics.

Choice of the exact translation technique depends on the problem that is solved by the developer. Flexible modeling language should provide an option for the user to choose what way is used to translate TDTs. As the default technique it is reasonable to use the proposed combined translation of templates that shows average results.

Conclusions

Analysis of OOL templates translation techniques that was done for the research allowed defining three similar techniques of modeling language templates translation. These techniques are studied and compared for modeling language that has ability to define signature constraints on template type parameter.

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A developer of a translator for modeling language should take into account not only common characteristics as productivity, compilation time, size of generated code but also readability and maintainability.

The actual problem for further research is creating techniques for translation TDTs of modeling language into constructs of procedural programing languages like C.

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INVESTIGATION OF THE FRACTAL TIME SERIES OF TEMPERATURES IN THE ELECTRIC ARC FURNACE FURNACE USING METHOD OF NORMALIZED R/S-ANALYSIS

Abstract: this paper is devoted to study the fractal parameters of the process of steelmaking. We described an algorithm of the R/S-analysis and estimated degree of the fractal output signal (estimated temperature of the metal melted in an electric arc furnace (EAF)) using the Hurst parameter and fractal dimension

Tags: method normalized range, hurst exponent, fractal dimension, persistence degree, metal's temperature in the electric arc furnace.

Introduction

The theory of fractals and multifractals now is widely used to describe the properties of self-similarity and scaling complex, and is observed in a variety of applications. Fractal time series represent a whole class of fractal curves are widely used in the description and modeling of various phenomena. One fairly simple and effective methods of time series analysis, having a scale of self-similarity is the so-called R/S-analysis. This method, in particular, we analyze series of meteorological and geophysical observations - changes in temperature, pressure, amount of rainfall, variation of the magnetic field of the Earth, and others [4]. In turn, this approach has also been successfully applied to assess current conditions and trends in the commodity, stock and other markets on the basis of analysis of the relevant stock exchange series [5]. Parameters of technological processes, in particular electric steel production, can be considered to some extent fractal.

Algorithm of R/S-analysis

Method of R/S-analysis of studying fractal time series was proposed by Hurst [3,4]. It is based on an analysis of amplitude parameter (the highest and lowest values in the target segment) and the standard deviation.

Hurst parameter estimation method is based on the normalized amplitude of the fact that for a random process, which has a long-term dependence for large values of τ the following relation:

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$$\mathrm{M}\left[\frac{R(\tau)}{S(\tau)}\right] = (c \cdot x(t))^H, \quad (1)$$

where c - a constant;

τ - time interval;

$R(\tau)$ - the scope of the cumulative number of $x^{acc}(t, \tau)$;

$S(\tau)$ - the standard deviation of the original series.

Rescaled range method proposed by Hurst, is the most popular and is used in many scientific studies. Use H-step algorithm for finding time series $X(t)$ [2].

1. For the calculation it is necessary to convert the initial number of $X(t)$, $t = 1,2 \ldots, N$, first by finding a difference: $x(t) = X(t+1) - X(t)$. If the original series are already a series of increments, this step is skipped.

2. The resulting number is divided by the length A of adjacent frames τ so that $\mathrm{A} \cdot \tau = \mathrm{N}$. Each period is marked as I_a, where in $a = 1, 2, 3, \ldots, A$. I_a length for each average value τ is determined:

$$\bar{\mathrm{x}}(\tau) = \frac{1}{\tau}\sum_{t=1}^{\tau} x(t) \quad (2)$$

3. Time series accumulated deviations from the mean $x^{acc}(t, \tau)$ for each time period is defined as I_a:

$$\mathrm{x}^{acc}(t,\tau) = \sum_{t=1}^{\tau} x(i) - \bar{\mathrm{x}}(\tau), \quad t = \overline{1,\tau}. \quad (3)$$

4. For each period is determined by the scope of I_a cumulative number of:

$$R(\tau) = max\left(\mathrm{x}^{acc}(t,\tau)\right) - min\left(\mathrm{x}^{acc}(t,\tau)\right), t = \overline{1,\tau} \quad (4)$$

and sample standard deviation of the number of increments

$$\mathrm{S}(\tau) = \sqrt{\frac{1}{\tau-1}\sum_{t=1}^{\tau}(\mathrm{x}(t) - \bar{\mathrm{x}})^2}\ . \quad (5)$$

5. The normalized scale for each period equal to $I_a\frac{R(\tau)}{S(\tau)}$. Mean R/S for the length τ is defined as

$$\frac{R}{S}(\tau) = \frac{1}{A}\sum_{a=1}^{A}\frac{R_a(\tau)}{S_a(\tau)}. \quad (6)$$

6. Length τ is increased to the next higher value. The values τ, including start and end points of the time series, and steps 1-6 are repeated until $\tau = N$.

7. Constructed linear regression by least squares log (τ), as the independent variable and log (R/S), as the dependent variable. The slope is an estimate of the Hurst exponent *(H)*.

Hurst exponent *(H)*, called the self-similarity parameter is in the range $0 < H < 1$, and is a key measure of self-similarity measure and duration of long-term dependence stochastic process [6].

In the case of $0{,}50 < H < 1{,}00$ - analyzed time series and is characterized by the persistent effect of long-term memory, i.e. if the number increases (decreases) in the previous period, it is likely that it will maintain this trend for some time in the future. Trends are evident, and the power of persistence increases when H unit.

In the case of $H = 0{,}5$ - holds a stochastic process with independent increments.

In the case $0 < H < 0{,}5$ - antipersistent analyzed time series . In this case, the growth is likely to last decrease in the future, and vice versa, i.e. the likelihood that the process step $i+1$ deviates from the mean in the opposite direction is so large - extent parameter H is close to 0.

The main quantitative characteristic of fractals - the dimension D, Hausdorff introduced in 1919 for a compact set in an arbitrary metric space [1, 5]. However, for most natural time series analytical determination of the fractal dimension are impossible, therefore D is determined by the Hurst exponent [1,7]: $D = 2 - H$.

Practical implementation of the R/S-analysis

Researched the experimental data are given changes in temperature of the metal (the first temperature measurement), melted in an electric arc furnace (EAF) on LLC "Dneprostal" (Fig. 1).

Implementation of the algorithm of the method is executed in the normalized amplitude Matlab package in accordance with the above algorithm, R/S-analyzes. Figure 2 shows a fragment of the work program for the implementation of the 1-st step of the algorithm - the transformation of the original series in a series of increments.

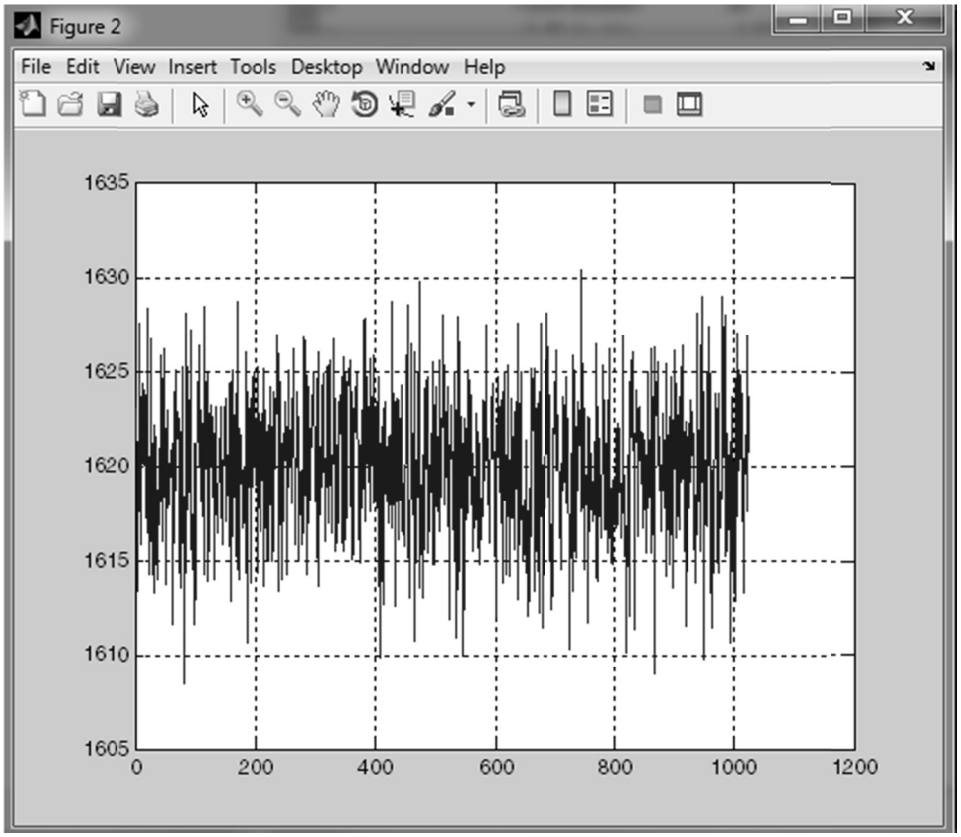

Figure 1 - Change in temperature of steel produced by EAF LLC "Dneprostal"

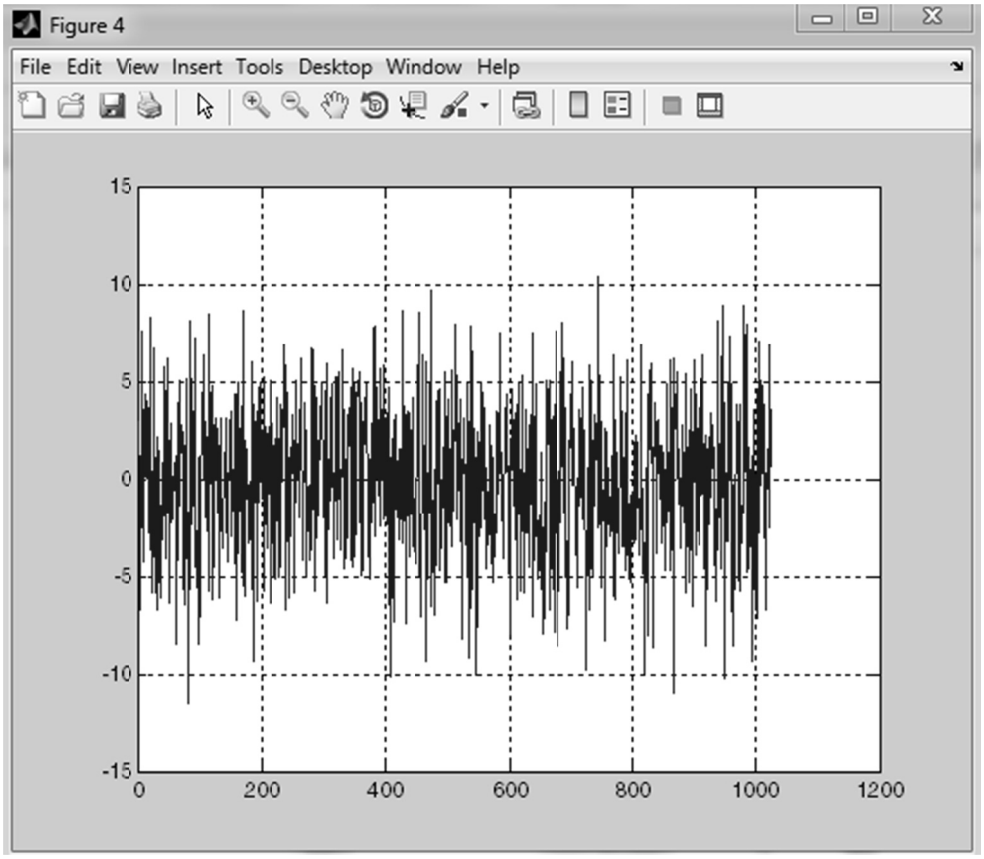

Figure 2 -A number of temperature increments of steel in EAF LLC "Dneprostal"

The application allows the fractal analysis of dynamic data, the result of which is an indicator of Hurst and the fractal dimension (Fig. 3). As is seen from the graph, for the analyzed time series H = 0,597, and the fractal dimension D = 1,403. The results of calculation show that the temperature of steel in EAF is in the range of persistence, i.e. have steady trend row. If the number increases (decreases) in the previous period, it is likely that it will keep this trend for some time in the future. Steady trend behavior or strength of persistence, increases as the value of H to 1. Resulting value of the Hurst exponent suggests the self-similarity of the time series of temperature change of steel in EAF.

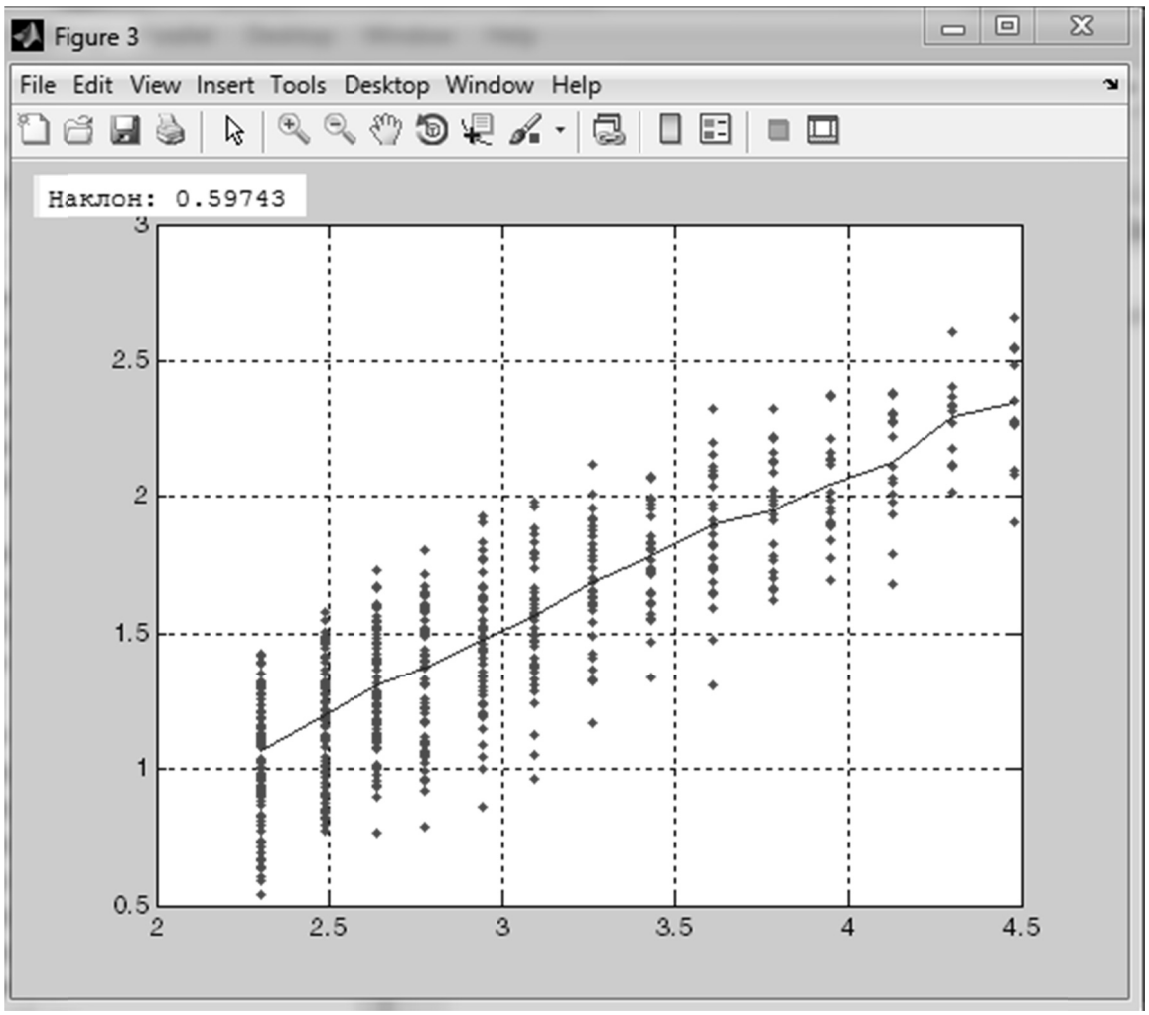

Figure 3 – Determination of the Hurst exponent

Conclusions and prospects for future research

In this paper, we made fractal analysis of time series of temperature of steel produced by EAF LLC "Dneprostal". To determine the fractal dimension method we used rescaled range (R / S- analysis). Method of R / S- analysis is a sustainable method to disclose the effects of long-

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term memory, fractal structure and availability of statistical time series of cycles, it is possible to distinguish fractal time series from other types of time series, revealing their self-similar statistical structure [7]. Possibilities of using fractal analysis are exemplified by the evaluation process of changing temperature of the metal in the EAF. We developed a software application that allows you to carry out the calculation of fractal characteristics of time series on the basis of Hurst R/S-analysis. The calculation results are obtained for the temperature of the analyzed time series: n = 0,597, D = 1,403, indicate that the steel temperature in EAF is the persistence interval, i.e. time series - steady trend. This suggests the fractal series, which, in turn, will further allow effectively predict the behavior of steel temperature in the actual process of optimal control modes chipboard.

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A.V. Mitsa, I.V. Fekeshgazi, F.E. Geche, V.M. Kotsovsky

MATHEMATICAL MODELING OF INFLUENCE OF LAYER NANODEFECTS ON THE LIGHT TRANSMISSION BY OPTICAL ELEMENTS WITH MULTILAYER INTERFERENCE SYSTEMS

The analysis of defects parameters influence on the light spectra transmission by optical elements with interference coating have been carry out. It is established that the maximum and spectral distribution of transmission curve essentially depend on parameters and space position of defect. The obtained results are important in fabrication of optical elements with multilayer coatings as for laser technique, as the spectacles lens.

Keywords: modeling, light transmission, multilayer interference coating, structure defects, interconnection of parameters.

Introduction

Production of qualitative interference optical elements (interference filters, antireflective coatings, light beam and spectra disconnectors and polarizers) demands the matters of the high level of cleanliness and stability of its parameters both for substrate and layers and also of technological regime of their deposition. The presence of non-uniformly distributed in the space nanodimension defects (emptiness or inclusions of foreign alien) give rise to change the transmission spectra of the interference systems. The results obtained for practically used interference coatings (in particular of spectacles optical lenses) are given in this report.

Experimental samples

All measurements were performed on the transparent substrates (spectacles lens) from material with refraction index equal to 1.9 [1]. The multilayer systems (MLS) was deposited on its working surfaces (see Fig. 1). It was formed by layers with unequal geometrical thicknesses. At the absence of defects the MLS consist on four layers (Fig. 1a and Fig. 1b: MLS-0), while at the presence of one (such as emptiness or inclusions of foreign alien) there are six layers (fig.1b: MLS-1, MLS-2 and MLS-3).

Shape forms of all defects may be represented as spherical (MLS-1), rectangular (MLS-2), cylindrical (MLS-3) and on more complicated one

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(see Fig. 1 b). The cross-section of defect by the plane that include the direction of light propagation are presented in Fig. 1.The layers parameters are given in the Table 1.

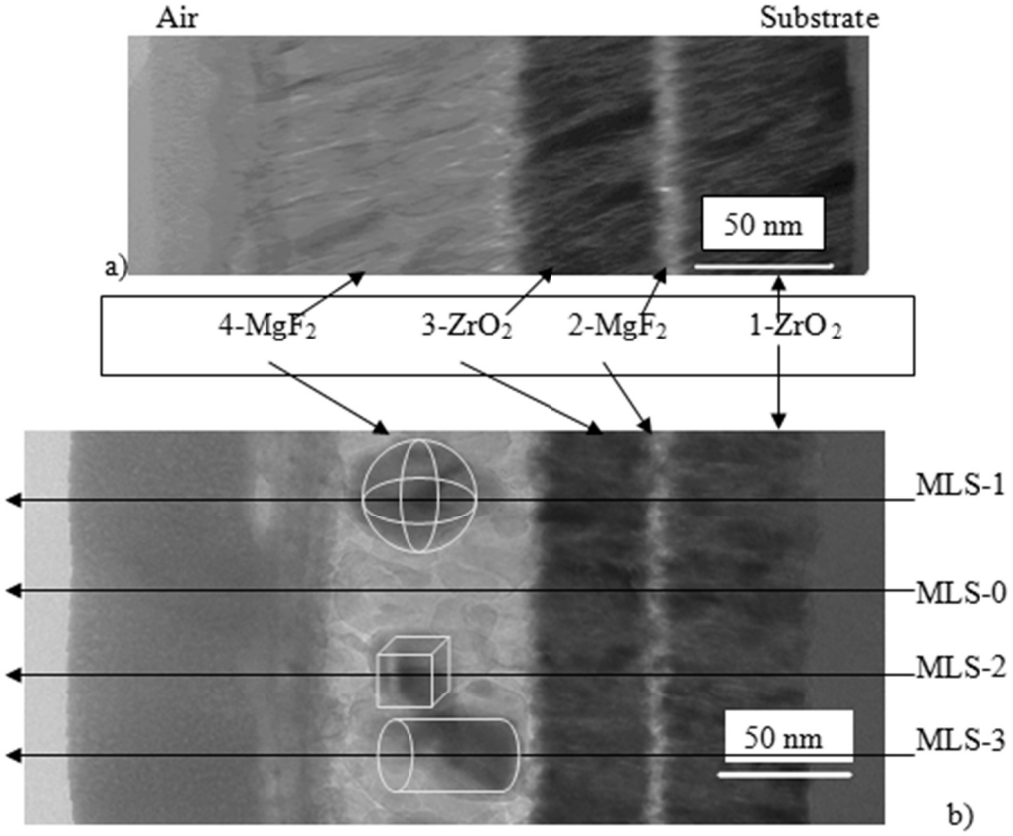

Fig.1. – Cross-section of MLS structures without defects (fig. 1a, 1b system MLS -0) and with defects (fig. 1b: systems MLS -1, MLS -2 and MLS -3).

Table 1.

Types of MLS and thickness of the layers, *nm*

Subst. of the layers	Types of MLS and thickness of the layers, *nm*													
	MLS-0		MLS-1-1		MLS-1-2		MLS-2-1		MLS-2-2		MLS-3-1		MLS-3-2	
	geom	opt.	geom	opt.	geom	opt.	geom	opt.	geom	opt.	geom	opt.	geom	opt.
ZrO_2	60	126,6	60	126,6	60	126,6	60	126,6	60	126,6	60	126,6	60	126,6
MgF_2	10	13.8	10	13.8	10	13.8	10	13.8	10	13.8	10	13.8	10	13.8
ZrO_2	50	105,5	50	105,5	50	105,5	50	105,5	50	105,5	50	105,5	50	105,5
MgF_2	80	110,4	22	30,4	22	30,4	30	41,48	30	41,48	10	13,8	10	13,8
ZrO_2 or Air	-	-	40	84,4	40	40	25	53	25	25	50	105,5	50	50
MgF_2	-	-	18	24,8	18	24,8	25	37,4	25	37,4	20	27,6	20	27,6

The first and the third layer of ML systems, were made from ZrO_2 (n_H = 2.11), the second, fourth and sixth layers – from MgF_2 (n_L = 1.38). It will be consider the two type of defect material: ZrO_2 or air.

The comparison of radiation transmission spectra shown that the spectra in the zone of MLS-0 (Fig.1a and Fig. 1b) without defects are identical to the transmission spectra of the MLS free on defects (fig.1b).

The analysis of results

The multilayer structures shown on Fig. 1a and Fig. 1b can be schematically represent as transparent substrate S with a refraction index n_S, on which one after another in consecutive order deposited the layers A with high refraction index n_A and layers B with low refraction index n_B (Fig.2), namely:

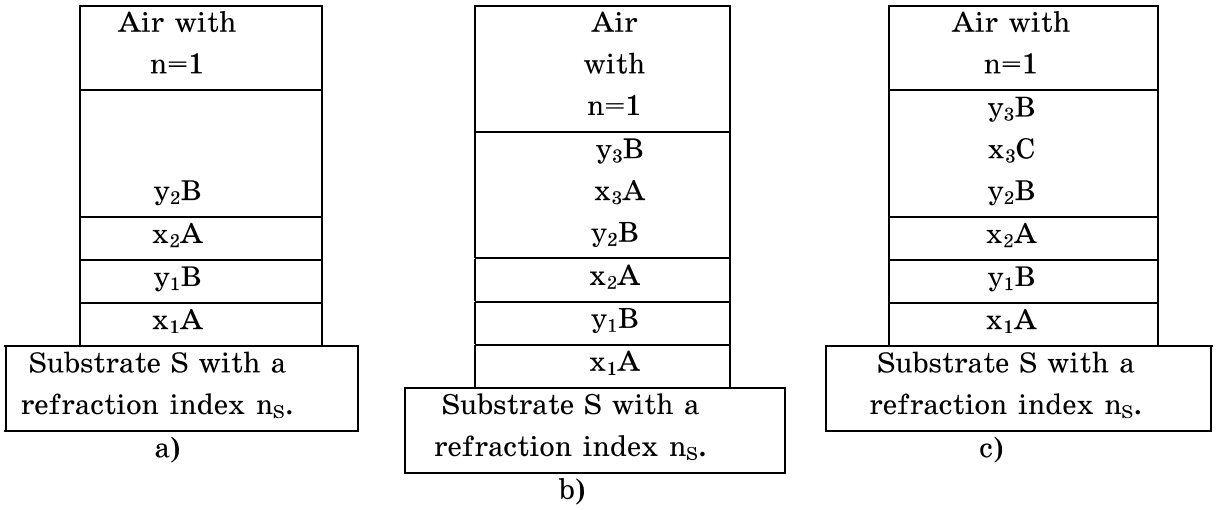

Fig. 2. Model of MLS structure without defects (a) and with the ZrO_2 (b) or air (c) defects.

The geometric and optical thicknesses of layers are determine by the factors x_i and y_i at the corresponding quarter-wave layers A and B for which the following ratio is correct $n_A d_A = n_B d_B = \lambda_0/4$. The geometrical view of defect structures MLS layer are present on Fig. 3. The MLS structure will be as in Fig 2b when the defects substance is from the same as B layer or as the Fig. 2c, when the defect is from the air.

To estimate the influence of changing interference systems parameters on the resulting transmission the matrix method was used. It based on the determination of a characteristic matrix [2]. If the geometrical thickness of a layer is equal to d, and refraction coefficient is equal to n, the characteristic matrix of the homogeneous dielectric film has the appearance:

$$M(n,d,\lambda)=\begin{Vmatrix} \cos\delta(n,d,\lambda) & -(i/p)\sin\delta(n,d,\lambda) \\ -ip\sin\delta(n,d,\lambda) & \cos\delta(n,d,\lambda) \end{Vmatrix}, \quad (1)$$

where $\delta(n,d,\lambda)=2\pi nd\cos\theta/\lambda$ - is the phase thickness of a layer, p=√ε/μ cosδ. In the case when the direction of propagation of radiation coincides with a perpendicular to the interface, $\delta = 0$ and correspondingly $p = n$.

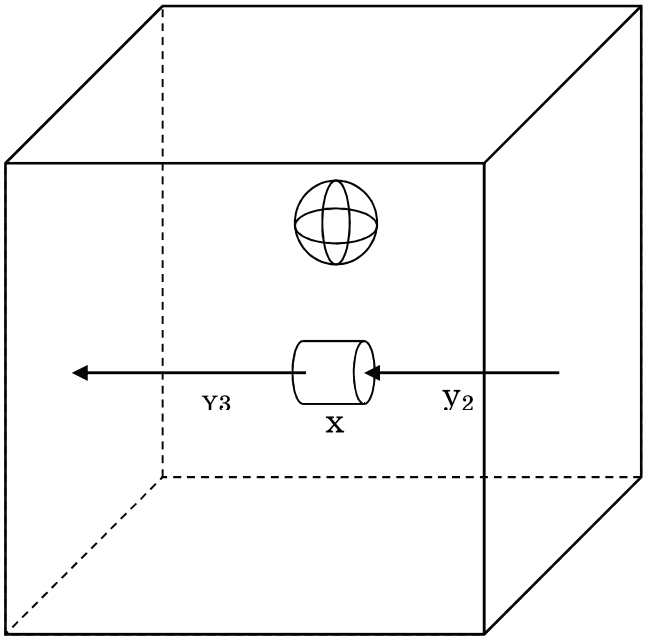

Fig.3. Geometrical view of the structures the MLS defect layer.

Knowing a characteristic matrix of one layer (1), we can determine a characteristic matrix of k-th layer of MLS, as a product of matrixes of each layer:

$$M(\overline{n},\overline{d},\lambda)=M_k(n_k,d_k,\lambda)\cdot M_{k-1}(n_{k-1},d_{k-1},\lambda)\cdots M_2(n_2,d_2,\lambda)\cdot M_1(n_1,d_1,\lambda), \quad (2)$$

where Mj – is a characteristic matrix of j-th layer; $\overline{n}=(n_1,n_2,...,n_{k-1},n_k)$ - is a vector of the values of refraction indices of layers; $\overline{d}=(d_1,d_2,...,d_{k-1},d_k)$ - is a vector of geometrical thicknesses of layers.

From (2) it is easy to find a value of a MLS transmission at the fixed values of $\overline{n}$, $\overline{d}$ and λ:

$$T(\overline{n},\overline{d},\lambda)=1-\left[\left|\frac{n_0(M_{11}(\overline{n},\overline{d},\lambda)+n_S\cdot M_{12}(\overline{n},\overline{d},\lambda))-(n_S\cdot M_{22}(\overline{n},\overline{d},\lambda)+M_{21}(\overline{n},\overline{d},\lambda)}{n_0(M_{11}(\overline{n},\overline{d},\lambda)+n_S\cdot M_{12}(\overline{n},\overline{d},\lambda))+(n_S\cdot M_{22}(\overline{n},\overline{d},\lambda)+M_{21}(\overline{n},\overline{d},\lambda)}\right|\right]^2, \quad (3)$$

where n_0, n_S – are the refraction indices of external environment and substrate accordingly, M_{11}, M_{12}, M_{21}, M_{22} - are the elements of a characteristic matrix Mj.

For the numerical calculation of the transmittance spectra of MLS the objective function is represented as [3-5]:

$$\max_{\bar{n},\bar{d}} F\left(\bar{n},\bar{d}\right)=\left(\frac{1}{L}\sum_{i=1}^{L}T^2\left(\bar{n},\bar{d},\lambda_i\right)\right)^{1/2}, \quad (4)$$

where L – is a number of a grid points for a spectral interval from λ_1 to λ_2. At the its uniform distribution with a step $\Delta\lambda$

$$L=\frac{\lambda_2-\lambda_1}{\Delta\lambda}+1, \quad (5)$$

where λ_1 and λ_2 – are the short-wave and the long-wave boundary accordingly of researched wave spectral region.

The spectral dependences of the MLS transmission was calculated by using the formula (3) and represented in Tables 1 and in the Fig. 3 layers parameters are presented in Fig. 4. It was shown, that the existence of the defects in the volume of MgF_2-layer give rise to essential change of MLS transmittance, decreasing of a spectra maximum and to its displacement in the short wave range. The more considerable effects observed when the defect is from the substance with higher refractive indices (curves 3.0, 3-1 and 3-2 in Fig. 4).

The more detailed examination of transmittance dependences were made by changing the defect parameters. The data for layers structure at the different type of defect with the constant longitudinal geometric value equal to 20 nm, but different optical thicknesses determined by the refractive indices of defect substances are presented in Table 2. The correspondence spectra of MLS-n are presented in fig. 5.

Table 2

Types of MLS-n systems with 20 *nm* geometric value of defect from substance with different refractive indices

Substance of the layers	Types of MLS-n and thickness of the layers, *nm*									
	MLS-0		MLS-n=1		MLS-n=2		MLS-n=3		MLS-n=4	
	geom.	opt.	geom.	opt.	geom.	opt.	geom.	opt.	geom.	opt.
ZrO_2	60	126,6	60	126,6	60	126,6	60	126,6	60	126,6
MgF_2	10	13,8	10	13,8	10	13,8	10	13,8	10	13,8
ZrO_2	50	105,5	50	105,5	50	105,5	50	105,5	50	105,5
MgF_2	80	110,4	30	41,4	30	41,4	30	41,4	30	41,4
Mater with n-	-	-	20	20	20	40	20	60	20	80
MgF_2	-	-	30	41.4	30	41.4	30	41,4	30	41,4

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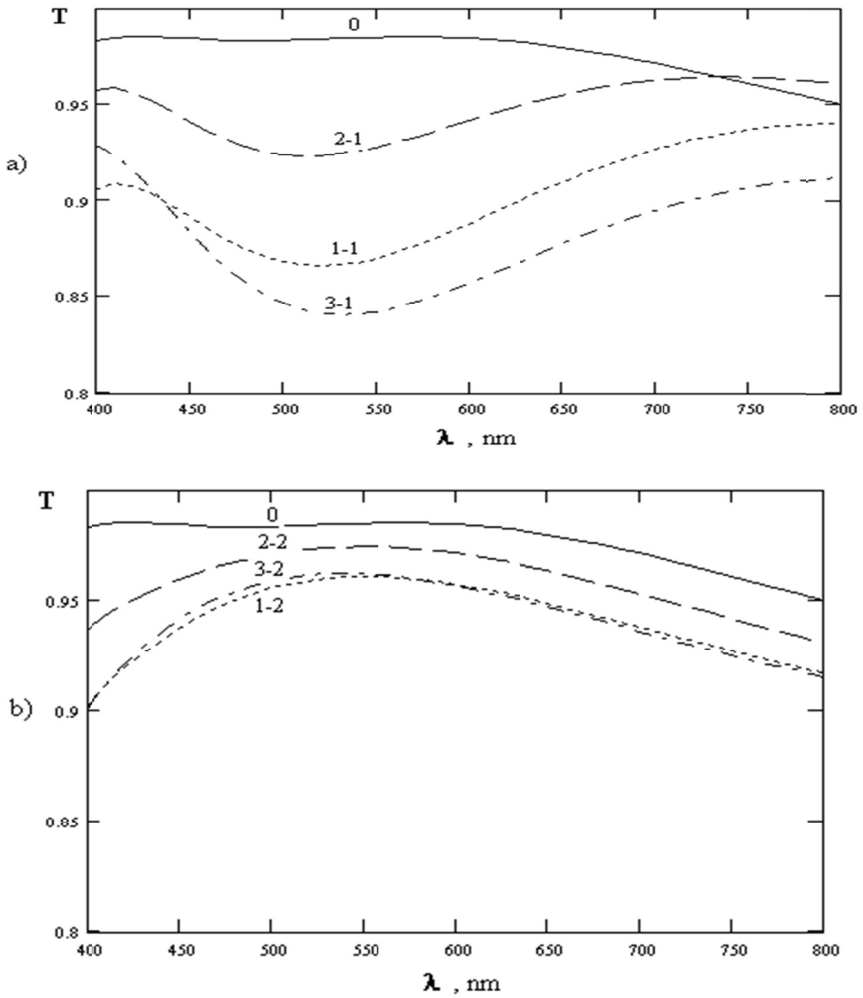

Fig. 4. The transmission spectra of MLS without defects (curve 0) and with defects from ZrO_2 (curves 1-1, 2-1, 3-1 on fig. 4a) or defects from air (curves 1-2, 2-2, 3-2 on fig 4b).

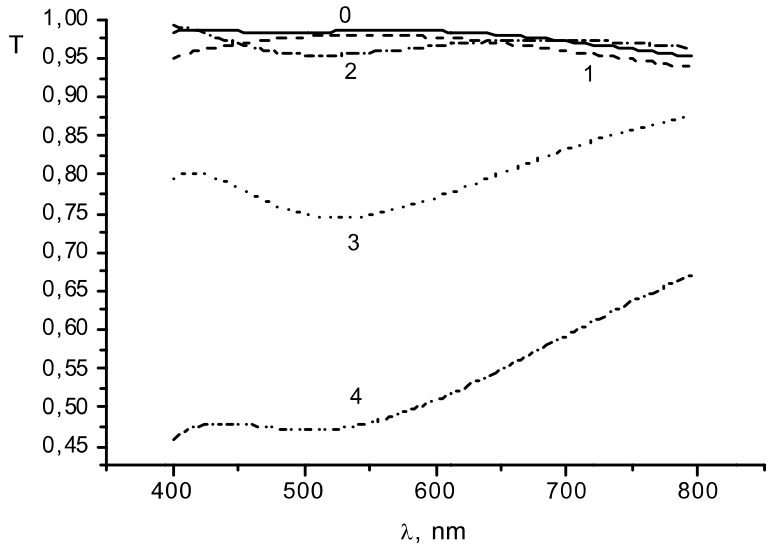

Fig. 5. The transmittance spectra of MLS-n without defects (curve 0) and with the defects from substances with refractive indexes $n = 1$ (curve 1), $n = 2$ (curve 2), $n = 3$ (curve 3), $n = 4$ (curves 4).

The diagram of interdependences between the of the MLS layer parameters at longitudinal values of defects from ZrO_2 are presented in Table 3 and Fig. 6a and on its space dislocation - in Table 4 and Fig. 6b for the longitudinal X_3A=20 nm value of defect .

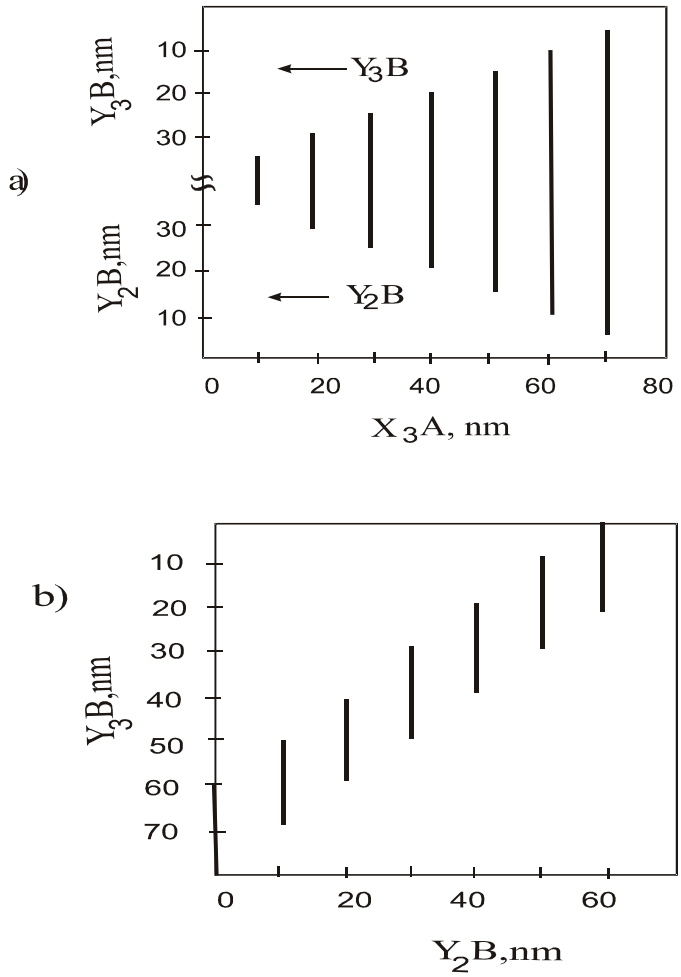

Fig.6. Diagram of interdependences between the MLS-D layer parameters at lon-gitudinal scale of defects (Fig. 6 a) and on its space dislocation MLS-P (Fig. 6 b).

Table 3.

Interdependency of MLS-D layers dimensions Y_2B and Y_3B at different longitudinal values of X_3A for defects from ZrO_2

Substance and designation of layers	Types of MLS D and thickness of the layers, *nm*																	
	MLS-D0		MLS-D1		MLS-D2		MLS-D3		MLS-D4		MLS-D5		MLS-D6		MLS-D7		MLS-D8	
	geom.	opt.	geom	opt.	geom.	opt.	geom	opt.	geom.	opt.	geom.	opt.	geom.	opt.	geom.	opt.	geom	opt.
ZrO_2X_1A	60	126,6	60	126,6	60	126,6	60	26,6	60	126,6	60	126,6	60	126,6	60	126,6	60	126,6
MgF_2Y_1B	10	13,8	10	13,8	10	13,8	10	13,8	10	13,8	10	13,8	10	13,8	10	13,8	10	13,8
ZrO_2X_2A	50	105,5	50	105,5	50	105,5	50	105,5	50	105,5	50	105,5	50	105,5	50	105,5	50	105,5
MgF_2Y_2B	40	555,	35	48,3	30	41,4	25	4,5	20	27,6	15	20,7	10	13,8	5	6,9	0	0
ZrO_2X_3A	0	0	10	13,8	20	42,24	30	63,3	40	84,4	50	105,5	60	126,6	70	147,7	80	168,8
MgF_2Y_3B	40	55,2	35	48,3	30	41,4	25	4,5	20	27,6	15	20,7	10	13,8	5	6,9	0	0

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Table 4.

Interdependency of MLS-P layers dimensions Y_2B and Y_3B at different space position of the defects from ZrO_2 with the longitudinal geometric value of X_3A= 20 nm

Substance and design- nation of layers	Types of MLS P and thickness of the layers, *nm*															
	MLS-P0		MLS-P1		MLS-P2		MLS-P3		MLS-P4		MLS-P5		MLS-P6		MLS-P7	
	geom.	opt.	geom.	opt.	geom.	opt.	geom.	opt.	geom.	opt.	geom.	opt.	geom.	opt.	geom.	opt..
ZrO_2X_1A	60	126,6	60	126,6	60	126,6	60	126,6	60	126,6	60	126,6	60	126,6	60	126,6
MgF_2Y_1B	10	13,8	10	13,8	10	13,8	10	13,8	10	13,8	10	13,8	10	13,8	10	13,8
ZrO_2X_2A	50	105,5	50	105,5	50	105,5	50	105,5	50	105,5	50	105,5	50	105,5	50	105,5
MgF_2Y_2B	40	55,2	0	0	10	13,8	20	27,6	30	41,4	40	55,2	50	69,4	60	82,8
ZrO_2X_3A	0	0	20	42,2	20	42,2	20	42,2	20	42,2	20	42,2	20	42,2	20	42,2
MgF_2Y_3B	40	55,2	60	82,8	50	69,4	40	55,2	30	41,4	20	27,6	10	13,8	0	0

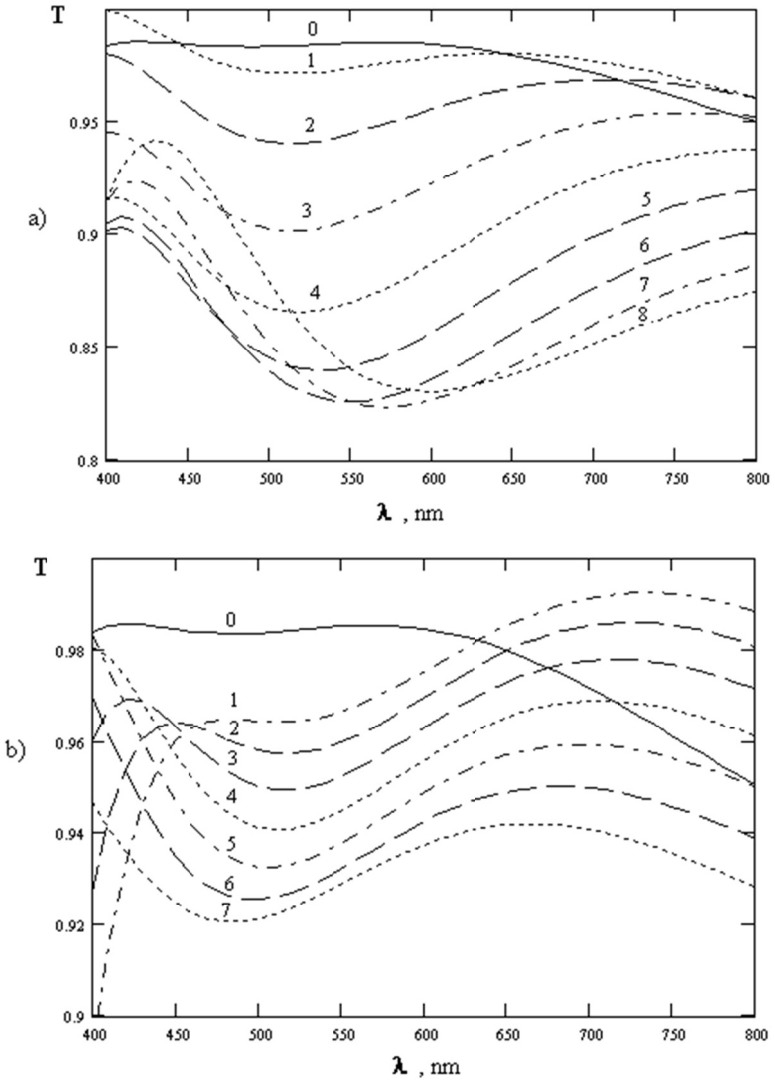

Fig. 7. The dependence of MLS spectra on longitudinal value of defects (fig.7a curves 0-8, data from table 3, diagram of Fig 6a) and on its space dislocation (fig.7b curves 0-7, data from table 4 , diagram on Fig 6b).

The transmittance spectra of corresponding to fig. 5 a diagrams and layer parameters from table 3 and table 4 are presented in Fig. 7a. At the increasing of longitudinal scale of defects (from high refractive substances) the minima of transmittance appear in the wavelength region of 500-550 nm while its position are shifted lo long wave. The similar dependence are observed at the changing of defect space position from the central points (table 4 and diagram of Fig. 5a) but the observed minima are shifted lo short spectra region.

Conclusion

The appearance of nanodefects in the MLS layer of antireflective coatings that give rise to declination the optical parameters of real optical elements from experimentally necessary are observed.

The model of defect layer structure is proposed for establish the interdependences between the MLS layer parameters at the different type of defects, their longitudinal scale and space dislocation. The numerical evaluation of the layers parameters influence of layers parameters on the transmission of MLS with defect are performed.

The decreasing of maximum transmission of the optical element with defect coating is established. At the increasing of longitudinal scale of defects from high refractive substances the minima of transmittance appear in the wavelength region of 500-550 nm while its position are shifted to the long wave. The similar dependences are observed at the changing of defect space position from the central points of defect layer but the observed minima are shifted to short spectra region.

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SEGMENTATION OF SPEECH SIGNAL BASED ON AGREGATE MATRIX OF INFORMATION FUNCTIONS AND ENTROPY

Abstract. It has been suggested the methods of speech signal segmentation by quasistationary areas, which are built by the extremums of mutual informativity of discrete distribution of algebraic characteristics of elementary areas. The algebraic characteristics are obtained from the solution by the Moore-Penrose method of degenerated system of linear equations, which is built out of the algebraic aggregate matrix operator of information functions. Pseudorotation of aggregate matrix-operator is conducted on the base of the singular distribution. It has been compared the similarity coefficients of segmentation results by the developed method and the DELCO one. Based on these results, the developed method efficiency has been established in case of segmentation of speech signal areas not depending on power values.

Key words: speech signal, segmentation, aggregate matrix of information functions, pseudoinverse matrix, Moore-Penrose algorithm, singular decomposition, entropy, similarity coefficient, mutual informativity.

Introduction and literature analysis. Up-to-date artificial intelligence systems, established on the technologies of language recognition, are typically built by two-stage procedure. The first stage lies in previous processing of speech signal and, as a rule, comprises solution of the following: signal normalization, signal parameterization and separation of quasistationary areas. At the second stage an original and parameterized signal is transferred for processing to some “machine”, which solves the problem of recognition.

As a rule, the segmentation is considered as an important stage (preprocessing) of the speech recognition. The point of segmentation is to separate the continuous signal into a se t of close-by-parameters (in the given metrics) areas of speech signal. This can lead to neglecting influence of transition areas of speech signal structure units, what results in impossibility to separate optimum characteristics, which change can be easily detected and is a feature of a phoneme boundary in the continuous speech flow. This means that the solution of formally formulated segmentation problem cannot take into consideration linguistic peculiarities of speech signals, which can be generated by different factors, for instance by the excitation signal.

On the other side, the speech signal segmentation into areas which can be considered stationary by the main characteristics (quasistatonary areas), can substantially simplify lasting solution of general language recognition problem.

Today, there are three main approaches of quasistationary area separation. The 1st one is based upon the speech signal spectrum analysis, the 2nd one – upon the methods of statistical analysis, and the 3rd one – on the analysis of some separated speech signal characteristics (parametric segmentation).

The spectral analysis uses the language signal presentation in the spectrum area with the further analysis of spectral characteristic gradients. The local extreme points of these gradients are typically used for determining quasistationary area boundaries. The main spectrum analysis problems are either the necessity of the whole signal availability or the threshold value definition problem. [7, 11, 12].

The base of up-to-date probability analysis methods lies in the formation of network models on the base of statistical or power parameters. The most widespread approaches are the use of hidden Markov models or artificial neural network technologies [5, 6]. The main issue is arrangement of learning process [6], especially in those cases when good set of observations is not available.

The 3rd direction lies in defining of some parameters, which sufficiently characterize the speech signal, usually such parameters are time dependencies [8, 11]. The main advantage of the methods of time characteristic analysis is low dependency upon time scale, and the typical issue – the dependency of segmentation efficiency upon the speech signal power distribution.

Goal of research. The research objectives are development of the method of quasistationary area separation on the base of determining the mutual informativity minimum in the characteristic vectors of elementary areas. The characteristic vectors are probabilities of the discrete value distribution on the elementary area, which is obtained as a result of matrix norming of solutions of degenerated linear system, built on the base of the aggregate matrix of information functions.

1. Formulation of separation problem of speech signal quasistationary area. Let the time interval $\tau = [0; T]$, $T \in R^{1,+}$ is given. On the interval τ the system of open sets

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$$\Gamma = \{T_i\}_{i = 1, 2, ...},\ T_i = [t \mid t_{i-1} \le t < t_i,\ t_{i-1}, t_i \in \tau], \quad (1)$$

with the diameter $|T_i| = \sup_{t_a, t_b \in T_i} d(t_a, t_b)$ (where d – metrics of the space R^1), let's determine the topology Γ. As far as the interval τ is closed limited set, in the topology Γ there is always disjunctive (with trivial intersection) finite covering $\chi = \{T_i \mid i = 1..n\}$, i.e.

$$\forall i, j \in [1; n]: T_i, T_j \in \chi \wedge i \ne j \to T_i \cap T_j = \varnothing; \quad (2)$$

$$\tau = \bigcup_{i=1}^{n} T_i . \quad (3)$$

Let's consider that all the elements of the covering χ have the same diameter equal to l: $\forall i \in [1, n]: |T_i| = l$. This determines χ as l-covering of the interval τ.

Let on the interval τ the speech signal $x(t)$ be determined as the continuous surjective reflection

$$x: \tau \to R^1. \quad (4)$$

As far as $x(t)$ is the continuous reflection, in case of existence of the covering χ we will obtain the covering η (not necessarily disjunctive) of the area of the $x(t)$ function values

$$\eta = \{X_i \mid i = 1..n\}, \quad (5)$$

where $X_i = \{x(t) | t \in T_i\} = \{x(t) | t \in T_i\}$ – element of the covering η.

The quasistationary areas Y_i of the speech signal $x(t)$ is a combination of elements of the disjunctive covering η on the base of the given criterion of belonging

$$Y_i = \bigcup_{j=a_i}^{b_i} X_j . \quad (6)$$

where $X_j \in \eta$ – consecutive elements of the covering η, which meet the criteria of belonging; a_i, b_i – indexes of the sequence $\{X_i\}$, which determine the subset of elements, which combination forms Y_i. The difference of values of indexes $m_i = b_i - a_i$ determines the number of elementary areas X_i, that determines the power of the quasistationary area Y_i: $|Y_i| = m_i l$.

By (5) and (6) the set $\{X_i\}$ forms a new disjunctive covering η' of the signal space $x(t)$, that is why there is the following equality

$$x(t) = \bigcup_{i=1}^{m} Y_i \,, \tag{7}$$

where $m \le n$ – a number of quasistationary areas Y_i.

Taking into consideration that (6) and (7) are dimension of the signal $x(t)$, the number of discretization points on the interval T is determined as follows

$$\dim\,(x(t)) = nl = l \sum_{i=1}^{m} m_i \,. \tag{8}$$

According to (5), (7) and (8) the problem of separation of the $x(t)$ signal quasistationary areas can be considered as the operator transformation formation problem of the topologies f: $\chi \to \chi'$ or F: $\eta \to \eta'$.

2. Formation of aggregative matrix of information functions. On the contrary to [2], while building the matrix operator the speech signal is not normalized and not shifted into the positive area. The speech signal amplitude values of the element X_i, which correspond to the elementary areas T_i, without any additional transformations, are used to build some matrix operator ∇_i: $T_i \to X_i$.

The operator ∇_i: $T_i \to X_i$ of transformation of l-dimensional vectors, determined within the interval T_i, that corresponds to the element X_i of the covering η, is built as the aggregate matrix of information functions [10, 15] (the aggregate matrix of absolute convergence measures) by the following rule:

$$\forall i \in [1;n] : \nabla_i = \begin{pmatrix} \min(x_{i,1}, x_{i,1}) & \min(x_{i,1}, x_{i,2}) & \dots & \min(x_{i,1}, x_{i,l}) \\ \sum_{j=1}^{2} \min(x_{i,j}, x_{i,1}) & \sum_{j=1}^{2} \min(x_{i,j}, x_{i,2}) & \dots & \sum_{j=1}^{2} \min(x_{i,j}, x_{i,l}) \\ \dots & \dots & \dots & \dots \\ \sum_{j=1}^{l} \min(x_{i,j}, x_{i,1}) & \sum_{j=1}^{l} \min(x_{i,j}, x_{i,2}) & \dots & \sum_{j=1}^{l} \min(x_{i,j}, x_{i,l}) \end{pmatrix}, \tag{10}$$

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where i – an index of the elementary area X_i, $x_{i,j} = x(t_j)$, $t_j \in T_i$. The matrix dimension (10) is equal to: dim $\nabla_i = l$ Ч l, and its elements $\delta_{i,(z,j)}$ are determined as follows: $\delta_{i,(z,k)} = \sum_{j=1}^{z} \min\left(x_{i,j}, x_{i,k}\right)$.

To solve the task of separating vectors, which take a part of characteristics of the elementary area of the speech signal for every element of the covering χ, let's consider the equation

$$\nabla_i g_i = x_i , \tag{13}$$

where $x_i = \left\{x\left(t_p\right) \in X_i \mid p = 1..l\right\}$; $g_i = (g_{i,1}, ..., g_{i,l})$ – l-dimensional vector of the amplitude values of the speech signal $x(t)$ on the i interval.

By (13), the vector g_i will be determined as follows

$$y_i = \nabla_i^{-1} x_i . \tag{14}$$

As far as the matrix ∇_i is degenerated ($\det(\nabla_i) = 0$), the inverse matrix ∇_i^{-1} doesn't exist. That is why to solve the problem (13) by the theorem of minimization of the brokens $\|x_i - \nabla_i g_i\|^2$ of the linear system (14) [3], the following method of determining the vector y_i

$$g_i = \nabla_i^{+} x_i + \left(1 - \nabla_i^{+} \nabla_i\right) r_i , \tag{15}$$

where ∇_i^{+} – general Moore-Penrose inverse matrix (pseudo inverse to the ∇_i matrix [1, 3]); $\left(1 - \nabla_i^{+} \nabla_i\right)$ – the projection operator onto the kernel of the operator ∇_i; r_i – the random vector of the dimension l. The first item in (15) takes a part of the pseudo inverse solution, and the second – the solution of the uniform system $\nabla_i g_i = 0$. Exemplified via (15) the method of determining the vector of characteristics of the i element of the covering χ is possible as far as in accordance with [3] the matrix $\nabla_i^{+} \nabla_i$ is not degenerated.

The Moore-Penrose matrix ∇_i^{+} is determined by the singular matrix distribution ∇_i in the following way [1]

$$\nabla_i^{+} = V_i \Sigma_i^{+} U_i^{T} , \tag{16}$$

where U_i, V_i – unitary matrices of the order lЧl of the singular matrix distribution ∇_i; Σ_i^{+} – the matrix of the order lЧl, which is pseudo in-

verse to the diagonal matrix Σ_i of the singular distribution [4] of the matrix ∇_i. As far as the matrix Σ_i is degenerated as well, the matrix Σ_i^+ is obtained out of Σ_i via substitution of all non-zero singular numbers $\sigma_{i,q}$ ($\sigma_{i,1} \geq \sigma_{i,2} \geq ... \geq \sigma_{i,l} \geq 0$) by appropriately inverse to them $1/\sigma_{i,q}$.

In the iteration process of finding by g_i^{j+1} (14), the random vector r_i^{j+1} – is determined by the broken: $r_i^{j+1} = \|x_i - \nabla_i g_i^j\|_l$, here $\|\cdot\|_l$ – l-norm [4].

3. Speech signal segmentation by quasistationary areas

With the vectors $g_i = (g_{i,1}, ..., g_{i,l})$, obtained by (15), let's form the matrix Y

$$Y = \begin{pmatrix} g_1 \\ g_2 \\ \dots \\ g_n \end{pmatrix} = \begin{pmatrix} g_{1,1} & g_{1,2} & \dots & g_{1,l} \\ g_{2,1} & g_{2,2} & \dots & g_{2,l} \\ \dots & \dots & \dots & \dots \\ g_{n,1} & g_{n,2} & \dots & g_{n,l} \end{pmatrix}, \quad (17)$$

which elements are necessary to be shifted into the positive area and normalized

$$P = \frac{Y + \left|\max_{i,j}\left(y_{i,j}\right) - \min_{i,j}\left(y_{i,j}\right)\right|}{\left\|Y + \left|\max_{i,j}\left(y_{i,j}\right) - \min_{i,j}\left(y_{i,j}\right)\right|\right\|}, \quad (18)$$

where $\|\cdot\|$ – matrix norm.

The matrix P is the set of vectors $\{p_i = (p_{i,1}, ..., p_{i,l}) \mid i = 1..n\}$, for which elements the following inequality is true:

$$\forall i \in [1; n], \forall j \in [1; l] : 0 \leq p_{i,j} \leq 1. \quad (19)$$

Due to (19), the elements $p_{i,j}$ of the matrix P can be considered as discrete distribution of probability of the value X_i on the time interval T_i. This makes possible to determine mutual information of two elements p_i, and p_j [9, 14]

$$I(p_i, p_j) = H(p_i) + H(p_j) - H(p_i, p_j). \quad (20)$$

where $H(p_i) = \sum_{i=1}^{l} p_{i,j} \log_2 p_{i,j}$ – the entropy of the random value p_i [9, 15]; $H(p_i, p_j) = \sum_z p_{i,z} H(p_j \mid p_{i,z})$ – the general conditional entropy of two random values p_i and p_j [9, 15]. The elements $p_{i,j}$ are "scales" of the η covering elements. As a result of this the descriptive set $p(X)$ is obtained [13]. Then by [15], the measure of interdependence X_i, $X_j \in \eta$ will be determined as follows

$$\mu(X_i, X_j) = 2I(p_i, p_j). \quad (21)$$

With the use of (20), the set of values of mutual information measures of consecutive areas $X_i \in \eta$ is obtained

$$M = \{\mu_{i,i+1} = \mu(X_i, X_{i+1}) \mid i = 2..n\} \quad (22)$$

The next stage is the separation of local extremum points out of I by the threshold value $\Delta_{\max}$, $\Delta_{\min}$, > 0

$$\Lambda = \{i \in [2, n] \mid \min(\mu_{i,i+1}) < \Delta_{\min} \vee \max(\mu_{i,i+1}) > \Delta_{\max}\}. \quad (23)$$

The Λ set dimension is equal to m, and the values $i \cdot l$, $i \in \Lambda$ – are boundaries of dividing the signal $x(t)$ by the quasistationary areas $Y_j \in \eta'$.

4. Results of experiments and conclusions. The developed method of speech signal segmentation into quasistationary areas has been approbated via primary division of the word "mysha" ("mouse" in English), which wave representation is presented in the Fig.1.

The speech signal characteristics are the following: the word duration – 1,03 s, discretization frequency 11 025 Hz, elementary area length – l = 120 segments. The speech signal comprises main phoneme types: stressed and non-stressed vowels, voiced and unvoiced consonants.

The results of the signal segmentation have been chosen as an appraisal by the DELCO algorithm with the threshold value 1.6 and the same elementary area size.

By the developed method 17 segments have been separated, and by the DELCO method – 10. Herewith, in the points t = 0.0240 s, t =

0.7920 s, t = 0.9 s the segmentation results fully coincide. On the rest signal areas, the results are close with different closeness measures.

Basing on the results, it can be stated that the developed method in comparison with the DELCO method is more sensitive to energy change with time in the whole power range. It is obvious within the appropriate periods [0.12 s; 0.6 s] and [0.6 s; 0.8 s].

The distribution of mutual informativity values calculated by (20) is presented in the Fig. 2. The results of segmentation exemplified in the Fig. 1 have been obtained on the base of (21)-(23) and on the above mentioned values. As a result of numerous experiments, the following regularity has been established: selection of local maximum points in (20) provides finding of segmentation points in the areas of average and high power, and separation of local minimum points –in the areas of low power. Such possibility is an advantage of the developed method, as far as makes possible determining segmentation areas by power ranges.

In the Fig. 3 the numeral values of similarity coefficients (Jaccard index, Sorensen coefficient, Kulchynskyy coefficient, Ochiai Coefficient, Shynkevich-Simpson coefficient, Braun-Blanquet coefficient [9], which are topologically equivalent) of the segmentation results by the DELCO method and the developed one are exemplified.

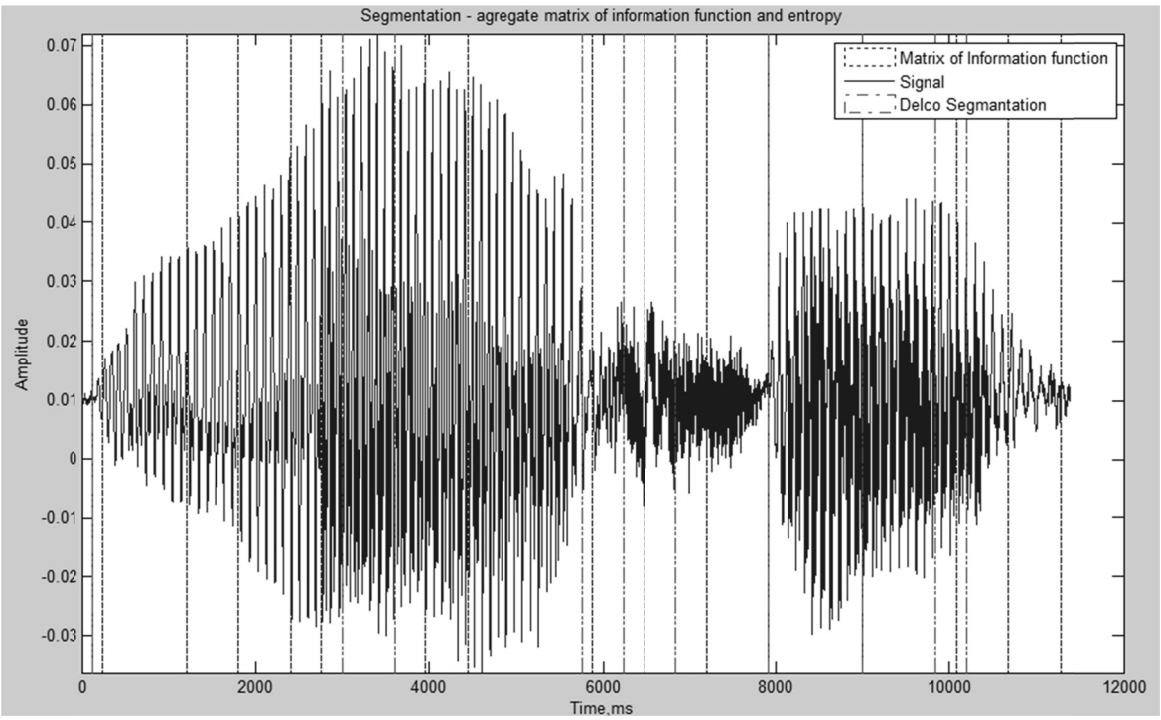

Fig.1. The results of speech signal segmentation (the word “mysha” (“mouse” in English)) by the DELCO algorithm and by the method on the base of the matrix of relative asymmetric convergence measures

Not high values of similarity coefficients (the biggest one is observed only in the Shynkevich-Simpson coefficient) prove that on the contrary to Delco, which demonstrates good segmentation results in the areas of low and average power, the developed method is equally efficient within the whole power range.

Fig.2. Distribution of mutual informativity values in the elementary areas

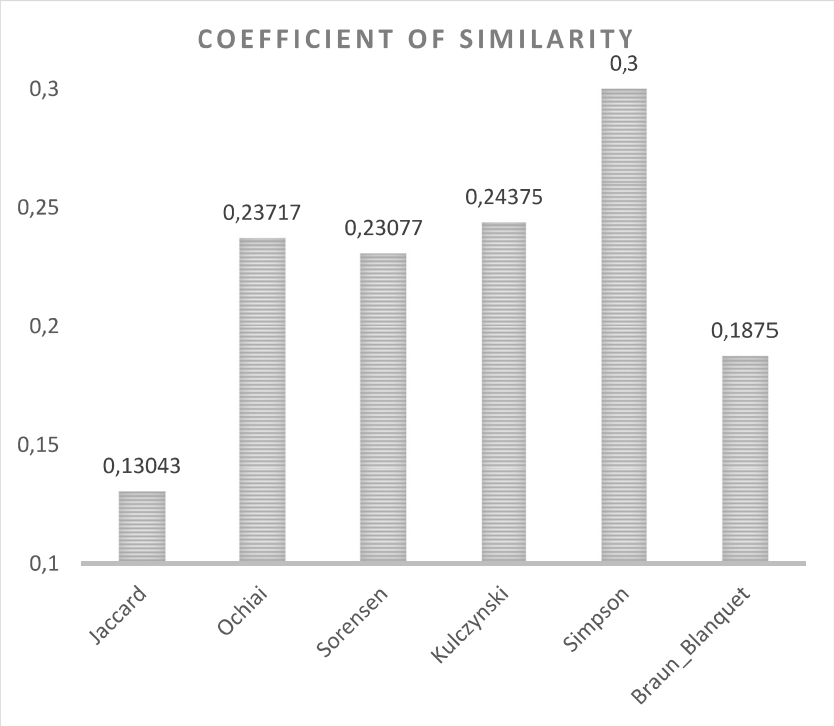

Fig.3. Coefficients of results similarity of segmentation by the DELCO algorithm and by the developed method

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UDK 004-896

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METHOD OF AUTONOMOUS MOBILE ROBOTIC SYSTEM MOTION CONTROL BASED ON FUZZY LOGIC

Abstract. The different motion modes is proposed to use to the control system of mobile robotic system. The method to control of mobile robotic system that carried out by combining fuzzy logic with linear regression is developed.

Keywords. fuzzy logic, autonomous mobile robotic systems, linear regression, the method of fuzzy inference, rule base.

Problem statement

The branches of application of mobile robotic systems are expanding today. The autonomous motion control of such systems in a complex and uncertain environment is of particular interest now because such systems can be used to implement various tasks in which is no information about the environment or communication with the operator. Such mobile robotic systems can be implemented for liquidations accidents or work at a dangerous environment for human.

The main requirements for the motion control system of autonomous mobile robotic system include: ensuring of rapid response for changing environmental conditions and unexpected events; ensuring of real-time operation in deterministic and non-deterministic environments; achieving all the goals set by the operator or higher control level, adjusting behavior according to the changing conditions of the environment to achieve goals; making decisions based on incomplete and ambiguous input data etc. The intelligent methods for mobile robotic control systems are necessary to use for performing the requirements. The usage of fuzzy logic technology ensures fulfillment of the requirements and effective control of mobile robotic systems because of a result of the mobile robotic control system in many cases is difficult to formalize, but it can be easily described with the usage of common language. Therefore, an effective solution is the usage of fuzzy logic, as this provides the possibility of control even in an uncertain environment with noisy input data that can be obtained from sensors.

Thus, the vital task is to develop a fast and accurate method of mobile robot control system that ensures performing the assigned tasks.

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Analysis of recent research and publications

Analysis of recent research and publications showed [1-4] that there are different methods of fuzzy inference. The most widespread of such methods are: the method of fuzzy inference Mamdani and Sugeno. The disadvantages of aforementioned methods for implementation of mobile robot control systems are the following:

• low accuracy due to the result value of the output variable dependence of method of defuzzification and low speed (Mamdani method);

• complexity of use, if the values of consequents of the rules are represented as fuzzy values and not intuitive approach for a rule base building (Sugeno method).

The antecedents and consequents of rule base which are used for the motion control of mobile robotic systems are fuzzy variables. The usage of Mamdani method does not provide adequate accuracy and speed. Therefore, it's necessary to develop a method of control that provides the adequate accuracy, speed and takes into account the fuzzy variables of rules for the implementation of mobile robotic control system

The proposed method

In general, the structure of mobile robotic system motion control is shown in Figure 1, that consists of four modes of motion: motion mode to the target, motion mode obstacles avoidance, motion mode along the right wall, motion mode along the left wall and appropriate activation coefficients for each mode of motion. The input data of motion mode obstacles avoidance and motion mode along the walls are the distance to the obstacles that represents by linguistic variables. There are three terms of every linguistic variable which define small, medium and large distance to the obstacles. The input data of motion mode to the target is rotation angle that calculates as difference between the direction of mobile robotic system motion and the direction of the target. The output value of the motion modes is the rotation angle of mobile robotic system that represents by linguistic variables with terms corresponding to the turning to the right, straight motion and turning to the left. The output value of activation coefficients is formed by using the input linguistic variables that represents the distance to obstacles from different sides of robotic system and the value of the rotation angle that calculates as difference between the direction of mobile robotic system motion and

the direction of the target. The output value of the linguistic variable of activation coefficients is formed with five terms, which define the value of each motion mode from not activated (which represents as zero) to activated (which represents as one).

Input data coming from sensors of mobile robotic system and the machine vision system. The resulting value of the mobile robotic system rotation angle comes to block for control signals forming, where the rotation angle converts to the corresponding control signals according to the actuators of mobile robotic system.

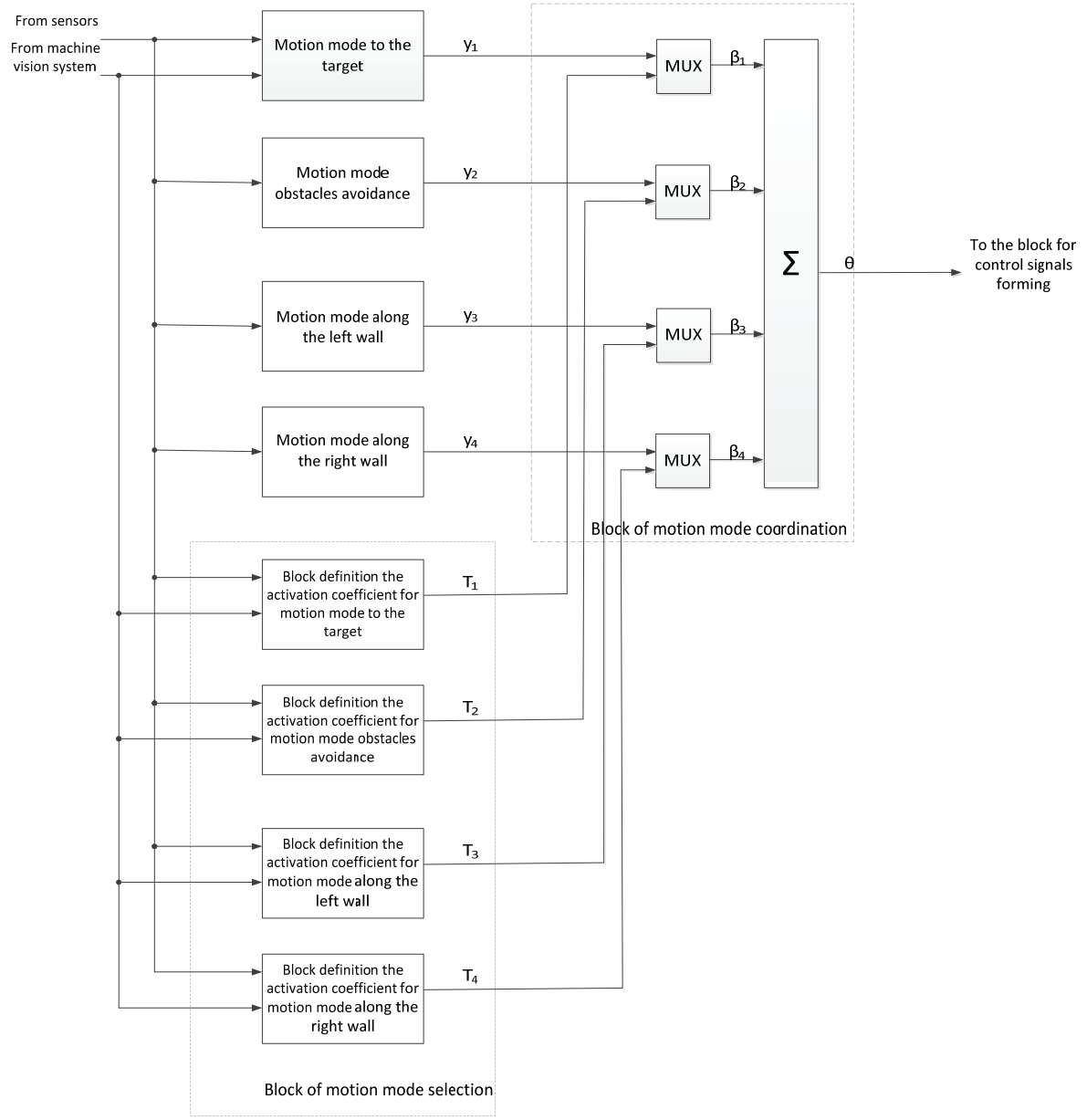

Figure 1 – Structure of mobile robotic system motion control.

In general, a fuzzy inference system consists of the following main steps: fuzzification , aggregation , activation , accumulation and defuzz-

ification. The large number of operations is required for implementation of these steps [5]. We propose to replace the operations that take a long computation time to the linear regression model. This method would reduce the number of operations and improve performance of control. In the general case the structure of the algorithm of developed fuzzy method of mobile robotic system motion control consists of two blocks: the block of fuzzy inference (BFI) and block of linear regression (BLR). The membership functions of each term for output linguistic variable is calculated with the usage of a given input data and the rules of the rule base at BFI. The output value of control variable is calculated using linear regression models at the BLR as [6]:

$$y = a_0 + a_1 Fy_1 + ... + a_q Fy_q, \quad (1)$$

where $a_0,...a_q$ - linear regression model coefficient; $Fy_1...Fy_q$ - the value of membership functions of each term for output linguistic variable; y - output control variable. The main problem in the implementation of this method is to find the coefficients of the linear regression model.

As can be seen from Figure 1, which shows the structure of mobile robotic system motion control, it is necessary to use this method for finding the rotation angle of each of the four motion modes and each of the four activation coefficients.

Three terms of result output linguistic variable is used to calculate the rotation angle of each of the four motion modes of mobile robotic system. Thus equation (1) takes such form for this purpose:

$$y_i = a_{0i} + a_{1i} Fy_{1i} + a_{2i} Fy_{2i} + a_{3i} Fy_{3i}, \quad (2)$$

where $a_{0i},...a_{3i}$ - linear regression model coefficients of an appropriate motion mode; $Fy_{1i}...Fy_{3i}$ - the value of membership functions of each term for output linguistic variable of appropriate motion mode, y_i - output control variable, $i = \overline{1,4}$.

Five terms of result output linguistic variable is used to calculate the activation coefficients of each motion modes of mobile robotic system. Thus equation (1) takes such form for this purpose:

$$T_i = b_{0i} + b_{1i} Ft_{1i} + b_{2i} Ft_{2i} + b_{3i} Ft_{3i} + b_{4i} Ft_{4i} + b_{5i} Ft_{5i}, \quad (3)$$

where $b_{0i},...b_{5i}$-linear regression model coefficients of appropriate activation coefficient; $Ft_{1i}...Ft_{5i}$ - the value of membership functions of each

term for output linguistic variable of appropriate activation coefficient; T_i - output variable of activation coefficient of appropriate motion mode; $i = \overline{1,4}$.

At first, the crisp values of the rotation angles and activation coefficients of appropriate motion modes as output variables must be calculated to determine the linear regression model coefficients. We propose to use fuzzy-neural T-Controller for this purpose which is based on fuzzy geometrical transformation model.

T-Controller provides higher accuracy than methods of fuzzy inference by usage of zero methodological error of defuzzification and higher performance, due to lack of accumulation of fuzzy rules consequents. T - Controller Workshop is software where T- controller is implemented. [7-9].

The same input data are sent to the BFI. So values of membership functions of each term for output linguistic variable of appropriate activation coefficients and rotation angles of each motion modes are calculated for all data base. A fuzzification (receiving fuzzy values from crisp values with the usage of triangular membership function), determining the degree of fulfillment antecedents of individual linguistic statements of rules from fuzzy inference system, determining the degree of fulfillment consequents of individual linguistic statements for each rule from rule base, determining the membership function of each output linguistic variable are implemented at BFI.

The method of least squares is proposed to use for calculating the linear regression model coefficients. The resulting rotation angle of mobile robotic system is the sum of the products of the rotation angles values and activation coefficients of the appropriate motion modes.

Conclusion

1. The combination of different motion modes and corresponding activation coefficients is used for implementation the autonomous mobile robotic system motion control. Such approach enhances adaptation to the requirements of the particular application by developing and adding new motion modes to system of motion control.
2. A new method to control of mobile robotic system is proposed, which is the combination of fuzzy logic and linear regression

model. The usage of this method provides increasing performance due to reduction of the number of computational operations.

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UDC 621-83 681.51

V.B. Zvorykin , G.U. Stanchits

TUNING OF PARAMETERS OF A CONTOUR OF SPEED IN TWO-MASS SYSTEM WITH A BIG RANGE OF INERTIAL MASSES

Annotation. Methods of adjusting of system of the subordinated regulation of speed in the presence of flexible connection of the engine with the mechanism and great values of coefficient of inertia are considered. Expressions for calculation of the regulator of the speed are received. They allow receiving transition process on the speed of executive mechanism with the reregulation, corresponding to tuning for a modular optimum.

Keywords: systems of the subordinated regulation, a speed control, two-mass system, flexible connection, big inertial masses.

As shown in [1] at big coefficients of inertia $\gamma > 5.8$ change of speed of executive mechanism at start-up happens without reregulation (fig. 1). In this case you must choose coefficient of amplification of the regulator of speed on the equation:

$$k_{pc} = \sqrt{\frac{T_{M1}}{T_C(\gamma - 1)}\gamma\sqrt{\gamma}}, \qquad (1)$$

where T_{M1} and T_{M2} - respectively, the electromechanical constants of time caused by inertia of the first and second masses; T_C - constant of time of rigidity of kinematic connection; $\gamma = \frac{T_{M2} + T_{M1}}{T_{M1}}$ - inertia coefficient, k_{pc} - coefficient of amplification of the regulator of speed.

In these cases it is also expedient to choose k_{pc} so that the coefficient of damping made $\xi_Э = 0.707$. It will allow increasing fast-acting of System Automatic Regulation (SAR) of speed.

Thus the working point will settle down on the line of equal value $\xi_Э = 0.707 = const$ on the Vyshnegradsky's chart [1]. It can be reached both reduction k_{pc} $(A < B)$, and its increase$(A > B)$, in comparison

with the value calculated on (1).

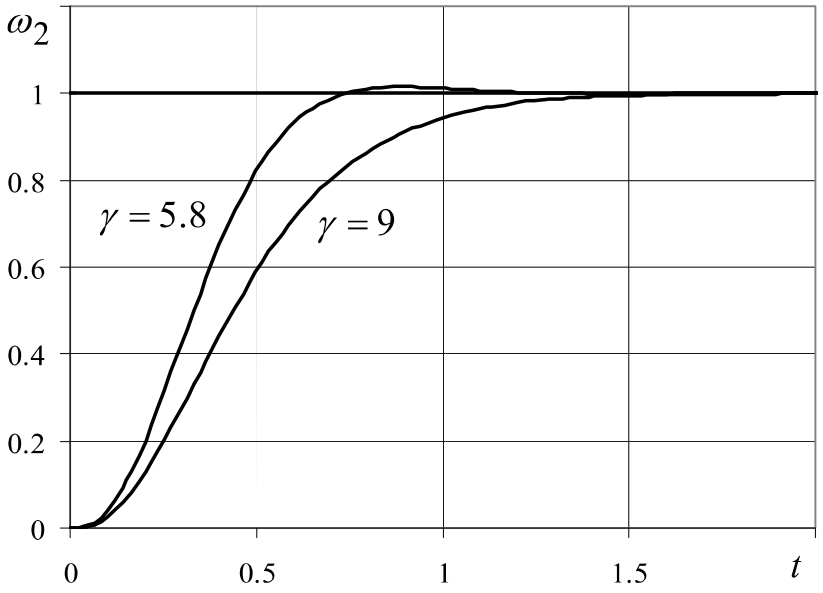

Fig. 1. Change of speed of executive mechanism at a choice k_{pc} on a formula (1)

In the first case transient process will be longer, than at a calculated value k_{pc}. Therefore practical interest represents the second case (a curve *бв* in fig. 4 [2]).

Let's find the expression connecting coefficient of inertia γ and coefficient of damping $\xi_э = 0.707$ with the demanded size of coefficient of amplification of the regulator of speed k_{pc}.

Let's compare expressions for transfer function $W_з^{в}(s)$, normalized on Vyshnegradsky [1] and transfer function of the closed system of regulation of speed /1/ $W_з(s)$.

$$W_з^{в}(s) = \frac{1}{s^3 + As^2 + Bs + 1}, \qquad (2)$$

$$W_з(s) = \frac{1}{\tau_1 \tau_э^2 s^3 + \left(2\xi_э \tau_1 \tau_э + \tau_э^2\right)s^2 + \left(\tau_1 + 2\xi_э \tau_э\right)s + 1}, \qquad (3)$$

where A and B - Vyshnegradsky's coefficients.

Comparing expression (3) to normalized transfer function (2), we will receive:

$$\begin{cases} \tau_1 \tau_э^2 = 1 \\ 2\xi_э \tau_1 \tau_э + \tau_э^2 = A \\ \tau_1 + 2\xi_э \tau_э = B \end{cases}. \quad (4)$$

Let's express from the first equation (4) τ_1. Let's substitute the received value in the second and third equations of system (4):

$$\begin{cases} \tau_э^3 - A\tau_э + 2\xi_э = 0 \\ 2\xi_э \tau_э^3 - \tau_э^2 B + 1 = 0 \end{cases}. \quad (5)$$

In /1/ it is shown that

$$B = \frac{\gamma}{A}. \quad (6)$$

Taking into account (6) we will resolve the second equation of system (5) relatively A.

$$2\xi_э \tau_э^3 - \frac{\gamma \tau_э^2}{A} + 1 = 0,$$

$$A = \frac{\gamma \tau_э^2}{2\xi_э \tau_э^3 + 1}. \quad (7)$$

Let's substitute value A in the first equation of system (5):

$$\tau_э^3 - \frac{\gamma \tau_э^3}{2\xi_э \tau_э^3 + 1} + 2\xi_э = 0. \quad (8)$$

Having reduced to a common denominator, we will receive the equation of the sixth power relatively $\tau_э$.

$$2\xi_э \tau_э^6 - \left(\gamma - 1 - 4\xi_э^2\right)\tau_э^3 + 2\xi_э = 0 \quad (9)$$

For the solution of the equation (9) we will use substitution $x = \tau_э^3$. Let's receive a quadratic equation relatively x:

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$$2\xi_Э x^2 - \left(\gamma - 1 - 4\xi_Э^2\right)x + 2\xi_Э = 0\,. \qquad (10)$$

Quadratic equation roots:

$$x_{1,2} = \frac{\left(\gamma - 1 - 4\xi_Э^2\right) \pm \sqrt{\left(\gamma - 1 - 4\xi_Э^2\right)^2 - 16\xi_Э^2}}{4\xi_Э}\,. \qquad (11)$$

Required value $\tau_Э$:

$$\tau_Э = \sqrt[3]{x_1} = \sqrt[3]{\frac{\left(\gamma - 1 - 4\xi_Э^2\right) + \sqrt{\left(\gamma - 1 - 4\xi_Э^2\right)^2 - 16\xi_Э^2}}{4\xi_Э}}\,. \qquad (12)$$

Taking into account $\xi_Э = 0.707$ and according to (6) and (7), coordinates of a new working point on the Vyshnegradsky's chart will register:

$$\begin{cases} A = \dfrac{\gamma\tau_Э^2}{2\xi_Э\tau_Э^3 + 1} = \dfrac{\gamma\tau_Э^2}{1.414\tau_Э^3 + 1}\,. \\ B = \dfrac{\gamma}{A} \end{cases} \qquad (13)$$

With the value A calculated on (13), coefficient of amplification of the regulator of speed will be defined from a formula /1/:

$$A = \sqrt[3]{\frac{k_{pc}^2 T_C\left(\gamma - 1\right)}{T_{M1}}}\,. \qquad (14)$$

Let's raise left and right part equality (14) to the third power and take a square root:

$$k_{pc} = \sqrt{\frac{A^3 T_{M1}}{T_C\left(\gamma - 1\right)}}\,. \qquad (15)$$

The choice k_{pc} according to (15) allows to adjust two-mass SAR of speed with flexible connection on transient processes with damping at $\xi_Э = 0.707$ if $\gamma > 5.8$.

The curve changes of speed of executive mechanism with k_{pc}, calculated on (15) are shown in fig. 2. As appears from curve fig. 2, fast-

acting speed of the electric drive increases both at inertia coefficient $\gamma = 9$, and at $\gamma = 14$.

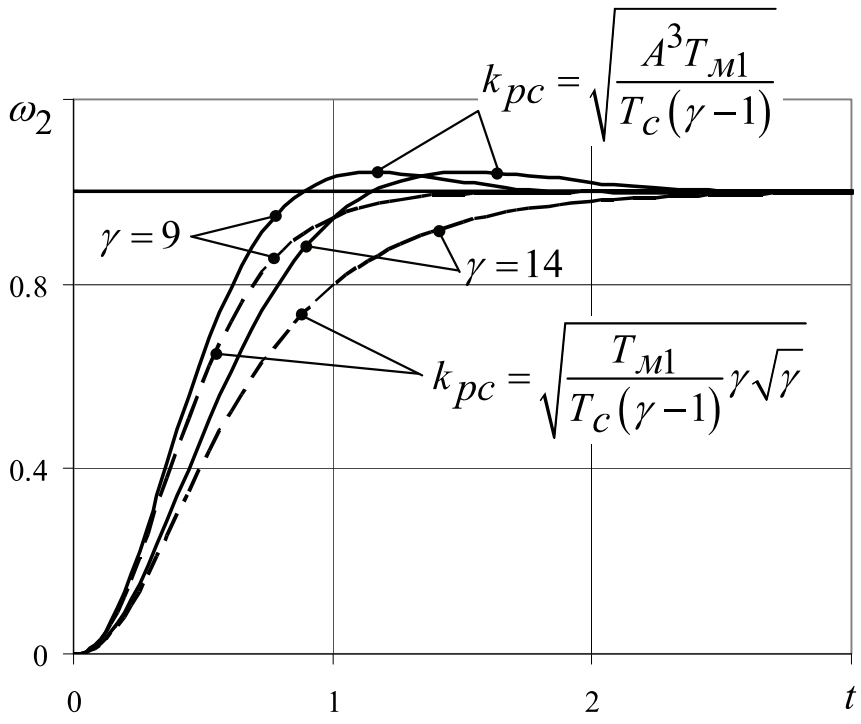

Fig. 2. Change of speed of executive mechanism at a choice k_{pc} on a formula (15).

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