фективность алгоритма и качество построения сеток продемонстрированы с использованием механической модели.

Ключевые слова: *усовершенствованный сеточный метод, геометрические особенности, построение шестигранной сетки, конформное перестроение, шаблоны „перестроения на 27 ячеек“, качество сетки*

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THE ALGORITHM OF ARTIFICIAL IMMUNE SYSTEM SIMULATION WITH SAATY SELECTION OPERATOR AND ONE-DIMENSIONAL LOCAL SEARCH

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АЛГОРИТМ МОДЕЛЮВАННЯ ШТУЧНОЇ ІМУННОЇ СИСТЕМИ З СЕЛЕКТИВНИМ ОПЕРАТОРОМ СААТІ ТА ОДНОВИМІРНИМ ЛОКАЛЬНИМ ПОШУКОМ

Purpose. Development of an algorithm which implements a certain method of modelling an artificial immune system for solving the task of multidimensional constrained optimization of multiextremum continuous functions and which provides increasing performance indicators.

Methodology. A hybrid adaptive immune algorithm is proposed. It uses an operator of clonal selection based on the evaluation of fitness of solutions using the method of Saaty’s hierarchy; pair adaptive crossover; the adaptive mutation based on polynomial and normal distribution laws; limited coordinate wise local search using the method the Golden section.

Findings. The use of the algorithm for multidimensional constrained optimization that simulates the behavior of the artificial immune system as the operator of selection is mathematically justified by the operator based on the method of analysis of Saaty’s hierarchies. It is proposed for the first time. Unlike any of known implementations of heuristic operators, it ensures a high precision and speed of the ascent up to the same level of problems.

Originality. The results show high efficiency of the proposed algorithm for optimization of standard objective functions used as a test on the spacial dimensions up to 100 iterations. The algorithm shows stable convergence and a higher speed when there is a task of training neural networks of direct distribution.

Practical value. The main advantages of the proposed algorithm lie in the fact that it remains effective with the growth of the of the problem; it finds not one solution, but many of them (alternatives); use much less time for a comparable solution. These properties allow the application of the proposed algorithm to solve multi-criteria multi-factor optimization problems of decision making in the processes of complex systems control.

Keywords: *immune system, optimization, Saaty’s method, local search*

Introduction. A lot of engineering, social and economic problems can be formulated as problems of optimization some objective functions which include many variables. However, in most cases there appears to be multimodal objective functions. The existence of multiple local optimums of the objective function in the same time with one or more global optimums is traditionally seen as a significant drawback. There are a number of methods and algorithmic techniques aimed at the withdrawal of the local optimums to achieve a single global solution.

The problem is compounded when the issue is not about one, but about a number of criteria and a set of decisions which are not dominated by each other among which we still trying to find a single optimum. In real usage there is often the need to find not a single optimum solution for the problem, but their families. Each of the resulting solutions that, in general is suboptimal, allows us to consider several possible outcomes.

Problem definition. Metaheuristic, known as a method of simulation of the artificial immune system, provides this multivarious problem solution.

The immune algorithm (IA) offered here imitates properties of the natural immune system. It is based on

the principles of the somatic theory [1] a network hypothesis. Somatic theory states that increasing the diversity of antibodies is due to somatic recombination and the mutation of genes. The assumption that control of breeding clones occurs because of mutual recognition of antibodies that function as a network is justified within the network hypothesis [1, 2].

In the course of evolution, the immune system of the highest mammals had gained the ability to destroy antigens by antibodies (Fig. 1).

In Fig. 1, the work of the immune system from the point of view of the processes governing the handling and control of the information is shown. Using this scheme it is possible to present informational processes in the immune system in the form of an algorithm which is put in the following sequence described in:

1. Discernment of an antigen. This process corresponds to the form of the optimization problem $f^* = f(X^*) = \min\limits_{X \in D \subseteq R^n} f(X)$, where n-dimension of the vector X of real variables $x_i \in X$, defined on the region of valid values D.

2. Generation of antibodies by memory cells. It corresponds to the mention of a successful solution of the same problem (or similar) in the past.

3. Evaluation of affinity of the cell X_j, which is equivalent to finding the optimal solution: $\varphi_j = -f(X_j)$ for the minimization problem.

4. Differentiation of lymphocytes: saving the corresponding solution for the next step of the search while avoiding any redundancies.

5. Inducing and suppressing antibodies, depending on the affinity. Research of local optimums is accompanied by maintainance of the diversity of the search directions.

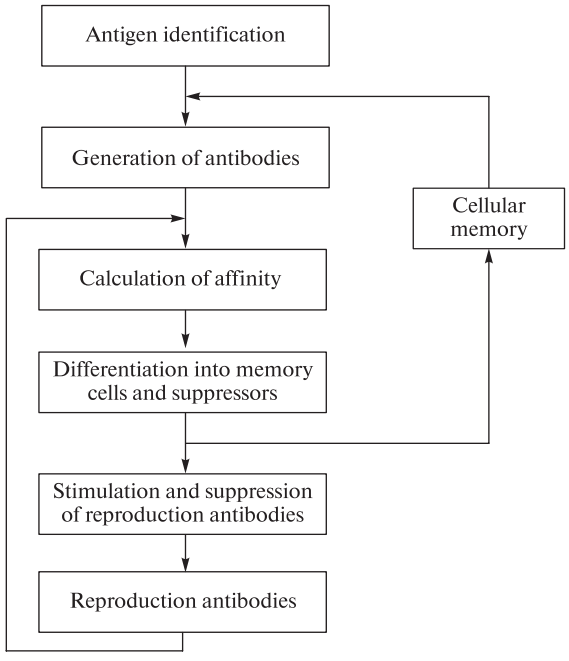


Fig. 1. Mechanism of formation of antibodies in the immune system

6. Breeding of antibodies using the memory and random genes.

In nature, the process described is continuous antibodies are produced by an organism – both for met antigens, and also for any possible mutations. In the computer simulation process of algorithm, it can be stopped after a certain amount of generations or after a set time.

The result of the algorithm is a family of solutions which correspond to antibodies in memory cells, most of which are adapted to the antigen. In the case of searching extremums of multimodal functions, this family corresponds to an array of vector-solutions, the affinity of which is the closest to the global optimum, while solutions are different in pairs no less than on the given threshold.

The time of performance and the number of calls to the objective function during searching the global optimum can be performance indicators of the algorithm, and also the reliability (repeatability) of the solutions in repeated runs. The last is quite important, because the heuristic method, which is described herein, belongs to a class of random search methods and has convergence only in probability.

Analysis of existing algorithmic solutions. Historically, the first realization of the idea of modelling the artificial immune systems was the idea of selection and exclusion of independent search agents proposed in the algorithm CLONALG [3]. This algorithm, which is a combination of the main ideas of genetic algorithms and evolutionary strategies, use binary encoding of real search space, selection of a specific part (about half) of the best individuals and their even cloning, inversely proportional to the utility mutation, the exclusion of the least useful antibodies and the compression of the population.

The population contraction operator removes excess population, except the worst one from close solutions which satisfy the requirement

$$\|X_a - X_b\| < r, \quad a \neq b, \quad a, b \in [1 : N_p], \qquad (1)$$

where r – a fixed threshold of proximity; $\|*\|$ – the symbol of a norm, depending on the metric of space; N_p – size of the population.

The disadvantages of the algorithm CLONALG are a lack of adaptation, limited accuracy due to the binary coding and non-usage of the memory mechanism.

Another algorithm for modelling the immune system is the algorithm BCA [4]. In fact, it is a version of an evolutionary strategy with a binary coding and compression operator. It uses two mutation operators at once: in 3/4 case bits, and 1/4 cases – adjacent (a few bits that are close by are inverted at once). The method shows high search performance in a small population $N_p = 3 \div 5$, however, as CLONALG, it is worse for multivariate testing problems than well-known evolutionary strategies because of the quality of solutions.

A step forward is an opt-AiNet algorithm, the main feature of which is a work directly in real space and saving all the locally-found global optimums of the objective function in the memory, the size of which is

dynamically changing. The algorithm also uses dynamic population size, controlled by compression mechanism. The mutation of each clone is performed proportionally to its usefulness to its parent cell by the formula

$$X_j^{C_i} = X_j^{C_i} + \alpha_j \cdot N(0;1), \quad \alpha_j = \rho e^{-\hat{\varphi}_j}, \quad j = \left[1 : N_p\right], \quad (2)$$

where $X_j^{C_i}$ – i-clone of the j-cell of the previous population; α_j – radius of mutation to the clones of the j-cell; $\hat{\varphi}_j$ – the relative affinity of the j^{th} cell in generation $\hat{\varphi}_j = \dfrac{\varphi_{\max} - \varphi_j}{\varphi_{\max} - \varphi_{\min}}$; ρ – free positive parameter of the method; $N(0; 1)$ – normally distributed random variable with the expectation 0 and standard deviation equal to 1.

The practical implementation of this algorithm on a number of functions [5] showed a significant advantage over CLONALG algorithm in the speed of finding the solutions comparable in quality.

In [2] it is proposed to complement an opt-AiNet algorithm with an operator of a random local search. The last makes some implementation of the algorithm comparable in the efficiency with known genetic algorithms and evolutionary strategies for the class of solving problems. Not accidentally – and this is the main value of opt-AiNet – it is the basis for a number of more advanced algorithms that implement the foregoing method of modelling immune systems.

The HIA algorithm, proposed in [1] and improved in [5], is used in solving many of the applied problems using the immune systems modelling method. It can be viewed as a modification of the method of opt-AiNet. Unlike the latter, the size of the population in the HIA algorithm stays constant during the entire iterative process and supported by the operator of compression (1). In addition, each cell has an additional attribute T, called the age of the cell. With its help the so-called "elite" cells that lived are determined. These are solutions that have not been improved by mutation for a long time, that is why they are considered as local optimums. They are recorded in memory and are used to generate clones in each new generation.

Mutation of clones is performed in two ways. The first, which is responsible for intensification of the search in the vicinity of the found solution, is to change the coordinates of clone using the normal adaptive distribution of mutation level.

$$X_j^{C_i} = X_j^{C_i} + N\left(0; \alpha_j\right), \quad (3)$$

where $\alpha_j(t)$ – the standard deviation of the normal distribution, for each iteration t determined by the relationship

$$\alpha_j(t) = \begin{cases} 2\left(X_j(t-1) - X_j^{C_i}(t-1)\right), \\ \quad \text{if } f\left(X_j^{C_i}(t-1)\right) < f\left(X_j(t-1)\right). \\ \alpha_j(t-1) \quad \text{overwise} \end{cases} \quad (4)$$

The second method aims to diversify of the search direction by examination areas which has not been reviewed and to change the one of the coordinates on a random number from the entire search area

$$x_{j,\,i} = U(x_{\min,\,i}; x_{\max,\,i}), \quad i = [1 : n]. \quad (5)$$

Here n – the dimension of the space; $U(x_{\min,\,i}; x_{\max,\,i})$ – uniformly distributed random variable within $D = \{x_i | x_{i,\,\min} \le x_i \le x_{i,\,\min}\}$.

The HIA algorithm, compared to previous ones, demonstrates the reliability of searching the global optimum of multiextremum functions for quite a limited time.

Some researchers, in particular [6, 7], include local search operators based on the above methods of unconditional optimization to the algorithms for modelling the immune system. However, the use of climbing up methods, Nelder-Mead and Lagrange multipliers, in particular, in the SIA [6] method for solving problems with limitations, though amplify the local convergence of algorithms, however, they did not significantly affect the probability of obtaining a global optimum.

The algorithm Dopt-AiNet [7] applies the operator of copying coordinates, which works as follows: if after mutation in any of the coordinate affinity of the clone is improved then, the new value for this coordinate is trying to be applied to the rest of the measurements. This operator shows high efficiency in the case of symmetry of functions for coordinates, typical for most test functions such as Rastrigina, Ackley, Shvefelya, Hrivanka and others. However, in solving real problems such as training of neural networks of direct distribution or based on radial basis functions, this operator is absolutely not effective.

The integration of the operator of information exchange between agents of search (recombination) to the general algorithm of the artificial immune system seems more appropriate. The last, known from genetic algorithm as crossover, allows significant improvement of the quality of solutions and achieves the desired quality in real time due to the information exchange.

In particular, in [8] it is proposed to perform its crossover with random cell memory for each of the clones formed with a small probability $P_{cross} \le 0{,}2$. Moreover, each gene will remain unchanged or they will be replaced by the memory cell genes.

The aim of this work is to develop an algorithm which would implement the method of modelling the artificial immune system to solve the problem of multivariate conditional optimization of multimodal continuous functions and would provide the most possible performance indicators.

Basic materials and improved optimization algorithm HINO-SF. Given the above implementations of algorithms which implement the modelling method of artificial immune systems, the following algorithm that does not require binary coding of real variables and applies a number of operators known as genetic and memetic algorithms. The aim of the last

ones should be the intensification of adaptive local search and study, as much as possible, and the entire search area.

We will call the proposed algorithm HINO-SF (*Hybrid Immune Network Optimization algorithm with Saaty selection and Fibonacci search*). It consists of the following:

1. The population of antibodies is generated randomly. A counter of generations is set to $t = 0$.

2. If a preassigned maximum number of generations is achieved then transition to step 11 should be made; otherwise – transition to step 3.

3. Depending on the cells' adaptability assessment of the current generation, the number of clones is assigned for each cell of the current generation. It is an operator of selection.

4. Cloning cells in an amount determined by the operator of selection.

5. Recombination of cloned individuals by using the operator of probability crossover.

6. Calculation of the dynamic probability of mutation for clones and implementation of adaptive mutation operator.

7. Execution of the one-dimensional local search on a random coordinate using method of golden ratio (Fibonacci) for each clone with a certain probability.

8. Compression of the general population of parents and clones using the appropriate to a specified level N_p operators.

9. Destruction of cells, whose age has reached the set value $t_{\max}$, from the current generation. Their place in the main population is occupied by cells, randomly generated uniformly in the search area.

10. The counter of generations $t = t + 1$. Transition to the step 2.

11. The output of the current generation as a set of suboptimal solutions.

12. Stopping the algorithm.

Consider each of the above operators of the algorithm in details.

Operator of selection. To determine the number of clones per each of the individuals of the current generation, it is proposed to use the operator which applies the hierarchy analysis method (HAM) of Saaty with cuttings off was first applied in the operators of of the clonal of evolutionary optimization strategies [9]. The author calls his operator h as the cut of set of the current generation of cells, described by the equation

$$M_h = \{X_j \in D \,|\, \mu(f(X_j)) > h_{\min}\}, \quad j = [1 : N_p], \quad (6)$$

where $h_{\min} = 1/N_p$ – the critical adaptivity of the cell; D – search area; $\mu(f(X_j))$ –function of the cell's appurtenance to the set of qualitative values.

Function of the cell's appurtenance is defined as follows:

- solutions are normalized by the value of the affinity for the segment [0; 1];

- the rating of each of them $a_j = 1 + \lfloor \varphi(X_j) * k \rfloor$ is calculated, k – the dimension of the scale (default $k = 9$);

- construction of a matrix of pairwise comparisons for the first line of which an expression $b_{1i} = a_1/a_i$ is used, and for the rest – $b_{ij} = b_{1j}/b_{1i}$;

- functions of appurtenance is calculated as $\mu(f(X_i)) = 1/\sum_j b_{ji}$;

- cells, with $\mu(f(X_j)) > h_{\min}$, are cloned in an amount proportional to the functions of appurtenance $n_c = N_c \cdot \mu(f(X_i))$, the other parent generation rejected.

For the effectiveness of the work of further crossover and mutation operators, it is desirable that individuals with high affinity would produce a sufficiently large number of clones. Therefore it is recommended to choose $N_c = 10 \ldots 20 \cdot N_p$.

Clonal selection by HAM is one of the key differences of the proposed algorithm from the rest of the algorithm implementations in which the tournament, proportional or equal principles of distribution of clones between parental individuals are applied. Besides the fact that this method, unlike the others, is mathematically justified, its practical application provides better convergence in solving typical problems in comparison with other operators of selection.

Operator of crossover. Another key difference of the proposed algorithm is applying the adaptive operator of crossover, which involves the exchange of genetic information. Since it was suggested not to encode real information as binary, then for the recombination of genes it is proposed to use simulated binary crossover (Simulated binary crossover, SBX) [8], which allows immune cells to perform bonding of vectors of real coordinates similar to binary vectors in genetic algorithms.

SBX operator has three parameters set by the user:

- P_{cross} – the probability that the operator of crossover will be executed for the clone (usually a value close to 0.5);

- P_{ind} – the probability of crossing implementation on a given coordinate (may vary widely from 0.4 to 1 – in latest case the crossover is performed simultaneously in all coordinates);

- index of variation η – shows how much a descendant of the crossing should be like a parent (values 0 and 1 is likely to give offspring resembling one parent, the value of 0.5 – maximum mixing genes).

If a random number equally distributed between 0 and 1 (here and after denoted $U(0; 1)$) is less than the probability P_{cross} for two random clones with numbers j and k, and another random number $U(0; 1)$ is less than P_{ind}, then the current coordinate i of clones is exposed hybridization by the formula

$$\begin{cases} x'_{j,i} = \frac{1}{2}\left((1+\beta)x_{j,i} + (1-\beta)x_{k,i}\right) \\ x'_{k,i} = \frac{1}{2}\left((1+\beta)x_{k,i} + (1-\beta)x_{j,i}\right) \end{cases}, \quad (7)$$

where β – so-called degree of hybridization, which is calculated by the formula

$$\beta = \begin{cases} \left(\alpha \cdot U(0;1)\right)^{\frac{1}{1+\eta}}, & \text{if } U(0;1) \le \dfrac{1}{\alpha} \\ \left(\dfrac{1}{2-\alpha \cdot U(0;1)}\right)^{\frac{1}{1+\eta}}, & \text{if } U(0;1) > \dfrac{1}{\alpha} \end{cases}. \quad (8)$$

The parameter α is defined through the degree of the difference of the j and k cell on the coordinate, namely

$$\alpha = 2 - \frac{1}{1+2\dfrac{\min\left\{x_{\max,i} - \max\left(x_{j,i};x_{k,i}\right); \min\left(x_{j,i};x_{k,i}\right) - x_{\min,i}\right\}}{\max\left(x_{j,i};x_{k,i}\right) - \min\left(x_{j,i};x_{k,i}\right)}}.$$

Operator of mutation. The main operator that is responsible for finding a solution in the proposed algorithm, as in most implementations of the method of artificial immune systems, is the operator of mutation. An adaptive operator is proposed, it uses the following random mutation

$$x_{j,i}^{C} = x_{j,i} + \delta_i \cdot \left(x_{\max,i} - x_{\min,i}\right), \quad i = [1:n], \quad (9)$$

where the random component δ_i can be determined based on the Gaussian distribution according to (2) by the formula

$$\delta_i = 0.1 \cdot N(0;\ 1), \quad (10)$$

or polynomial distribution by the formula

$$\delta_i = \begin{cases} \left(2 \cdot r_i + \left(1-2r_i\right)\Delta_i^{\mu+1}\right)^{\frac{1}{\mu+1}} - 1, & \text{if } r_i < \dfrac{1}{2} \\ 1 - \left(2 \cdot \left(1-r_i\right) + 2\left(r_i - 0{,}5\right)\Delta_i^{\mu+1}\right)^{\frac{1}{\mu+1}} - 1, & \text{if } r_i \ge \dfrac{1}{2} \end{cases}, \quad (11)$$

where $r_i = U(0;\ 1)$ – random number equally distributed for each of the coordinates; $\Delta_i = \dfrac{\max\left\{x_{\max,i} - x_{j,i}; x_{j,i} - x_{\min,i}\right\}}{x_{\max,i} - x_{\min,i}}$ – the relative position of the current cell in the search area for the i coordinate; μ – index of density of the polynomial distribution (higher values correspond to the less dispersion of mutations).

Getting conventional parameters $P_{mut}^{\min}$ – the minimum level of mutation, *mut_rate* – the relative importance of mutation (part of the genes that will be changed by the operator) and $T_{\max}$ – maximum number of generations, the algorithm calculates the degree of gene mutations at each

$$mut\_level = \begin{cases} P_{mut}^{\min}\left(1 + mut\_rate - mut\_rate\dfrac{2t}{T_{\max}}\right), \\ \quad \text{if} \quad t < \dfrac{T_{\max}}{2} \\ P_{mut}^{\min}, \quad \text{if} \quad t \ge \dfrac{T_{\max}}{2} \end{cases}, \quad (12)$$

where t – number of current generation (of iteration).

If during the iteration of the coordinates the random number is less than *mut_level* then the coordinate is exposed to a particular mutation, otherwise it remains unchanged.

It is recommended to set $P_{mut}^{\min}$ at a level of 0.2–0.5, and *mut_rate* – at 0.5 ... 1. Then, regardless of the time of the algorithm on the initial iterations, mutation will be performed for all clones on final – less than for a half of them.

The decision about the type of mutation that will be performed (wide (10) or a brief (11)) is made based on the synthetic evaluation of the current cell in the scale of estimates of utility for the current iteration across a population. The latter is determined for each cell individually by the formula

$$mut\_select_j = \frac{1}{2}\left(1 - \gamma\frac{t}{T_{\max}}\right)\frac{\varphi_{\max} - \varphi_j}{\varphi_{\max} - \varphi_{\min}}, \quad j = [1:N_c], \quad (13)$$

where $g = 0.8 \div 0.95$ – maximum allowable portion of polynomial mutations in the total number.

If during appeal to the clone the random equal number is less than *mut_select*, then for the genes of the clone will be applied only mutation (10), otherwise – (11).

From the analysis (13) it is clear that the broader Gaussian mutation will be applied to cells with low affinity and often in the initial steps of optimization. The number of Gaussian mutations decreases linearly with the number of iterations and proportionally to the affinity cells in favor of polynomial mutation. It should be noted that the choice of the type of mutation is performed for the whole cell, and only then it is checked if this mutation will be performed for each of the coordinates (12).

Operator of local search. To intensify local search solutions and make it even more targeted, the operator of one-dimensional local search of the golden section method (Fibonacci) is applied to the clone that has passed the crossover and mutation with probability $P_{ls} = 0.1 \ldots 0.25$. This operator consists of the following operations [10]:

- equiprobably selected one of the coordinates $k = [1:n]$;
- equiprobably selected search direction – to the lower border of the search area $\min X_j^{C_i}$ or to the top $\max X_j^{C_i}$;
- one-dimensional local search is performed in the direction of the current location of the clone in the space $X_j^{C_i}$ to the border search area.

If the search improves the affinity of the solution, then earlier found solution is saved.

Operator of compression. After all search operators the cells of the new generation are estimated for quality. With the previous generation, they form a conflict set, from which N_p cells with the highest affinity, which are not closer than in the radius r of each other are select using the principle of (1). For this the following operations are applied:

- sorting clones according to descending of the affinity;

- cyclically from the first cell to the devastation of not-considered set;

- removal all cells that are close to the current cell and worst than it.

It should be also emphasized the need of removal the cells with age above a specified limit $t_{\max}$ after compression. It is proposed to delete the cell with $t_{\max} = 10 \ldots 20$ from iterations regardless of its affinity. These cells are replaced by new ones, in which each cell is generated by (5).

Modelling the algorithm. To compare the work of the proposed algorithm with renowned implementations of artificial immune systems modelling and with other heuristic methods, traditionally used for solving multidimensional optimization problems, they have been tested on a number of standard multiextremum functions. It was also compared to the work of the proposed algorithm, with previously known factors in solving practical problems – training the neural network of direct distribution.

Fig. 2, *a* represents a screen shot of the results of the algorithm for Rastrihin functions $F(X) = 20 + x_1^2 + x_2^2 - 10\cos(2\pi x_1) - 10\cos(2\pi x_2)$. minimization. For clearer understanding of the graph displayed are not objective functions, but the return value to it – affinity of the cells. From the picture you can easily see the main feature of the method of modelling the immune system – getting more than one solution, a certain set, which includes both global optimum and the closest by the affinity local optimums.

Fig. 2, *b* shows the dependence of the affinity of the best cell in the generation and average affinity of the population on the number of iteration while minimization of the Rastrihin twentieth order function. Graphics which are usual for heuristic algorithms have an important feature: even the best solutions are discarded and replaced by random ones if they have not been modified within a certain period in life.

Table 1 shows the comparative results of the algorithms in solving common problems. As the problem of training neural network has been used, the task of identifying the mechanical properties of long products depends on its chemical composition in an abridged and full version.

In the Table 1 following notation is used: f^* – minimum value of the objective function, which was found by 10 repeat runs; $\tilde{f}^*$ – statistical evaluation of the expectation value of the minimum value of the function at random launch; $\tilde{n}^*$ – statistical evaluation of the expectation value of the number of calls to the objective function before the end of the algorithm in a random launch.

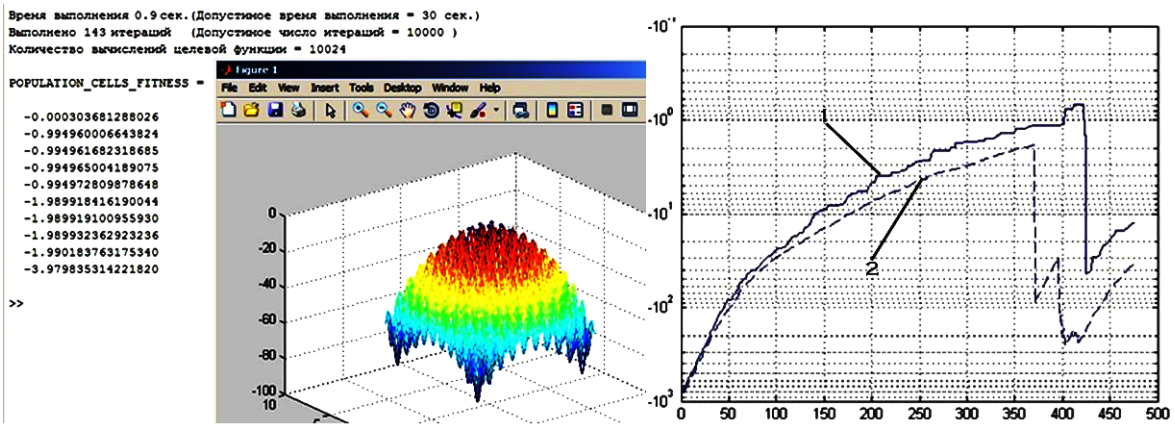
As can be seen, the proposed algorithm finds globally optimal solutions more often than analogues, herewith it is spending significantly less time. In particularly difficult problems, such as neural network training, on real data the winning of the time can be almost two orders of magnitude.

To understand the effectiveness of each of the operators that form the algorithm we summarized the frequency with which they improve the value of affinity cells to the Table 2.

It should be noted that the findings fully correspond to theoretical principles because mutation is the main tool for the local search in the method of artificial immune systems modelling. The absence of the proposed operator of selection in the table is substantiated by the fact that it does not lead to improvement of solutions, and only selects candidates for cloning.

Conclusion. Analysis of main modern algorithms that implement the modelling method of artificial immune systems showed the benefits of its advantages over other methods of multivariate conditional optimization in real space. It has been proposed a hybrid adaptive immune algorithm that uses operator of clonal selection, crossover, adaptive mutation and limited local search.

Selection is made by assessing the adaptability of solutions using the Saaty hierarchy. The proposed op-



a *b*

Fig. 2. Testing the proposed algorithm with the Rastrihin functions:

a – the result of minimization n = 2; b – changing affinity in time n = 20;1 – the dependence of the affinity of the best cell in the generation; 2 – average affinity of the population on the number of iteration while minimization of the Rastrihin twentieth order function

Table 1

Comparison of the algorithms in solving

Testing function (problem)	The dimension of the problem (number of variables)	The method of solving the problem								
		RC-GA			HIA			HINO-SF		
		Quality parameters of the algorithm								
		f^*	$\tilde{f}^*$	$\tilde{n}^*$	f^*	$\tilde{f}^*$	$\tilde{n}^*$	f^*	$\tilde{f}^*$	$\tilde{n}^*$
Rastrihin	20	0	3.472	$4.4*10^6$	0	6.626	$2.4*10^5$	0	1.929	$1.0*10^5$
	100	1.999	15.94	$1.6*10^7$	0.999	13.33	$8.6*10^6$	0	2.616	$2.0*10^6$
Ackley	20	0	0.142	$2.0*10^6$	0	1.086	$7.2*10^5$	0	0.007	$8.1*10^4$
	100	1.258	21.42	$2.1*10^7$	1.314	11.24	$9.4*10^6$	1.101	7.240	$2.1*10^6$
Training neural networks	72	4.974	16.37	$1.4*10^6$	2.994	11.33	$2.4*10^6$	2.039	10.20	$2.1*10^5$
	144	14.94	39.52	$5.1*10^8$	13.99	21.07	$1.4*10^8$	12.07	16.75	$4.1*10^6$

Table 2

The effectiveness of the proposed algorithm operators

Operator	Gaussian mutation	Polynomial mutation	Local search	Crossover
Cases of improvement of the objective function, %	23.33	47.99	17.23	11.45

erator of selection is more efficient than the traditional operators, in addition, it is the only one which is mathematically justified.

Doubles adaptive crossover of cell-clones provides intensification of the local search, allowing the combination of the best genes of two successful solutions from previous generations. The operator of one-dimensional golden section optimization method (Fibonacci) is applied to a random coordinate of a clone to increase the directionality of the search.

Operator of mutation by coordinates applies a polynomial or normal probability distribution. Moreover, if the clone is generated cells with high affinity, the probability of "narrow" polynomial mutation, corresponding to intense local search is higher. Clone generated by the cell with low affinity has a bigger probability of the "broad" mutation with the deviation by a Gaussian law.

The results show the high efficiency of the proposed algorithm for standard objective functions with dimensions up to 100, as well as in solving the training of neural networks of direct distribution.

The main benefits of the proposed algorithm are that it stays effective while increasing the dimension of the problem, it finds not one solution, but a set of solutions (alternative) and it uses significantly less time (in order) for the comparative solution to the problem.

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Желдак Т. А. Метод моделювання штучної імунної системи в задачах оптимізації мультимодальних функцій: матеріали 2-ї міжнар. наук.-техн. конф. „Обчислювальний інтелект (результати, проблеми, перспективи)“ (Черкаси 14–17 травня 2013 р.) / Т. А. Желдак. – 2013. – С. 33–36.

Мета. Розробка алгоритму, що реалізує метод моделювання штучної імунної системи для вирішення задачі багатовимірної умовної оптимізації багатомодальних безперервних функцій та забезпечує підвищення показників ефективності.

Методика. Запропоновано гібридний адаптивний імунний алгоритм, що використовує оператор клональної селекції на основі оцінки пристосованості рішень з використанням методу ієрархії Сааті, парний адаптивний кросовер, адаптивну мутацію на основі нормального й поліноміального законів розподілу, а також обмежений покоординатний локальний пошук методом золотого перетину.

Наукова новизна. Уперше запропоноване використання в алгоритмі багатовимірної умовної оптимізації, що імітує поведінку штучної імунної системи, в якості оператора селекції математично обґрунтований оператор на основі методу аналізу ієрархій Сааті, який, на відміну від відомих реалізацій з евристичними операторами, забезпечує вищу точність рішень і швидкість сходження на аналогічних класах задач.

Результати. Результати дослідження показують високу ефективність запропонованого алгоритму для оптимізації стандартних цільових функцій, що використовуються в якості тестових на розмірності простору до 100 вимірів. Також алгоритм показує стабільну збіжність та вищу швидкість роботи при вирішенні завдань навчання нейронних мереж прямого поширення.

Практична значимість. Основні переваги запропонованого алгоритму полягають у тому, що він залишається ефективним при зростанні розмірності задачі, знаходить не одне рішення, а їх множину (альтернативи) та використовує значно менше часу (на порядок) для порівняного розв'язання задачі. Ці властивості дозволяють застосовувати запропонований алгоритм для розв'язання багатокритеріальних багатофакторних задач оптимізації прийняття рішень у процесах керування складними системами.

Ключові слова: *імунні системи, оптимізація, метод Сааті, локальний пошук*

Цель. Разработка алгоритма, который реализует метод моделирования искусственной иммунной системы для решения задачи многомерной условной оптимизации многоэкстремальных непрерывных функций и обеспечивает повышение показателей эффективности.

Методика. Предложен гибридный адаптивный иммунный алгоритм, который использует оператор клональной селекции, на основе оценки приспособленности решений с использованием метода Саати, парный адаптивный кроссовер, адаптивную мутацию на основе нормального и полиномиального законов распределения, а также ограниченный покоординатный локальный поиск с использованием метода золотого сечения.

Научная новизна. Впервые предложено использование в алгоритме многомерной условной оптимизации, имитирующей поведение искусственной иммунной системы, в качестве оператора селекции математически обоснованный оператор на основе метода анализа иерархий Саати, который в отличие от известных реализаций с эвристическими операторами обеспечивает высокую точность решений и скорость схождения на аналогичных классах задач.

Результаты. Результаты исследования показывают высокую эффективность предложенного алгоритма для оптимизации стандартных целевых функций, используемых в качестве тестовых на размерности пространства до 100 измерений. Также алгоритм показывает стабильную сходимость и более высокую скорость работы при решении задач обучения нейронных сетей прямого распространения.

Практическая значимость. Основные преимущества предложенного алгоритма заключаются в том, что он остается эффективным при росте размерности задачи, находит не одно решение, а их множество (альтернативы) и использует значительно меньше времени (на порядок) для сопоставимого решения задачи. Эти свойства позволяют применять предложенный алгоритм для решения многокритериальных многофакторных задач оптимизации и принятия решений в процессах управления сложными системами.

Ключевые слова: *иммунные системы, оптимизация, метод Саати, локальный поиск*

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