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THE INDUCTIVE METHOD FOR THE SYNTHESIS OF COOPERATIVE IMMUNE NETWORK TO MEET THE CHALLENGES FORECASTING

Запропоновано та описано GMDH алгоритм синтезу кооперативної імунної мережі у вирішенні задач прогнозування часових рядів. Проведено порівняльні експерименти показали, що використання зовнішніх критеріїв підвищує адаптивність, надійність і точність одержуваних рішень.

Ключові слова: індуктивне моделювання, GMDH, кооперативний імунний алгоритм, часові ряди, прогноз, зовнішній критерій.

The article suggests and describes a GMDH algorithm for the synthesis of co-operative immune network in the solution of tasks of forecasting of time series. Conducted comparative experiments have shown that the use of external criteria improves adaptability, robustness and accuracy of the obtained solutions.

Key words: Inductive modeling, GMDH, Cooperative Immune Algorithm, time series, Forecasting, External Criteria.

Introduction

Recently a great attention is paid to of researchers the development of hybrid systems and algorithms. This is caused by that application of methods a corresponding computing paradigm does not always lead to success. In a hybrid architecture inefficiency of one approach, compensated by different approach. By combining different approaches can overcome the drawbacks that are each method alone. Integration and hybridization of different methods and information technology allows to solve complex tasks that can not be solved on the basis of any separate methods. In the case of the integration of diverse information technologies can be expected synergy effects of a higher order than when combining different models within the same technology. In the article [5] was a detailed analysis of hybridization methods of neural networks, fuzzy networks and evolutionary algorithms with GMDH. Using GMDH for hybridization with other computing paradigms because GMDH has some of unique properties [6]. Algorithms are tremendously noise-resistant - with a ratio of nois/signal θ = 20-30% algorithms are used to obtain an accurate physical model, the algorithms do not lose their health up to the ratio θ = 300-400% [7] . The noise-immune algorithm models of self-organizing algorithms when selecting the type and consistency of application of the criteria can obtain reasonably accurate forecasts in the conditions when the noise power exceeds the power of the useful signal. Immunity to interference algorithms for self-

organization with the right choice of species, and the sequence of criteria to be applied let you receive the fairly accurate forecasts in an environment where the noise power higher than the power the useful signal. The explanation for this effect is associated with the abandonment of the principle of "than the most more and more difficult model, that she more accurate" and the recognition of the principle of the existence of an optimal size and complexity of the model.

In [1] described a new type of algorithm for constructing artificial immune networks – “cooperative algorithm of artificial immune network”. We have investigated the advantages and disadvantages of this method. The algorithm has shown a high rate of convergence and accuracy in solving the problems of prediction and classification. The general idea of this algorithm is shown in Figure 1. The main idea of this algorithm is that, each antibody of population is only as the part of the solution or in the case of approximation problems is as the part of the model. Within the population, the antibodies connected to each other in some way (co-operating) and form a structure capable of solving the problem at the system level, i.e. at the level of the entire population, rather than at a single individual. This approach greatly reduced the time spent on training while maintaining an acceptable quality of approximation. A more detailed description of the cooperative immune algorithm can be found in [1-4]. In this article we propose a new scheme of the algorithm using the external criteria GMDH.

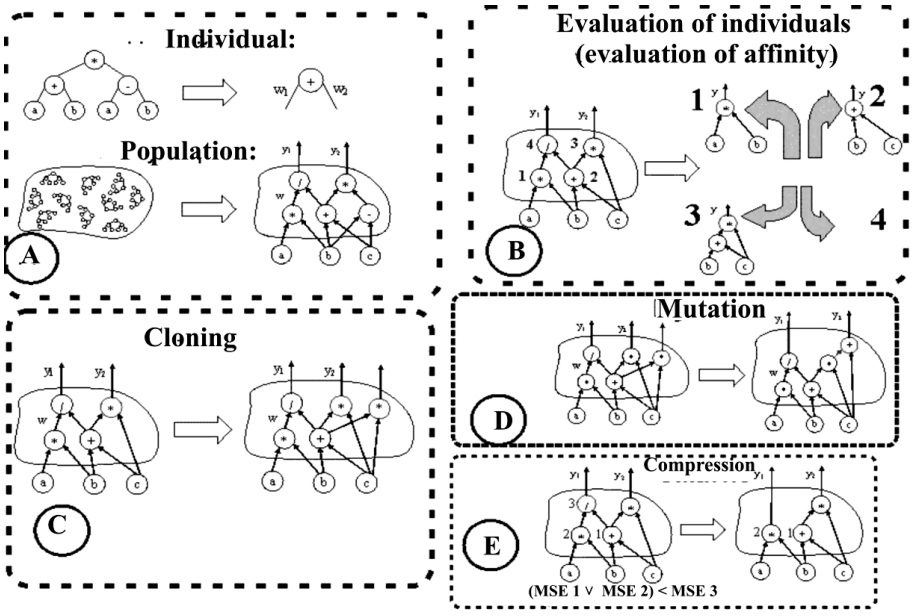


Fig. 1. The general scheme of the cooperative algorithm

Theoretical Part

The problem of the time series forecasting. Time series is a set of data that were collected or recorded via the serial (equal) intervals. Consider the dynamic system (i.e. a system whose properties change over time) with one output y. The value of output of the system at different times can be represented as the following sequence

$$(y_{t-n}, ..., y_{t-1}, y_t), \quad (1)$$

where t - time. If y_{t-j} and y_{t-i} are the two successively recorded in the time value of output of the system and $(t-i)-(t-j)=const,\ \ i, j=\overline{0,n}$, then the sequence (1) is the time-series of the dynamic systems behavior observations.

According to Takens’ theorem, the problem of time series forecasting is reduced to a typical function approximation problem of several variables for a given set of examples using the procedure of diving

series in l-*dimensional* lagged space. In this case the value of time series y_t is an arbitrary function of *l* past values of the same series. That is:

$$y_t = f(y_{t-1}, ..., y_{t-l}). \quad (2)$$

This feature provides an unambiguous prediction of the next value of series on *l* its previous value. The problem of model identification of the nonlinear structure object of the form:

$$\boldsymbol{y} = \boldsymbol{f}(\boldsymbol{x}_1, \boldsymbol{x}_2, ..., \boldsymbol{x}_n), \quad (3)$$

for which the relationship between inputs x_i and output y is presented in tabular form of the experiments data *T*:

$$T = \bigcup_{i=1}^{k} (x_{i1}, x_{i2}, ..., x_{in}, y_i), \quad (4)$$

where *k* is the number of table rows.

Representations of solutions. Dependence of (2) in general is a mathematical expression that can be written as a formula. For example, assume that our object has three inputs (x_1, x_2, x_3) and one output. Suppose also that the relationship between the inputs of the object and its output can be described by the formula:

$$y = a_{12} \cdot (a_1 x_1 + a_2 x_2) \cdot a_3 x_3, \quad (5)$$

where a_1, a_2, a_3, a_{12} are the some constants that serve as coefficients.

In this case, formula (5) can be presented as a graph shown in Figure 2.

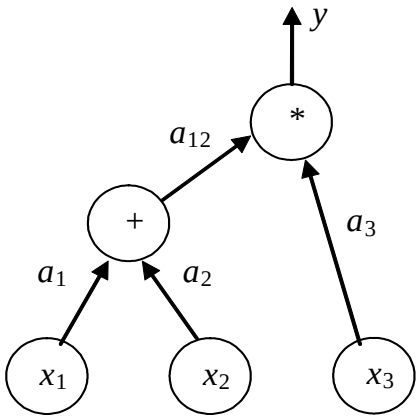


Fig. 2. Submission of a mathematical expression as a graph

In terms of the theory of evolutionary algorithms the such graph is called a genetic program. It includes the tops of two types:

- terminal top - top that has no incoming arcs in it and these tops are the variables in the task;

- functional top - the top, which has both incoming and outgoing arcs; the functional tops include the mathematical operations and functions.

Each top can have multiple outgoing arcs. Incoming arcs may have only functional tops. The number of incoming arcs in the top depends on the number of function arguments supplied by the top. Since most mathematical operations and functions are unary or binary, then most of the tops will have one or two incoming arcs. In contrast to the classical view of the genetic program in this paper all arcs of the graph are weighted. One of the main properties of the graph is that it contains no cycles and can always be presented as a tree. Consider another example of mathematical expression:

$$y = a_{123}(a_{12} \cdot (a_1 x_1 + a_2 x_2) \cdot a_3 x_3) + a'_{12}(a'_1 x_1 \cdot a'_2 x_2) \quad (6)$$

The genetic program, according to the expression (36), shown in Figure 3.

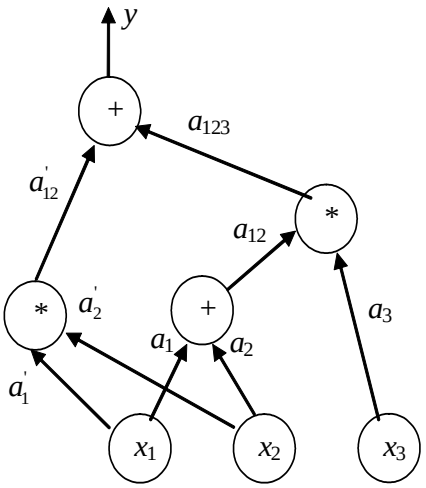


Fig. 3. Graph of the mathematical expression (genetic program) corresponding to the expression (6)

The encoding of antibodies. The design of artificial immune systems begin with defining of search space or "space forms." Each form is identified with the antibody of the immune system and is a string that encodes one possible solution of the problem. The proposed method in this paper, in contrast to classical approaches, uses no individual the programs genetic coding but population one, where each antibody is only part of the genetic program. The set of terminal vertices can not be any changed during the solution of the problem, so the immune algorithm population should be only antibodies that encode functional tops. In this case the line antibodies can be represented as (Fig. 4).

Code of function	Code of 1-st unit-descendant	Code of 2-nd unit-descendant	Weight of 1-st unit-descendant	Weight of 2-nd unit-descendant

Fig. 4. The proposed structure of the immune algorithm individual populations

As seen from the figure, the antibody has the mixed (integer and real) coding. The function code and codes of nodes serving as integers, and weights - as real. Under the function code, one can understand its number or index in the array of functions (functional set). The function set (F) may contain any number of mathematical operations, functions, polynomials, that is $F = \{+, -, *, /, sin, cos, tan, ln, poly1, poly2, ...\}$. Here, under $poly1, poly2, ...$ understanding the use of Kolmogorov-Gabor polynomials, like $f_1(x_1, x_2) = c + a_1x_1 + a_2x_1x_2$, $f_2(x_1, x_2) = c + a_1x_2 + a_2x_1^2$, etc. All tops of the genetic program graph are numbered. The top numbers, the output arcs of which directed to this top, are stored in the codes of the descendants of this node. Because all tops can contain any number of output arcs, then by either connection this top to the graph we cannot obtain the syntactically incorrect mathematical expression even when the codes of both node-descendants will be equal. This important feature allows you to give maximum freedom in the structure graph evolution during training.

The calculation of affinity. Any immune algorithm requires a population of antigen (*AG*), which will be recognized by population of antibodies (*AB*). In the tasks of identifying models as antigens population acts the set of data table rows experiments of T, $Ag_i = t_i, Ag_i \in AG, t_i \in T, i = \overline{1,k}$. There is also a possibility, suggested in [4], of table experiments splitting on a the subset of rows $Ag_i = T_i, T_i \subseteq T$, and in general $|Ag_i| \neq |Ag_j|$, $Ag_i \cap Ag_j \neq \varnothing$ at $i \neq j$. Evaluation of i-th genetic program and j-antigen are calculated as the Euclidean distance. In this paper, in values affinity calculation we use a similarity degree,

not the degree of complementarity of individuals. Therefore, we introduce an additional feature affinity, to keep the target area to maximize affinity, as:

$$f_{aff} = \frac{1}{1 + D_E}. \tag{7}$$

Because in our approach each antibody is the only part of the genetic program, its affinity is calculated based on the evaluation sub-graph formed by the current node and all its descendants. Thus, the function value f_{aff} varies from 0 to 1, i.e. $f_{aff} : \Re^+ \to [0,1]$.To control the sensitivity of antibody the affinity threshold (ε)is entered. The fact, when the antibody $Ab_i, Ab_i \in AB$ recognized the antigen Ag_j, is the affinity function value of $f_{aff} \geq \varepsilon$. Thus, the smaller the threshold affinity, the more robust are the results of the system. The number of antigens recognized by antibody Ab_i, called the antigen concentration and indicated as v_i^{Ag}. To calculate the concentration, define the function of antigen binding with antibody, such as:

$$b : [0,1] \times [0,1] \to \{0,1\}. \tag{8}$$

This function can take only two values: 1 - binding occurred (antigen is recognized by an antibody) and 0 - there was no binding (not recognized antigen by an antibody). Using the function value f_{aff} and the threshold ε the function b can be represented as:

$$b = \begin{cases} 0, & if \ f_{aff} < \varepsilon; \\ 1, & if \ f_{aff} \geq \varepsilon. \end{cases} \tag{9}$$

Then the concentration of antigen to antibody Ab_i can be calculated as follows:

$$v_i^{Ag} = \sum_{j=1}^{k} b_{ij}, \tag{10}$$

where b_{ij} is the function of the antibodies binding Ab_i with antigen Ag_j; k is the population size (of training sample). Cell is stimulated, if its values are $v_i^{Ag} > 0$.

Consider the sample population, shown in Figure 4.5. Using the value (7) - (10), the concentration v_3^{Ag} can be represented as some concentration composition v_1^{Ag} and v_2^{Ag}, that is $v_3^{Ag} = v_1^{Ag} \circ v_2^{Ag}$. In this case, are the following two ratio variants of these three variables.

Variant 1. $v_3^{Ag} > max(v_1^{Ag}, v_2^{Ag})$ - the antibody Ab_3 has a higher concentration of antigen as compared with antibodies Ab_1 and Ab_2. So, in terms of genetic program the involving of node Ab_3 improves the depends approximation, bringing us to the solution of the problem. In this case the cell Ab_3 is stimulated and antigen concentration is equal to v_3^{Ag}.

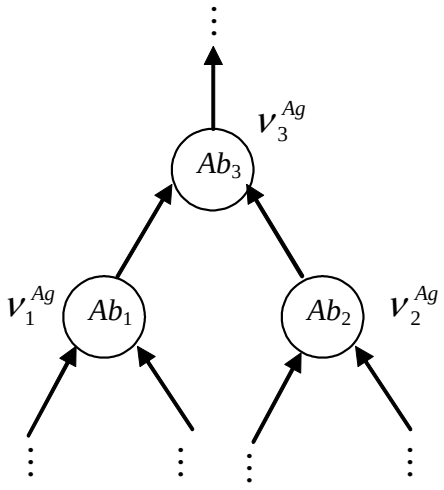


Fig. 4. Fragment populations of antibodies

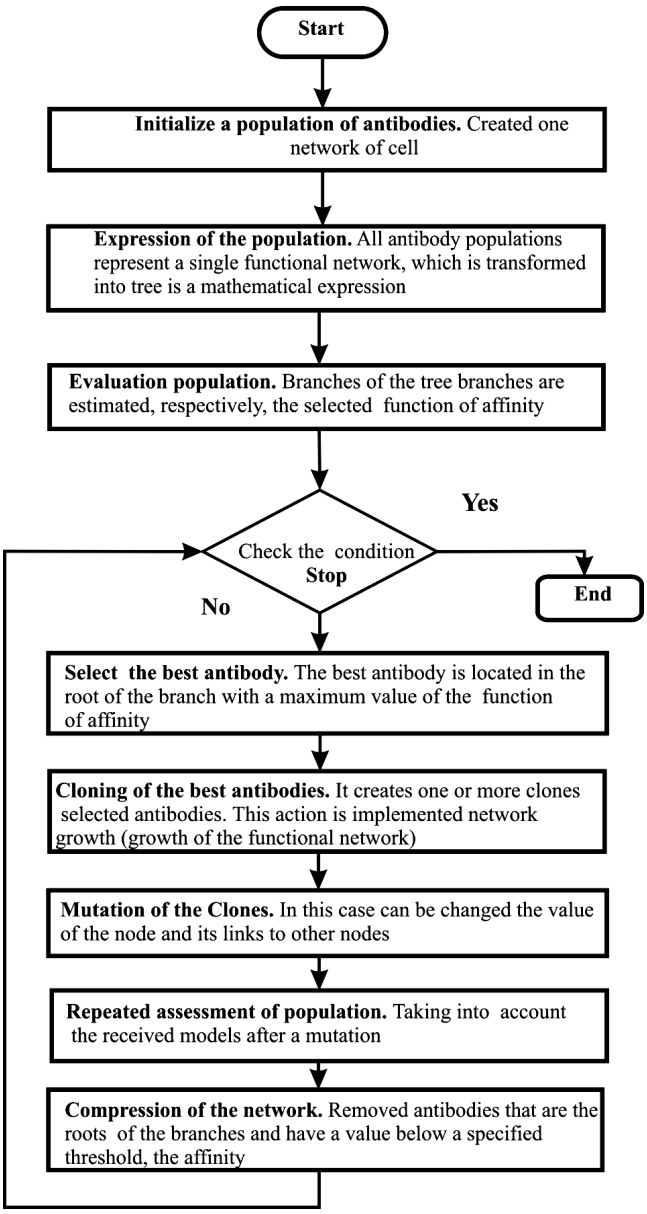


Fig. 5. Generalized procedure for cooperative learning of immune network for solving problems of approximation

Variant 2. $v_3^{Ag} \le max(v_1^{Ag}, v_2^{Ag})$. This introduction of node Ab_3 worsens or does not change the model approximation, from which it follows that the cell Ab_3 is not stimulated and its value v_3^{Ag} is equal to 0. Learning algorithm uses information about the stimulated and not stimulated cells to increase or decrease the size of the antibodies repertoire.

The procedure of training. In general, early learning assumed the existence of only one antibody in an antibodies population. During the study population of antibodies is structurized as a graph, like that shown in Figure 5. In the context of immune algorithms call this structure as a functional network of antibodies (FNA). As the basic properties of this network are the following: 1) growth of the network based on the principle of clonal selection, 2) compression network, based on the death of not stimulated cells (apoptosis), 3) evolution and structure of the network settings based on the evaluation mechanisms and somatic hyper mutation.

In the general form the learning procedure can be described as follows.

Step 1. Initialization. Creation of antibodies initial population AB. In this paper, the initial population consists of a single antibody, but of any specified size population can be initialized.

Step 2. Infection (presence of antigens). For each antibody on the basis of expression (10) the calculation of antigen concentration.

Step 3. Selection and cloning. Choosing the antibody with the highest concentration (most stimulated cells). Cloning the selected antibody. It is possible formation as one or several clones.

Step 4. Maturation of affinity. Subject the mutation of all selected cells clones with intensity inversely-proportional to their concentration of $\boldsymbol{v}_i^{Ag}$. While mutations the change the function code and code first and second generations (evolution of the network structure) are possible as well as the change of first and second generations weights (settings network evolution).

Step 5. Re-calculate the concentration of network antibodies like of step 2.

Step 6. Compression of network. Remove the all cell of network values for which ($\boldsymbol{v}_i^{Ag}$) is less than or equal to some given threshold $\boldsymbol{v}_{\min}^{Ag}$ (removal not stimulated cells).

Step 7. Go to step 2, if the condition of stop does not fulfilled.

Growth of network. This process is the selection and reproduction of the most stimulated population cell according to the principle of clonal selection. The choosing of cells for cloning are in accordance with the values of the antigen concentration, calculated for all cells of the network. Cell with the highest concentration for cloning is chosen. Consider a procedure growth of network in a specific example. Assume that the current network configuration is such, as shown in Fig. 7. In this case, the cell $\boldsymbol{Ab}_1$ chosen for cloning because $v_1^{Ag} > v_2^{Ag}$ (Fig. 6).

Because the top Ab_3 has no output arcs, the network forms after cloning two outputs ($\boldsymbol{y}_1, \boldsymbol{y}_2$), which in fact is not a problem and is well suited for the concept multi-gene individuals [9]. Total output network (y) can be calculated as the composition of outputs: y_1, and y_2 ($y = f(y_1, y_2)$).

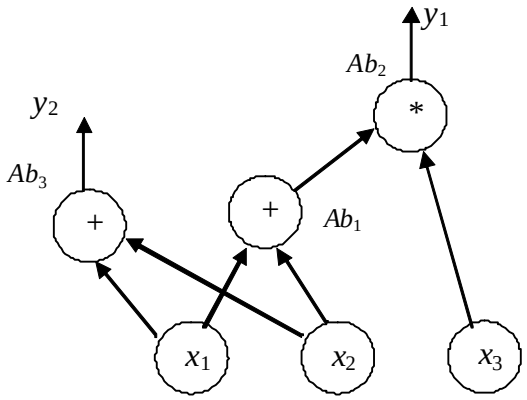


Fig. 6. Example of network configuration before starting growth

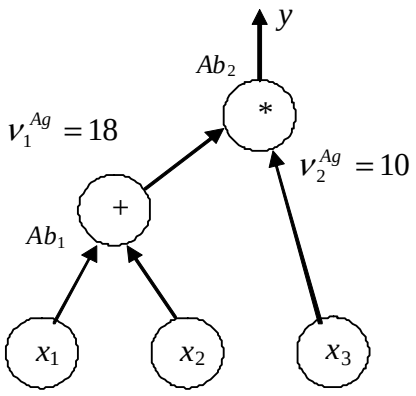


Fig. 7. Example of network configuration after starting growth

Hyper mutation of cells. Mutation plays an important role in shaping the immune response of the system to influence of antigen. Through the mechanism of mutation is adapting of antibodies structure and, as consequent, increasing in affinity population. In this paper, the intensity of mutation depends on the values of the antibody concentration ν^{Ag} in network. The higher the value ν^{Ag}, the lower the intensity of mutation. To mutations can be subjected the any part of the antibody line. Under the intensity β one can means the quantity of the elementary effects of operator mutations on antibody *Ab*. Elementary effect produced by one-point mutation scheme proposed in [10]. Since the operator can affects the any part of the antibody, it can updates not only the weight characteristics of arcs FNA, but also the structure of the FNA. Let antibody Ab_3 undergone by mutation so that both the function code and code of the 2nd node-descendant were changed. The new network structure might look like (Figure 8).

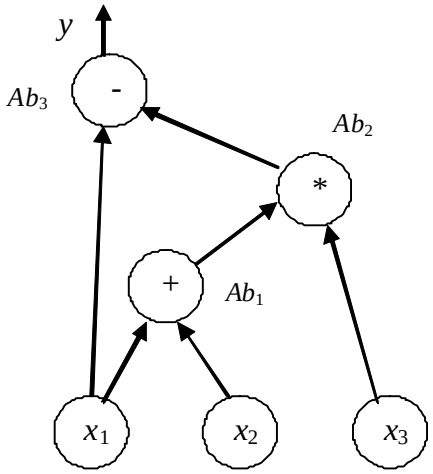


Fig. 8. The structure of the network (from example) after mutation

This structure does not contradict the syntax of mathematical expression that represents and can easily be shown as a tree (Figure 9).

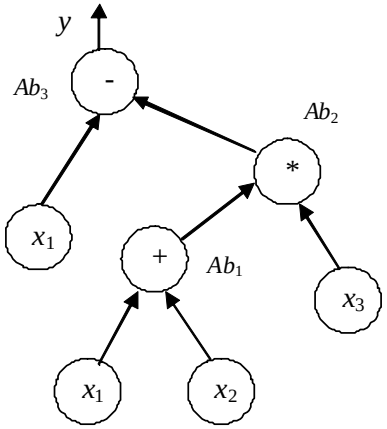


Fig. 9. Submission of network (from example) as a binary tree

To avoid the formation of a large number of the network outputs, the proposed method was set limitations under which any functional network top can forms a relationship with only terminal tops or other functional tops with no outgoing arcs.

GMDH cooperative immune algorithm. In the developed system is implemented the basic and additional external criteria. Using the basic criteria of training and testing occurs in the presence of three samples: training, checking (verification) and testing. Moreover, training and testing samples are as training set (Training set) (Figure 10).

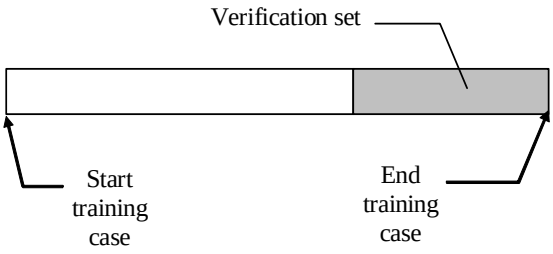


Fig. 10. Training, Verification and Training set

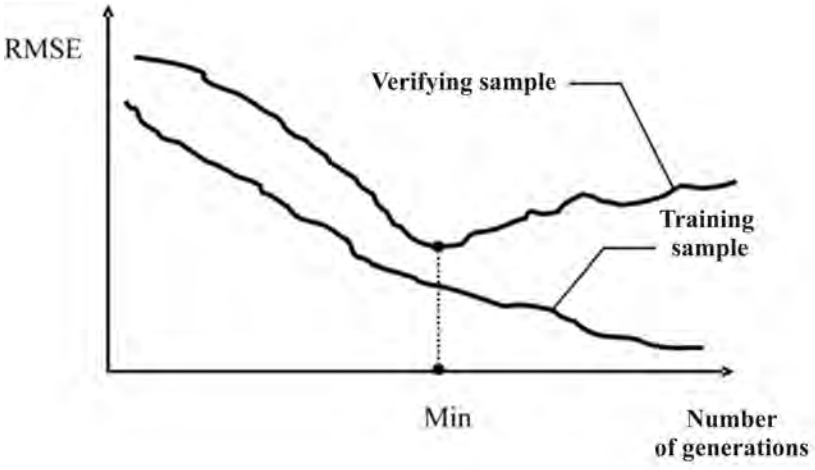


Fig. 11. An example of minimum achievement on the testing set

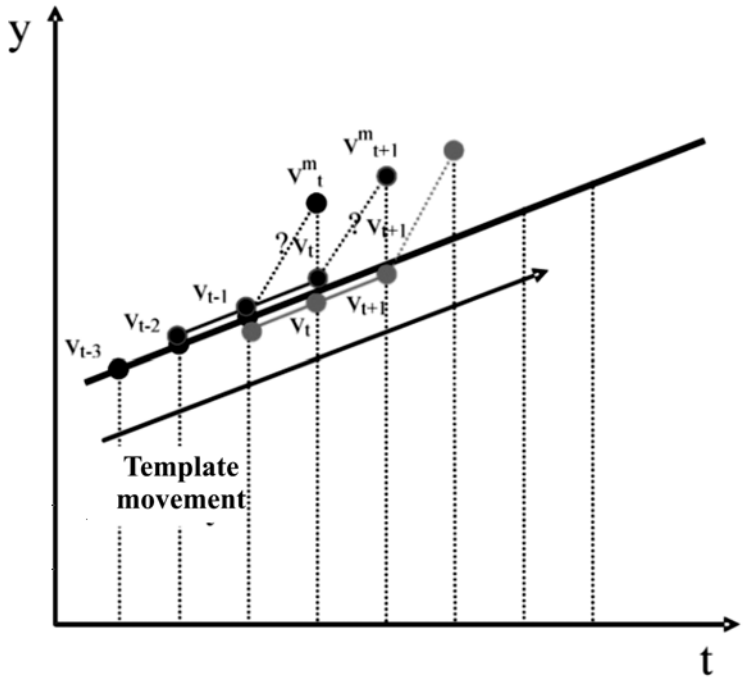


Fig. 12. The graphical interpretation of an external criterion based on the criterion of accuracy of step integration

As external criterion in our algorithm the regularity criterion was used. In this realization the initial set of N measurements shares in sampling N_A by which the model parameters are estimated and in N_B for checking of and to choice the suitable model. Regularity criterion defines standard deviation of model on the checking sub-sequence:

$$\Delta^2(B) = \frac{\sum_{t \in N_B} \left(y_t^M - y_t \right)^2}{\sum_{t \in N_B} y_t^2} \to min \tag{11}$$

The principle of self-organization using external criteria is as follows. While the system trains on the training sample, its error is gradually approaching zero. At the same time, system error in the verification set passes through a certain minimum value, which should not necessarily coincide with the minimum error in the study set (Figure 11).

It is proved that the achievement of a minimum on testing set is the moment of obtaining the most appropriate model [142]. To implement this criterion, we added two new parameters: the size of checking set and the parameter of study on the verification set only of best individual of current generation, and alternatively the all population is investigated. When using an external criterion at the end of each generation, when using only the best individual, is tested or: the better individual, or the entire population of the verification set. The error of this test is compared with the previous step error of procedure and, if it is less, then the individual structure who gave the error reduction is stored. At the end of the algorithm we have the best saved for two individual subsets. To explain an external criterion (it is based on the criterion of accuracy of step integration) turn to Figure 12.

The general scheme flow of cooperative GMDH algorithm of artificial immune network is presented in Figure 13.

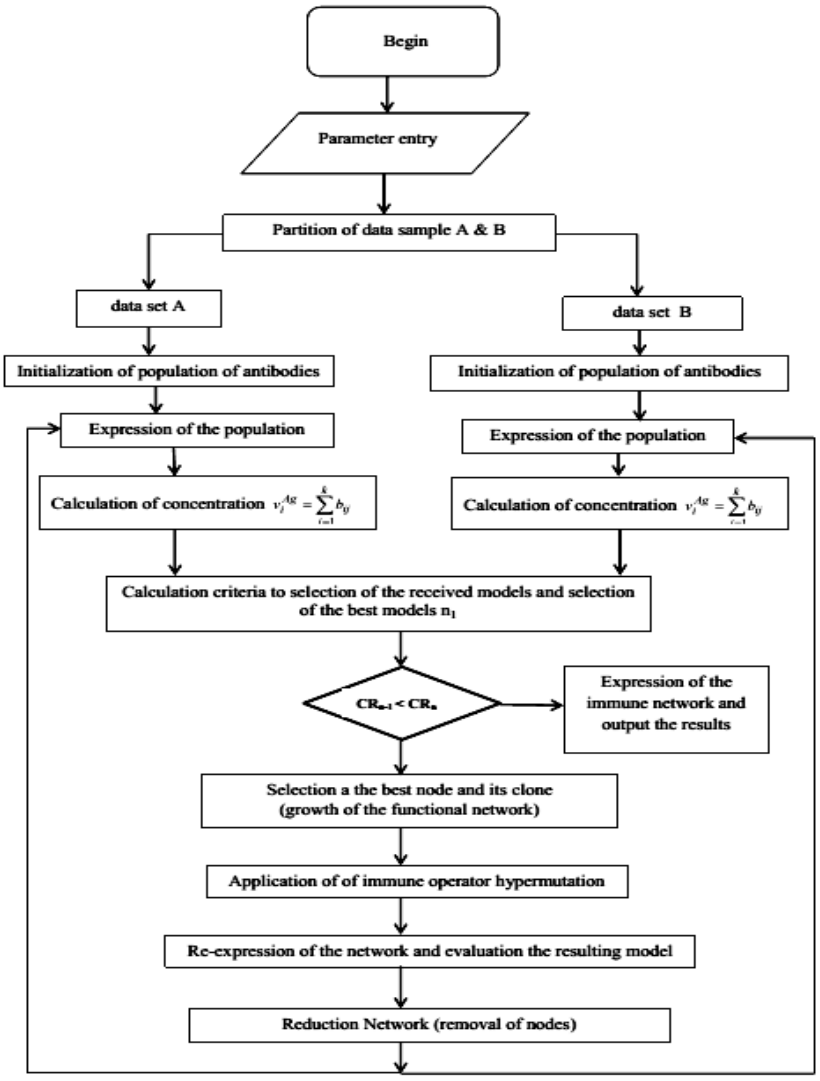


Fig. 13. Scheme flow of cooperative GMDH algorithm of artificial immune network

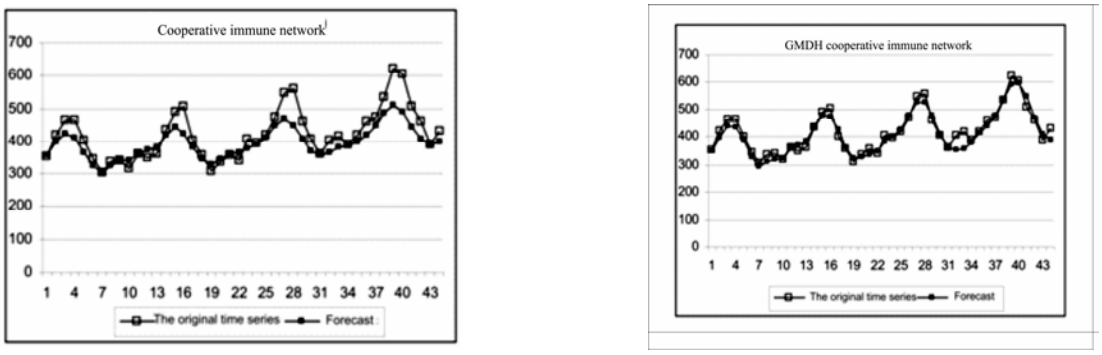
Numerical study of cooperative immune networks

Table 1

Set up the cooperative immune network for solving test problems

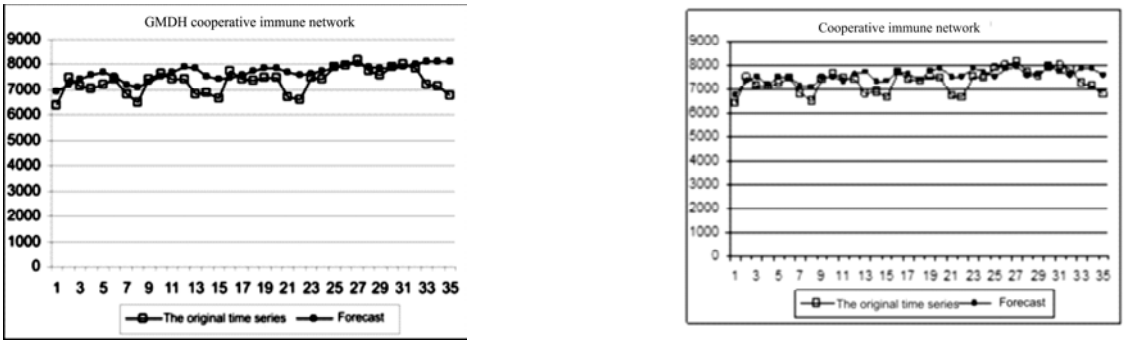
No.	Name of parameter	Parameter value
Time series of monthly volume of ticket sales		
1	Number of generations	10000
2	The period of compression (of generations)	70
3	Using the weights of arcs	So
4	The accuracy of weights representation	0,1
5	The level of cell mutation	5
6	Interval representation of weights	$[-1.0;1.0]$
7	Functional alphabet	$\{+,-,*,\backslash\}$
Time series of energy consumption		
1	Number of generations	10000
2	The period of compression (of generations)	170
3	Using the weights of arcs	So
4	The accuracy of weights representation	0,1
5	The level of cell mutation	3
6	Interval representation of weights	$[-1.0;1.0]$
7	Functional alphabet	$\{+,-,*,\backslash\}$

Charts of forecasts on 44 steps for a number of volumes monthly ticket shown in Figure 14 (a) and (b). Charts of forecasts on 35 steps ahead of time series of energy consumption shown in Figure 15(a) and (b).



a *b*

Fig. 14. Graphs of multistep forecasts of monthly tickets volumes sales. Predictions obtained using: a) neural network with radial basis package Neurosolution (MSE = 43.8; RMSE = 8.64%), b) cooperative immune algorithm (MSE = 21.9; RMSE = 5.16%)



a *b*

Fig.15. Graphs of multistep forecasts of energy consumption time series. Predictions obtained using: a) cooperative immune algorithm (MSE = 425.4; (%RMSE = 6.14%), b) GMDH cooperative immune algorithm (MSE = 542.5; %RMSE = 7.86%)

For numerical estimates we consider some additional statistical criteria. The average absolute error:

$$MAE = \frac{1}{n} \cdot \sum_{i=1}^{n} \left| y_i^M - y_i \right| . \quad (12)$$

where n is the size of the test sample.

The average relative error, in percent:

$$MAPE = \frac{1}{n} \cdot \sum_{i=1}^{n} \left| \frac{y_i^M - y_i}{y_i} \right| \cdot 100 . \quad (13)$$

The maximum absolute error:

$$WAE = \max_{i \in \{1, 2, ..., n\}} \left(\left| y_i^M - y_i \right| \right). \quad (14)$$

The maximum absolute error, in percentage:

$$WAPE = \max_{i \in \{1, 2, ..., n\}} \left(\left| \frac{y_i^M - y_i}{y_i} \right| \right) \cdot 100 . \quad (15)$$

The Tail coefficient:

$$U = \frac{\sqrt{\frac{1}{n} \cdot \sum_{i=1}^{n} \left(y_i^M - y_i \right)^2}}{\sqrt{\frac{1}{n} \cdot \sum_{i=1}^{n} \left(y_i^M \right)^2} + \sqrt{\frac{1}{n} \cdot \sum_{i=1}^{n} \left(y_i \right)^2}} . \quad (16)$$

By definition, the coefficient of U varies in the range of $[0;1]$. The closer the value of this coefficient to 0, the better the prognosis. As additional features one can also consider the prediction accuracy of the sign change of the process variable (*DA*), which determines the dynamic properties of the model. This characteristic is usually measured as a percentage of correctly prescribed signs. In Table 4.3 the predictions quality evaluation using the above statistical characteristics is shown.

Table 2

Comparative evaluation of the predictions quality evaluation obtained by different methods

No	Algorithm	MAE	MAPE	WAE	WAPE	U	DA
Time series of monthly volume of ticket sales							
1	GMDH Cooperative immune algorithm	17,7	4,20 %	57,7	13,8 %	0,026	81,4 %
2	Cooperative immune algorithm	32,3	7,00 %	116,2	19,5 %	0,053	74,4 %
Time series of energy consumption							
1	GMDH Cooperative immune algorithm	424,1	6,03 %	1354	20 %	0,036	50 %
2	Cooperative immune algorithm	338,5	4,80 %	934,3	13,7 %	0,029	53 %

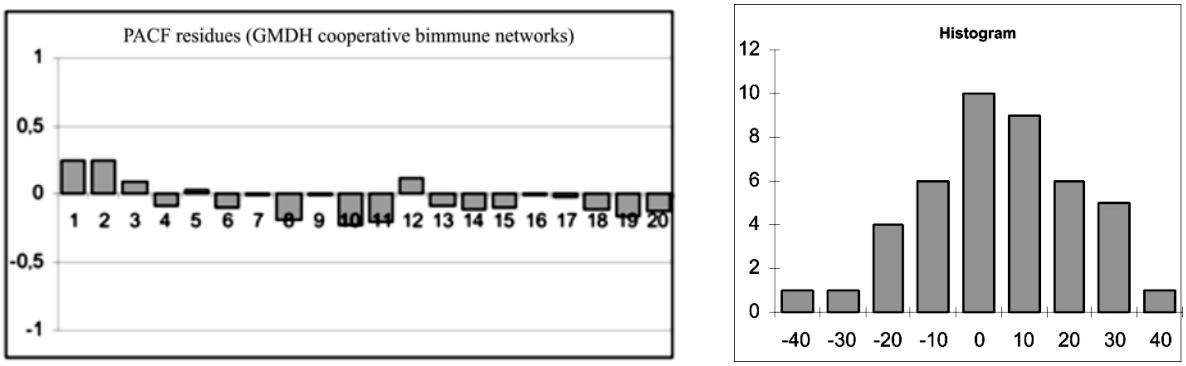
By comparing the results, we can conclude that, for the first and the second test series, the most high-quality model is obtained by the combined AIS-algorithm with the wavelet-neural network. However, according to Table 4.3, this algorithm is the slowest of all of the examples here. Here we present experimental results from the analysis obtained models residues to prove the possibility of using the developed algorithms for solving of the prediction problems.

Assessment of forecasting models quality using analysis of residues. In conducting the analysis of residues, we will use the following considerations:

- closer PACF (partial autocorrelation function) of forecast residues to 0, the more fully model uses the embedded in a row information, and thus more accurately reflects the behavior of the process represented by this series;

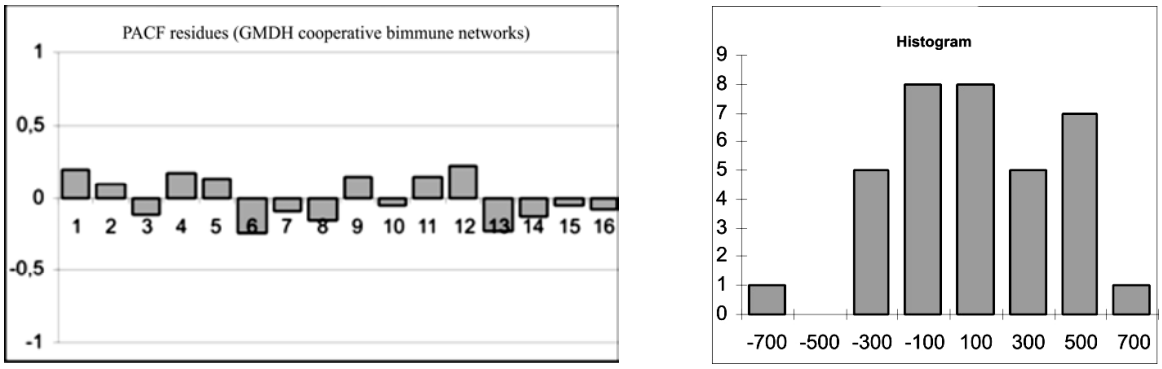
- for qualitative model the its residues distribution close to normal, which can be verified by a number of indicators of descriptive statistics.

Figures 16–19 show the PACF and residues distribution histograms for all obtained earlier forecasting models.



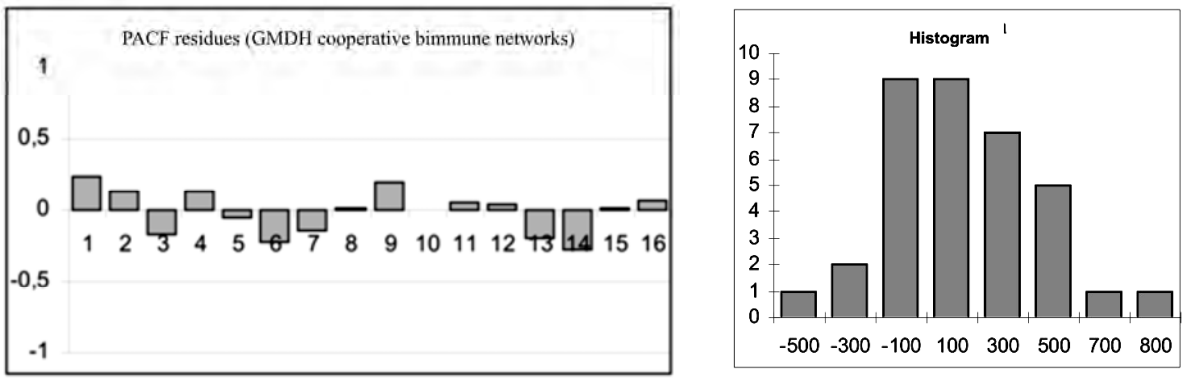
a *b*

Fig. 16. PACF (a) and histogram of model residues (b) distribution obtained through the GMDH cooperative immune algorithm for monthly volume of ticket sales



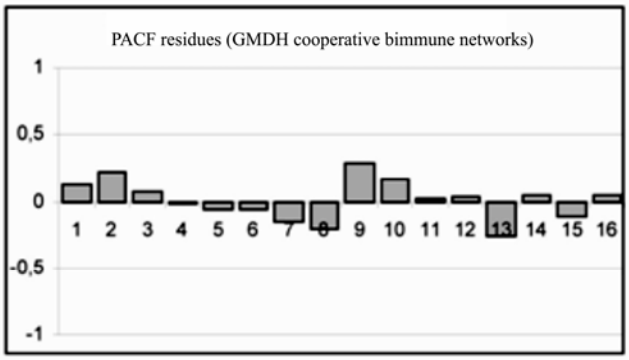
a *b*

Fig. 17. PACF (a) and histogram of model residues (b) distribution obtained using cooperative immune algorithm for monthly volume of ticket sales

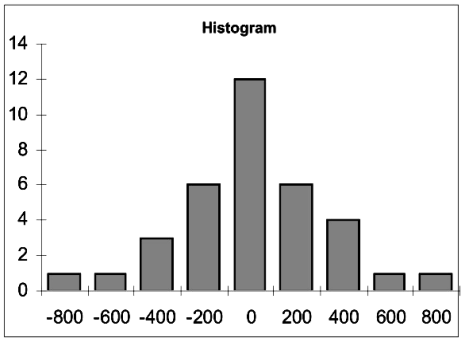


a *b*

Fig. 18. PACF (a) and histogram of model residues (b) distribution obtained through GMDH cooperative immune algorithm for the time series of energy consumption



a



b

Fig. 19. PACF (a) and histogram of model residues (b) distribution obtained using cooperative immune algorithm for the time series of energy consumption

The Table 3 presents the numerical characteristics of the residues distribution of considered models. In this case, the excess of the normal distribution, and to test Jarque-Bera the specified degree of null hypothesis likelihood may indicates that the distribution considered is normal. The results of the above analysis show that the model residues distribution, generated by the developed algorithms, with a high degree of confidence could attributed to normal. Therefore, the most developed algorithms are quite suitable for solving problems of forecasting.

Table 3

Numerical characteristics of the forecasting model residues distribution obtained by different methods

No.	Algorithm	Excess	Asymmetry	Test Jarque-Bera (probability)
Time series of monthly volume of ticket sales				
1	Cooperative immune algorithm	2,74	-0,24	0,75
2	GMDH Cooperative immune algorithm	3,02	-0,24	0,8
Time series of energy consumption				
1	Cooperative immune algorithm	2,58	-0,09	0,86
2	GMDH Cooperative immune algorithm	3,51	0,13	0,78

Conclusion

In the article for the first time is presented a GMDH hybrid immune algorithm, intended for solving the problems of forecasting. Shown that the use of external criteria significantly improves quality of the obtained models.

As a result we get a formal description of antibodies structure and ways of their association within the limits of a population in the functioning computer network. The way of estimation of antibodies as elements of a network is also considered. A description of the training algorithm based on a principle of clonal selection is resulted. Separately examples of basic phases of the algorithm are considered: growth of a network, a mutation of cells, compression of a network. Growth of a network is carried out due to selection and cloning of the best antibodies; the mutation of cells changes structure and adjustments of a network, and process of compression is provided by removal of not stimulated antibodies and results in reduction of the network size. This process plays exclusively important role, as owing to it the algorithm aspires to create solutions of minimal size. However removal even of one cell can essentially affect functioning of a network as a whole. Depending on position of the deleted cell, the given procedure can lead to strong redistribution of values of concentration of antigens among the remained antibodies. An analysis of the algorithm allows to tell, that it tends to delete only cells

of top level, i.e. the networks closest to outputs and, hence, will not cause global reorganizations of structure.

On the other hand it is possible to state with confidence, that process of compression allows a network to grow only aside increases in values of concentration of antigens, and the process of search initiated by clonal selection and a mutation, provides adding to a network of new cells consistently approaching a network to solution of a problem As the further research in this area it is possible to allocate to following directions:

- implementation of some alternative ways of estimation of antibodies as elements of the uniform computing system;
- further improvement of growth procedures and compression of a network;
- search and elimination of superfluous parts of a network with the purpose of simplification of its structure;
- comparative study of the effect of combined external criteria on quality of the obtained solutions.

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