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EXPERIMENTAL ANALYSIS OF MULTINATIONAL GENETIC ALGORITHM AND ITS MODIFICATIONS

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ABSTRACT

Context. Niching genetic algorithms are one of the most popular approaches to solve multimodal optimization problems. When classifying niching genetic algorithms it is possible to select algorithms explicitly analyzing topography of fitness function landscape; multinational genetic algorithm is one of the earliest examples of these algorithms.

Objective. Development and analysis of the multinational genetic algorithm and its modifications to find all maxima of a multimodal function.

Method. Experimental analysis of algorithms is carried out. Numerous runs of algorithms on well-known test problems are conducted and performance criteria are computed, namely, the percentage of convergence, real (global, local) and fake peak ratios; note that peak rations are computed only in case of algorithm convergence.

Results. Software implementation of a multinational genetic algorithm has been developed and experimental tuning of its parameters has been carried out. Two modifications of hill-valley function used for determining the relative position of individuals have been proposed. Experimental analysis of the multinational genetic algorithm with classic hill-valley function and with its modifications has been carried out.

Conclusions. The scientific novelty of the study is that hill-valley function modifications producing less number of wrong identifications of basins of attraction in comparison with classic hill-valley function are proposed. Using these modifications yields to performance improvements of the multinational genetic algorithm for a number of test functions; for other test functions improvement of the quality criteria is accompanied by the decrease of the convergence percentage. In general, the convergence percentage and the quality criterion values demonstrated by the algorithm studied are insufficient for practical use in comparison with other known algorithms. At the same time using modified hill-valley functions as a post-processing step for other niching algorithms seems to be a promising improvement of performance of these algorithms.

KEYWORDS: multimodal optimization problem, niching genetic algorithms, multinational genetic algorithm, hill-valley function, genetic algorithm convergence, real peak ratio, fake peak ratio.

ABBREVIATIONS

ASD is an adaptive species discovery;

GA is a genetic algorithm;

HillVallEA is a hill-valley evolutionary algorithm;

HTS is a history-based topological speciation;

HVcMO is a hill-valley-clustering-based variable mesh optimization;

HVF is a hill-valley function;

MMOP is a multimodal optimization problem;

MNGA is a multinational genetic algorithm;

$\mathrm{MNGA}_{\mathrm{c\_h\_v}}$ is a MNGA with $F_{c\_h\_v}$;

$\mathrm{MNGA}_{\mathrm{m\_h\_v}}$ is a MNGA with $F_{m\_h\_v}$;

$\mathrm{MNGA}_{\mathrm{m\_h\_v\_rand}}$ is a MNGA with $F_{m\_h\_v\_rand}$;

$\mathrm{MNGA}^{\mathrm{n}}$ is a MNGA with national selection to the mating pool;

$\mathrm{MNGA}^{\mathrm{w}}$ is a MNGA with weighted selection to the mating pool;

$\mathrm{MNGA}^{\mathrm{m}}$ is a MNGA with mixed selection to the mating pool;

NBC is a nearest-better clustering;

RS-CMSA is a covariance matrix self-adaptation evolution strategy with repelling subpopulations;

SCGA is a species conserving GA;

TCGM_S2 is a GA of tournament crowding based on Gaussian mutation, with S2 parameter set;

TS is a topographical selection;

TSC is a topological species conservation.

NOMENCLATURE

$d(x,y)$ is an Euclidean distance between individuals x and y;

f is a fitness function;

$f(s)$ is a fitness value of an individual s;

$F_{c\_h\_v}$ is a classic HVF;

$F_{m\_h\_v}$ is a modified HVF;

$F_{m\_h\_v\_rand}$ is a modified HVF with randomized intermediate points;

FPR is a ratio of the number of fake peaks found by the algorithm to the total number of species formed by the final population;

$g(k, t)$ is a number of politicians of the k-th nation at the t-th algorithm step;

GP is a number of real global peaks found in one run of the algorithm;

GPR is a ratio of the number of real global peaks found by the algorithm to the total number of global peaks to be localized;

$gr=[gr_1, gr_2, \ldots, gr_K]$ is a sample array, $0<gr_1<gr_2<\ldots<gr_K<1$;

i_j is a j-th politician;

K is a size of gr and a number of intermediate points used by HVF;

LP is a number of real local peaks found in one run of the algorithm;

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LPR is a ratio of the number of real local peaks found by the algorithm to the total number of local peaks to be localized;

n is a search space dimension;

NP is a number of real peaks found in one run of the algorithm;

NSeeds is a power of *Seeds*, i.e. a number of species or, equivalently, a number of peaks (real and fake) found in one run of the algorithm;

$O_\varepsilon(x^*)$ is an ε-neighborhood of the point x^*;

$<p_0, p_1, p_2, \ldots, p_K, p_{K+1}>$ is an ordered list of points used by HVF, $p_i \in X \subseteq R^n$;

p_0 is a first test point;

P_c is a probability of crossover;

p_i is an *i*-th intermediate point, $0<i<K+1$;

p_i^j is a *j*-th coordinate of the *i*-th point;

p_{K+1} is a second test point;

$pl_k(t)$ is a policy of the *k*-th nation at the *t*-th algorithm step;

P_m is a probability of mutation;

PR is a ratio of the number of real peaks found by the algorithm to the total number of peaks to be localized;

S is a set of individuals encoding $X \subseteq R^n$;

s_i is an individual encoding point p_i, $0 \le i \le K+1$;

Seeds is a set of the best individuals of each species;

SucRuns is a percentage of successful runs of the algorithm;

δ is a function accuracy parameter;

ξ is a random value from (0, 1);

σ is an argument accuracy parameter.

INTRODUCTION

Niching GAs, based on the phenomenon of speciation and specialization in natural ecosystems, are one of the most popular approaches to solve MMOPs. These problems aim to find multiple extremums (global, local) of a given function and arise in many areas of science and technology, see [1–5] for examples.

It can be shown that solving an arbitrary, including multimodal, optimization problem in the form

$$F(x) \to \max, x \in X \subseteq R^n \quad (1)$$

reduces to solving by a GA an optimization problem in the form

$$f(s) \to \max, s \in S. \quad (2)$$

Here with, an arbitrary feasible solution of problem (2) is called an individual of the population, and it is said about genotype and phenotype of the individual. The objective function of (2) is used to estimate the quality of solution of (1); crossover (the exchange of segments between different solutions) and mutation (disturbance) operators ensure transition from one solution to another.

A niche in GA is a subdomain of the search space (a region around a certain optimum of the fitness function), and species is a subpopulation of individuals located in a given niche. Niching GAs tend to structure population into stable subpopulations (species) in the search space in a way that each subpopulation is formed around one of the sought optimums. To date, several dozen niching GAs of different performance reflecting various approaches to solve MMOPs have been developed. Surveys of niching GAs and their classifications are available at [1, 6, 7].

In recent years topological niching GAs are of growing interest. To capture the landscape topography and identify basins of attraction for given individuals the topological niching GAs analyze relationships between locations and fitness values of individuals. Based on the basin identification method these algorithms can be roughly classified at the algorithms based on TS [8, 9], algorithms based on NBC [10–13], and algorithms using HVF. Last class includes but not limited to MNGA [14, 15], TSC and TSC2 [16, 17], ASD [18], HTS [19], Hill-VallEA [20, 21], HVcMO [22, 23], RS-CMSA [24, 25].

The object of study is a niching GA as a method to solve MMOPs.

The subjects of study are the HVF, MNGA and how MNGA parameters affect algorithm performance.

The purpose of the work is the development and performance analysis of MNGA and its modifications. Recall that the experimental analysis of heuristic algorithm performance is to evaluate statistical data collected as a result of conducting a series of independent runs of the algorithm for each problem from the benchmark suite.

1 PROBLEM STATEMENT

In this paper the MMOP (1) is considered in the following formulation. Let $F: X \to R$ be a function defined on some set $X \subseteq R^n$. A point $x^* \in X$ is called a point of local maximum of *F* over *X* if there exists a number $\varepsilon>0$ such that $\forall\ x \in X \cap O_\varepsilon(x^*)$: $F(x^*) \ge F(x)$. A point $x^* \in X$ is called a point of global maximum of *F* over *X* if $\forall\ x \in X$: $F(x^*) \ge F(x)$. The problem is to find all points of local and global maxima and the values of function *F* at these points.

The MNGA analysis is to compute well-known criteria characterizing the number and accuracy of problem solutions found by the MNGA and to compare the criterion values obtained for various values of the MNGA parameters.

2 REVIEW OF THE LITERATURE

A significant drawback of many niching algorithms is so-called niche radius problem. The performance of radii-based niching algorithms heavily depends on the niche radius value while estimation of this value is a complex task requiring prior knowledge of the search space landscape [1, 6]. As opposed to radii-based niching algorithms, the MNGA presented in [14, 15] divides popula-

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tion into subpopulations without using the niche radius concept. To determine whether two individuals occupy the same niche (whether the points encoded by these individuals are in the neighborhood of the same extremum) the fitness-topology function HVF is used. This function analyzes the search space landscape between two points based on the fitness values of individuals encoding points located on the straight line that connects two test points.

In MNGA the following metaphor is used. The population of individuals represents the world (the entire population of the planet), each subpopulation represents the nation, and the fittest individuals in the subpopulation represent the government of the nation; these individuals are referred to as the politicians. The government determines the policy of the nation, which is a single point representing the peak the nation is formed around; this point is the centroid of the subpopulation fittest individuals. Policy calculation is needed to determine possible migrations of individuals between nations as well as to distinguish nations from each other. The evolution of the world obeys the following rules.

1. Migration. This rule regulates movement of individuals between nations and creation of new nations in “uninhibited” areas of the search space.

2. Merge. Nations are merged when they are formed around the same extremum.

3. Selection to the mating pool. The following modifications of binary tournament selection are considered.

1) Weighted selection. In this case fitness value of an individual is divided by the total number of individuals in its nation. This approach reduces the probability for a nation to die out because of small subpopulation size.

2) National selection is conducted within each nation, therefore, the number of individuals in a nation after selection remains unchanged. This implies that migration is the only way to change the nation size.

3) Mixed selection is a combination of weighted and national selections.

4. Election. This rule describes how the government of a nation is elected and how its policy is calculated. Note that formula $pl_k(t) = \frac{1}{g(k,t)} \sum_{j=1}^{g(k,t)} i_j$ is computed coordinatewise. If the number of individuals in a nation is less than predefined value g, then the number of politicians is equal to the number of individuals in the subpopulation.

5. Mating. Only individuals belonging to the same nation may produce offspring. This limitation is because the crossover of two individuals located in the neighborhoods of two different optima may produce an offspring much worse than each of the parents. The mutation operator that adds noise generated by normal distribution to an individual is called in [15] the mutation based on the distance policy; this name looks reasonable as the operator provides minor changes to individuals that are close to the nation policy and significant changes to individuals located far from it. In literature, this operator is also known as Gaussian mutation. In [14] it is proposed to perform mutations within nations, i.e. an offspring is accepted only if it occupies the same niche as its parent. To reduce the algorithm execution time, this restriction was not applied in our research.

6. Initialization of the start nation. At the start of the algorithm, all individuals belong to the same initial nation.

MNGA works as follows. In every generation, each individual is compared to the policy of its nation. If the individual and the policy are located around different optima, the individual migrates to the nation with policy in the individual’s peak neighborhood. If such a nation does not exist, the individual founds a new one; this nation corresponds to a potentially new peak the individual is approaching. If a nation with a very small number of individuals is formed at the end of the migration process, this nation is strengthened by new individuals generated from the nation policy with the use of Gaussian mutation. Instead, the worst fitness individuals of other nations are removed from the population. After completion of all necessary migrations, the pairwise comparisons of policies of all nations are carried out to ensure there are no nations following the same peak; if two nations around the same peak are found, the corresponding subpopulations are merged. Thereafter, standard actions are performed to move to the next generation, i.e. selection to the mating pool and applying genetic operators. The MNGA scheme is provided below.

0. Encoding of solutions.
1. Initialization. The initial population is generated randomly.
2. Fitness calculation for all individuals in the population.
3. Initialization of the start nation. Determining politicians and calculation of the policy.
4. Migrations of individuals.
5. Recalculation of all nation policies.
6. Strengthening small nations.
7. Merging nations.
8. Selection to the mating pool.
9. Applying genetic operators (crossover, mutation).
10. Fitness calculation for all obtained offspring.
11. If the stop condition is fulfilled, then goto step 12, otherwise goto step 4.
12. Stop the algorithm.

To implement processes of migration of individuals and merging of nations the HVF is used. This function determines the positional relationship of two selected individuals, in fact of points encoded by these individuals. HVF returns TRUE if these points are located in the neighborhoods of different maxima (there is a "valley" in the fitness function landscape between the points). HVF returns FALSE if these points are located in the neighborhood of the same maximum (there is a "hill" in the fitness function landscape between the points).

The idea of the HVF is as follows. A set of points disposed on the line connecting two test points is generated; to calculate these intermediate points a predefined array *gr* is used. If fitness of all intermediate individuals is not less than fitness of the worst of the test individuals, these

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test individuals are considered to be located around the same maximum (the HVF returns FALSE); otherwise they are considered to be located around different maxima (the HVF returns TRUE).

The $F_{c\_h\_v}$ computation scheme proposed in [14, 15] is given below.

1. Put $i = 1$; *found* = FALSE.
2. If $i \le K$ and *found* == FALSE, then goto step 3 (intermediate point calculation); otherwise goto step 6.
3. For each j from 1 to n do: $p_i^j = p_0^j + (p_{K+1}^j - p_0^j) * gr_i$.
4. If $f(s_i) < \min(f(s_0), f(s_{K+1}))$, then put *found* = TRUE.
5. Put $i = i+1$.
6. Return *found*.

For example, let n=2 and gr=[0.25, 0.5, 0.75]. Then, to determine the relative position of points (0, 1) and (1, 2), the intermediate points (0.25, 1.25), (0.5, 1.5) and (0.75, 1.75) will be analyzed by the algorithm above.

In [15] the array [0.25, 0.5, 0.75] is used to ensure the migration process, and the array [0.02, 0.25, 0.5, 0.75, 0.98] is used to ensure the merging process. The extension of the sample array by two extra points is explained by the fact that merging subpopulations is more drastic operation than migration of an individual from one nation to another.

3 MATERIALS AND METHODS

In some cases the $F_{c\_h\_v}$ return values are wrong. Let us consider functions F_1 and F_2 of dimension 1, see Section 4, and determine the positional relationship of the points 0.13 and 0.97 by the $F_{c\_h\_v}$, gr=[0.02, 0.25, 0.5, 0.75, 0.98]. Notice that each of the functions has five peaks and test points are located on the first and the fifth peaks with respect to the left-to-right peak numeration alongside the X-axis. But $F_{c\_h\_v}$(0.13, 0.97)=FALSE. This means that points 0.13 and 0.97 are in the neighborhood of the same peak according to $F_{c\_h\_v}$. Table 1 provides F_1 and F_2 values at the test and intermediate points.

Table 1 – Values of F_1 and F_2 at the points analyzed by HVF

i	p_i	F_1	F_2
0	0.13	0.50036	0.49939
1	0.1468	0.16654	0.16575
2	0.34	0.28038	0.24749
3	0.55	0.125	0.08061
4	0.76	0.04124	0.01605
5	0.9532	0.09102	0.01881
6	0.97	0.00876	0.00170

The first proposed HVF modification $F_{m\_h\_v}$ is the following. Test points are considered to be located in the neighborhood of the same maximum if, moving along the list $<p_0, p_1, p_2,\ldots, p_K, p_{K+1}>$ from p_i to p_{i+1}, $0 \le i \le K+1$, fitness changes of individuals encoding these points conform to one of the rules below:

– from a smaller value to a bigger one;

– from a bigger value to a smaller one;

– from a smaller value to a bigger one and again to a smaller value.

Test points are considered to be located in the neighborhoods of different maxima in all other cases.

As an example, let test points p_0, p_{K+1} such that $f(s_0)$=2 and $f(s_{K+1})$=1 be given. The above modification considers these points as points located around the same maximum if the list of fitness values <2, 3, 4, 5, 7, 3, 1> is analyzed, and as points located around different maxima if the list of fitness values <2, 3, 5, 3, 7, 4, 1> is analyzed.

It is readily seen that $F_{m\_h\_v}$ returns correct value for the above example defined for F_1 and F_2 test functions: $F_{m\_h\_v}$(0.13, 0.97)=TRUE.

Assume that all the points (test as well as intermediate) are related to individuals of equal fitness. Notice that in this case the $F_{c\_h\_v}$ treats test points as being located around the same maximum (assuming a plateau), and the $F_{m\_h\_v}$ treats them as being located around different maxima (assuming existence of neighbor peaks). In general, the presence of plateaus in the fitness function landscape should be avoided since in this case GA can not compare individuals properly.

There exist cases when both $F_{c\_h\_v}$ and $F_{m\_h\_v}$ return wrong values. For instance, points 0.09 and 0.91 lie on different peaks of functions F_1 and F_2 of dimension 1, but they are in the neighborhood of the same peak according to both $F_{c\_h\_v}$ and $F_{m\_h\_v}$ when gr=[0.02, 0.25, 0.5, 0.75, 0.98] is used: $F_{c\_h\_v}$(0.09, 0.91)=FALSE and $F_{m\_h\_v}$(0.09, 0.91)=FALSE. Table 2 provides F_1 and F_2 values at the test and intermediate points. The F_1 graph with circles designating all target points is given in Fig. 1.

Table 2 – Values of F_1 and F_2 at the points analyzed by HVF

i	p_i	F_1	F_2
0	0.09	0.92837	0.92817
1	0.1064	0.97009	0.97000
2	0.2950	0.98165	0.90403
3	0.5	1.0	0.70711
4	0.705	0.98165	0.44425
5	0.8936	0.97009	0.24794
6	0.91	0.92837	0.22414

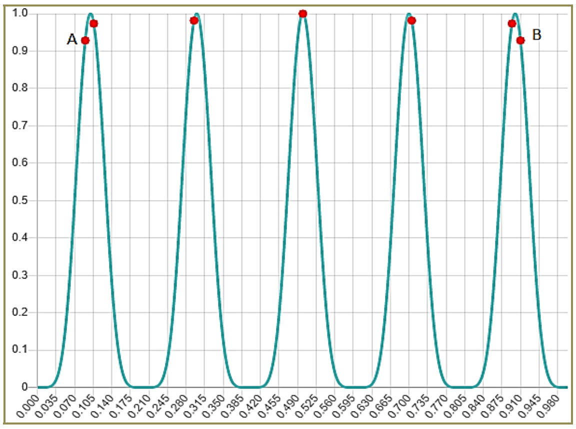

Figure 1 – Graph of F_1 with points from Table 2

The second proposed HVF modification $F_{m\_h\_v\_rand}$ is to add random values ξ_1, ξ_2 to the sample array gr=[0.25, 0.5, 0.75]; these random values should be generated at each iteration of the algorithm. Such a dynamic array re-

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duces the probability of wrong values returned by the $F_{m\_h\_v}$ as far as different sets of intermediate points may be used for two test points. In particular, in the example above there could be generated the sample array *gr*=[0.25, 0.35, 0.5, 0.6, 0.75] ensuring the $F_{m\_h\_v}$ correct return value. Table 3 provides F_1 and F_2 values at the test and intermediate points. The F_1 graph with circles designating all target points is given in Fig. 2.

Table 3 – Values of F_1 and F_2 at the points analyzed by HVF

i	p_i	F_1	F_2
0	0.09	0.92837	0.92817
1	0.295	0.98165	0.90403
2	0.377	0.00195	0.00165
3	0.5	1	0.70711
4	0.582	0.00047	0.00029
5	0.705	0.98165	0.44425
6	0.91	0.92837	0.22414

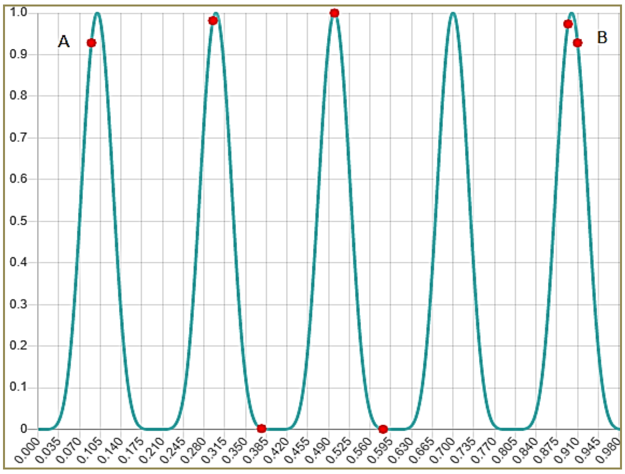

Figure 2 – Graph of F_1 with points from Table 3

Preliminary tests revealed significant differences in the $F_{c\_h\_v}$, $F_{m\_h\_v}$ and $F_{m\_h\_v\_rand}$ responses. The statistics of these function calls for one MNGA run on the F_1 test function is shown in Table 4. Following sections provide the benchmarking of the MNGA with $F_{c\_h\_v}$, $F_{m\_h\_v}$ and $F_{m\_h\_v\_rand}$.

Table 4 – Differences in responses of $F_{c\_h\_v}$, $F_{m\_h\_v}$, $F_{m\_h\_v\_rand}$ for one MNGA run on F_1

Number of different responses for:	*n*=1	*n*=3
$F_{c\_h\_v}$ and $F_{m\_h\_v}$	2 616	1 020 942
$F_{c\_h\_v}$ and $F_{m\_h\_v\_rand}$	1 900	1 114 164
$F_{m\_h\_v}$ and $F_{m\_h\_v\_rand}$	872	253 978
Total number of HVF calls:	23 265	5 209 793

4 EXPERIMENTS

Recall that in this paper the experimental analysis of performance of the MNGA and its modifications is used. Thus, test problems and performance criteria should be defined.

Test suite of benchmark functions used in this research is given below.

1) Equal Maxima function (Deb's 1):

$$y = F_1(x_1, x_2, ..., x_n) = \frac{1}{n}\sum_{i=1}^{n}\sin^6(5\pi x_i),$$

$$0 \le x_i \le 1,\ i = \overline{1,n}.$$

The function has 5^n equally spaced global maxima.

2) Decreasing Maxima function (Deb's 2):

$$y = F_2(x_1, x_2, ..., x_n) = \sum_{i=1}^{n} e^{-2(\ln 2)\left(\frac{x_i - 0.1}{0.8}\right)^2}\sin^6(5\pi x_i),$$

$$0 \le x_i \le 1,\ i = \overline{1,n}.$$

The function has 5^n equally spaced maxima of different heights.

3) Uneven Maxima Function (Deb's 3):

$$y = F_3(x_1, x_2, ..., x_n) = \frac{1}{n}\sum_{i=1}^{n}\sin^6(5\pi(x_i^{0.75} - 0.05)),$$

$$0 \le x_i \le 1,\ i = \overline{1,n}.$$

The function has 5^n global maxima that are at different distances from each other, and the distance between the points of maximum increases with increasing value of the argument.

4) Uneven Decreasing Maxima function (Deb's 4):

$$y = F_4(x_1, x_2, ..., x_n) =$$

$$= \sum_{i=1}^{n} e^{-2(\ln 2)\left(\frac{x_i - 0.08}{0.854}\right)^2}\sin^6(5\pi(x_i^{0.75} - 0.05)),$$

$$0 \le x_i \le 1,\ i = \overline{1,n}.$$

The function has 5^n maxima of different heights that are at different distances from each other, and the distance between the points of maximum increases with increasing value of the argument.

5) Six-Hump Camel Back function:

$$y = F_5(x_1, x_2) =$$

$$= -\left(\left(4 - 2.1x_1^2 + \frac{x_1^4}{3}\right)x_1^2 + x_1x_2 + 4(x_2^2 - 1)x_2^2\right),$$

$$-3 \le x_1 \le 3,\ -2 \le x_2 \le 2.$$

The function has 2 global and 4 local maxima.

6) Griewangk's function is considered in the following form:

$$y = F_6(x_1, x_2, ..., x_n) = n - \left(\sum_{i=1}^{n}\frac{x_i^2}{4000} - \prod_{i=1}^{n}\cos\left(\frac{x_i}{\sqrt{i}}\right) + 1\right),$$

$$-600 \le x_i \le 600,\ i = \overline{1,n}.$$

The function has 1 global and many local maxima, and the height of the local maxima decreases with increasing distance from the global maximum.

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7) Rastrigin's function is considered in the following form:

$$y = F_7(x_1, x_2, \ldots, x_n) = \sum_{i=1}^{n}\left(10\cos(2\pi x_i) - x_i^2\right) - 10n\,,$$

$$-5.12 \le x_i \le 5.12\,,\ i = \overline{1,n}\,.$$

The function has 1 global and 10^n local maxima, and the height of the local maxima decreases with increasing distance from the global maximum.

8) Modified Rastrigin's function:

$$y = F_8(x_1, x_2) = -10 - 9\cos(6\pi x_1) - 10 - 9\cos(8\pi x_2)\,,$$

$$0 \le x_1, x_2 \le 1\,.$$

The function has 12 global maxima.

9) Xin-She Yang's function:

$$y = F_9(x_1, x_2, \ldots, x_n) = \left(\sum_{i=1}^{n}|x_i|\right)\exp\left(-\sum_{i=1}^{n}x_i^2\right),$$

$$-10 \le x_i \le 10\,,\ i = \overline{1,n}\,.$$

The function has several global maxima located at a small distance from each other. In particular, for n=1 the function has 2 global maxima, and for n=2 the function has 4 global maxima.

Detailed description and plots of the functions above can be found in [26, 27].

To specify the performance criteria we begin with two definitions: the algorithm stop conditions and whether the extremum is found when the algorithm stops.

GA stops if either population convergence is detected, i.e. the changes in the average population fitness value do not exceed 0.0001 over the last 10 generations, or 40000 algorithm iterations are carried out. This means that if convergence was not detected the algorithm has been terminated after the specified number of iterations. The algorithm run stopped under the convergence condition is called *successful*.

The *maximum is found* if the algorithm convergence is detected and there is at least one individual of the final population such that the individual fitness value differs from the sought maximum value at most δ and the point encoded by this individual is located within the maximum's neighborhood of radius σ. Let us set δ=0.01 and σ=0.01 for all test functions.

As stated in [28], when algorithm stops under any condition including convergence, individuals of the final population may be located not only in the small radius neighborhoods of function peaks but individuals may also form clusters on the peak slopes and even in the valleys. Thus, to analyze the algorithms, standard performance criteria are used as well as proposed in [28] *FPR* criterion that in fact estimates number of clusters formed by individuals located far from the sought maxima. Note that big value of *FPR* criterion is a significant drawback of a niching algorithm as far as it makes use of such algorithms impractical for problems of finding all (local, global) maxima.

To determine species (and, consequently, niches) formed by the final population the algorithm of [28] presented below is used; ε=0.03.

1. Put *Seeds* = Ø.
2. Choose the best unprocessed individual *s* from the population; mark it as the processed one: s^*.
3. Put *found* = FALSE.
4. If there exists an individual $s \in$ *Seeds* such that $d(s^*, s) \le \varepsilon$, then put *found* = TRUE; otherwise, create a new species with the best individual s^*: put $Seeds = Seeds \cup \{s^*\}$.
5. If unprocessed individuals are remained in the population, then goto step 2.

To separate real species from the fake ones the elements from *Seeds* should be compared with real peaks of the fitness function using parameters δ and σ.

The criteria calculated for each run of the algorithm are the following ones: *NSeeds*, *NP*, *GP*, *LP*, *PR*, *GPR*, *LPR*, *FPR*. Note that $NP = GP + LP$, $0 \le PR \le 1$, $0 \le GPR \le 1$, $0 \le LPR \le 1$, $0 \le FPR \le 1$. The *FPR* criterion is calculated as $FPR = \frac{NSeeds - NP}{NSeeds}$.

For algorithm analysis average values of the *PR*, *GPR*, *LPR*, *FPR* criteria are computed over all runs as well as the *SucRuns* criterion; the *SucRuns* is computed as the ratio of the number of successful runs to the total number of runs, in percent. Criterion values of unsuccessful runs are not used to calculate averages; recall that the unsuccessful runs are the runs stopped under the condition of reaching maximum iteration number.

The software implementation of the MNGA with the classic HVF and its both modifications was developed. The criteria above were computed with the following purposes. First, to tune the parameters of the MNGA with $F_{c\_h\_v}$. Secondly, to conduct comparative analysis of the MNGA with $F_{c\_h\_v}$, $F_{m\_h\_v}$ and $F_{m\_h\_v\_rand}$.

To calculate averages of the criteria above there were conducted 10 runs of the algorithm for each set of parameter values and for each benchmark problem. Note that the initial population is the same for all sets of parameter values at the *i*-th run; this guarantees the same start point for corresponding runs of the algorithms using different sets of parameter values.

The authors of this research tried to follow the [14, 15] recommendations on setting the algorithm parameter values. If such recommendations were not provided in [14, 15], the algorithm parameter values have been set based on the authors' experience or by conducting experiments. The predefined MNGA parameter values used in this research are listed below.

– Number of individuals in the population: 500.

– Number of individuals in the government: 8.

– Array to implement migration of individuals and merging of nations:

  – [0.02, 0.25, 0.5, 0.75, 0.98] for functions $F_{c\_h\_v}$ and $F_{m\_h\_v}$;

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– [0.25, 0.5, 0.75]∪ $\{\xi_1, \xi_2\}$ for function $F_{m\_h\_v\_rand}$.

In [15], small nations are strengthened by the nation policy mutants, i.e. by addition of a small noise to the policy of the nation. To reduce the algorithm computation complexity the zero noise is used in our research, i.e. small nations are supported by copies of their policies. Since there is no information in [14, 15] about nations to be small or large, we define the small nation as a nation with population size less than 30% of the average number of individuals per nation at the current algorithm iteration, and the large nation as a nation with population size exceeding 50% of the average number of individuals per nation at the current algorithm iteration. This implies that the number of policy copies strengthening a small nation ensures population size of this nation to be not less than 30% of the average number of individuals per nation at the current algorithm iteration.

Let us remark that step 5 of the MNGA (the recalculation of all nation policies) is not specified in [14, 15]. We have added this step to ensure the use of actual nation policies while strengthening small nations and merging nations.

Further on, the following MNGA parameter values are analyzed experimentally.

– Encoding methods: real numbers and Gray codes encoding sample points to three decimal places. Notice that binary codes are used in [14] and real numbers are used in [15].

– Selection to the mating pool: the weighted selection, the national selection and the mixed selection. For mixed selection 50% of individuals are selected using weighted selection and 50% of individuals are selected using national selection [15].

– Genetic operators used for binary encoding are one–point crossover and density mutation. The analyzed values of P_c are 0.6, 0.8, 0.9 and 1. The analyzed values of P_m are 0.001, 0.01 and 0.025. In [14] values P_c=0.9 and P_m=0.025 are recommended. Gaussian density mutation is the only genetic operator used for encoding in real numbers, P_m=1 [15]. In this case noise determined by standard normal distribution is added to each gene encoded variable.

Generally, 39 parameter sets are analyzed in this research.

For MNGA parameter tuning the F_1–F_4 functions are used. These functions have different properties, e.g. existence of only global maxima (F_1, F_3) or global and local maxima (F_2, F_4), location of the maxima at equal (F_1, F_2) or at different (F_3, F_4) distances from each other. Therefore, Deb's benchmark functions are widely used for experimental analysis of algorithms solving MMOPs. Having regard to the function properties two test suites for parameter tuning are composed:

– T1 includes functions F_2 and F_4 having one global and many local maxima;

– T2 includes functions F_1 and F_3 having many global and no local maxima.

5 RESULTS

The convergence of the MNGA with $F_{c\_h\_v}$ was not observed for any parameter set using binary codes; experiments were conducted for both T1 and T2 test suites. Therefore, parameter sets with binary codes were excluded from further analysis.

Results obtained for real number encoding and Gaussian density mutation, P_m=1, are given in Table 5. It is easy to see from the table that the percentage of successful runs is poor in most cases. Moreover, it is worthwhile to consider only national selection method as far as $\mathrm{MNGA}^{w}_{c\_h\_v}$ converges only when n=1 while for $\mathrm{MNGA}^{m}_{c\_h\_v}$ the *SucRuns* criterion value is close to 0%.

We assume that proposed HVF modifications return wrong values more rarely in comparison with $F_{c\_h\_v}$; thus, using $F_{m\_h\_v}$ or $F_{m\_h\_v\_rand}$ instead of $F_{c\_h\_v}$ should improve the overall performance of the MNGA. With regard to above, the MNGA runs for classic HVF and its modifications were conducted using national selection method; results obtained for test suites T1 and T2 are given in Table 6. It is easy to see from the table that using HVF modifications gives higher percentage of successful runs for test suite T1, but decreases this percentage for test suite T2. Anyway, the *SucRuns* criterion value is still poor in most cases.

Assuming that another selection method tuned for appropriate HVF modification could improve the MNGA performance, the MNGA runs for different HVFs and different selection methods were conducted; both T1 and T2 test suites were used. Experiments have shown the thorough improvements of algorithm convergence. In particular, best results of *SucRuns* criterion were achieved by the $\mathrm{MNGA}^{w}_{m\_h\_v}$ (98.33%) and $\mathrm{MNGA}^{w}_{m\_h\_v\_rand}$ (91.67%) on T1 test suite (functions having one global and many local maxima), and by the $\mathrm{MNGA}^{m}_{m\_h\_v}$ (100%) and $\mathrm{MNGA}^{w}_{m\_h\_v\_rand}$ (100%) on T2 test suite (functions having many global and no local maxima). On the other hand, the quality criteria become worse with increasing the convergence criterion value, in particular, the *PR* criterion value decreased 1.7–8.6 times. Supporting data (averages computed over all runs for functions F_1–F_4) are provided in Table 7. Note that computation of averages over all benchmark functions makes sense as far as the function surfaces are not known in advance for most practical problems.

We have also developed the software implementation of the SCGA [29] intending to analyze this algorithm and to develop its hybridization with the MNGA; this seems to be a promising area [16, 17]. Parameter tuning conducted for this algorithm led to the following parameter values: SUS selection, one-point mutation, P_m=0.01, no crossover, Euclidean distance, σ_s=0.2. Experimental analysis of the SCGA with mentioned parameter values was conducted for functions F_1–F_4; results are given in Table 7. It is obvious from the table that though the SCGA provides satisfactory percentage of the algorithm convergence the quality parameter values of this algorithm are poor.

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Table 5 – Results of experiments: MNGA with classic HVF

Parameters	Test suite T1						Test suite T2			
Selection method	Criteria: average values over 10 runs					Comment	Criteria: average values over 10 runs			Comment
	SucRuns	*PR*	*GPR*	*LPR*	*FPR*		*SucRuns*	*PR=GPR*	*FPR*	
Weighted	31.67%	0.2	0	0.25	0	Convergence only if n=1	16.67%	1	0	Convergence only if n=1
National	45%	0.0898	0.4444	0.0749	0.7567		93.33%	0.5051	0.4287	
Mixed	0%						2%	0.9667	0.0040	Convergence only for F_1, if n=1 or n=2

Table 6 – Results of experiments: MNGA with classic HVF and its modifications

Algorithm	Test suite T1					Test suite T2		
	Criteria: average values over 10 runs					Criteria: average values over 10 runs		
	SucRuns	*PR*	*GPR*	*LPR*	*FPR*	*SucRuns*	*PR=GPR*	*FPR*
$\text{MNGA}^{n}_{c\_h\_v}$	45%	0.0898	0.4444	0.0749	0.7567	93.33%	0.5051	0.4287
$\text{MNGA}^{n}_{m\_h\_v}$	63.33 %	0.6158	0.5790	0.6173	0.4173	68.33%	0.6092	0.4361
$\text{MNGA}^{n}_{m\_h\_v\_rand}$	63.33 %	0.5737	0.6053	0.5680	0.3542	53.33 %	0.79	0.1919

Table 7 – Results of experiments: MNGA with classic HVF and its modifications, SCGA, TCGM_S2; functions F_1–F_4

Algorithm	Criteria: average values over all runs					Comment
	SucRuns	*PR*	*GPR*	*LPR*	*FPR*	
$\text{MNGA}^{n}_{c\_h\_v}$	69.17%	0.3700	0.4854	0.0749	0.5354	
$\text{MNGA}^{n}_{m\_h\_v}$	65.83%	0.6124	0.5946	0.6173	0.4270	
$\text{MNGA}^{n}_{m\_h\_v\_rand}$	58.33 %	0.6726	0.6897	0.5680	0.280	
$\text{MNGA}^{m}_{m\_h\_v}$	99.17%	0.1904	0.1799	0.0863	0.4622	
$\text{MNGA}^{w}_{m\_h\_v\_rand}$	95.83 %	0.1908	0.2023	0.0735	0.2783	
SCGA	90.83%	0.2680	0.4481	0.025	0.6773	
TCGM_S2	100%	0.9563	0.8908	0.4744	0.1538	see [28]

6 DISCUSSION

From the Table 6 it follows that using HVF modifications improves the performance of the MNGA solving optimization problems for functions having global and local maxima. Indeed, the *SucRuns* increased by nearly 41%, the *PR* increased nearly 6.86 times for $F_{m\_h\_v}$ and 6.39 times for $F_{m\_h\_v\_rand}$ (mainly due to the greater number of local peaks found), the *FPR* decreased significantly, to be exact by 55% for $F_{m\_h\_v}$ and by 47% for $F_{m\_h\_v\_rand}$. Let us remark that $F_{m\_h\_v\_rand}$ gives better results in comparison with $F_{m\_h\_v}$ in terms of *GPR* and *FPR*, but worse results in terms of *LPR*. Fig. 3 illustrates the forgoing via a histogram.

Now let us analyze the influence of $F_{m\_h\_v}$ and $F_{m\_h\_v\_rand}$ on performance of the MNGA solving optimization problems for functions having only global maxima. From the Table 6 we see that *SucRuns* decreased considerably, namely by 27% for $F_{m\_h\_v}$ and by 43% for $F_{m\_h\_v\_rand}$. At the same time, the *PR* increased by 21% for $F_{m\_h\_v}$ and by 56% for $F_{m\_h\_v\_rand}$. Note that $F_{m\_h\_v\_rand}$ gives better results in comparison with $F_{m\_h\_v}$ in terms of *GPR* and *FPR*, but provides worse algorithm convergence. Fig. 4 illustrates the forgoing via a histogram.

Consequently, the performance improvement of the MNGA using HVF modifications can be observed when the objective function has global and local maxima. If the objective function has only global maxima, the quality criteria improvement is accompanied by the decrease of the convergence criterion value.

Let us consider other test functions. Functions F_8 and F_9 have only global maxima. Experiments conducted for these functions of dimensions 1 and 2 showed 100% of convergence and *GPR* value close to 1 for all three kinds of the algorithm: $\text{MNGA}^{n}_{c\_h\_v}$, $\text{MNGA}^{n}_{m\_h\_v}$, $\text{MNGA}^{n}_{m\_h\_v\_rand}$.

Functions F_5, F_6 and F_7 have global and local maxima. Experiments conducted for functions F_5 of dimension 2 and F_7 of dimensions 1, 2 and 3 revealed the advantage of modified HVFs over classic HVF in terms of *PR* (mainly due to the greater number of local peaks found). However, modified HVFs provide worse algorithm convergence. Function F_6 is defined on the wide range of argument values; therefore, to find maxima of F_6 the population size parameter of the MNGA was increased to 1000 individuals. Experiments were conducted for function F_6 of dimensions 1, 2 and 3. The $\text{MNGA}^{n}_{m\_h\_v}$ algorithm demonstrated significantly better results both in terms of convergence and quality of found solutions: *SucRuns*=90% for $\text{MNGA}^{n}_{m\_h\_v}$ and *SucRuns*=50% for $\text{MNGA}^{n}_{c\_h\_v}$, *GPR*=0.4074 for $\text{MNGA}^{n}_{m\_h\_v}$ and *GPR*=0.2667 for $\text{MNGA}^{n}_{c\_h\_v}$.

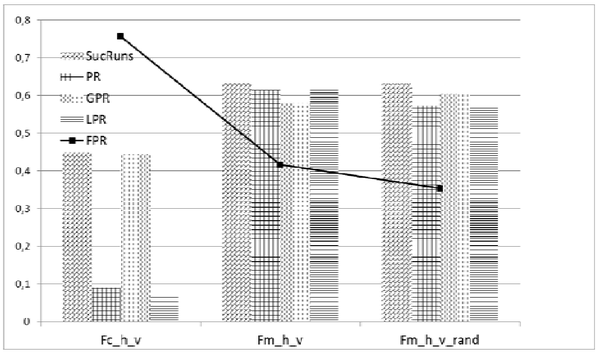

Figure 3 – Histogram with criteria values obtained for MNGA using different HVFs, test suite T1

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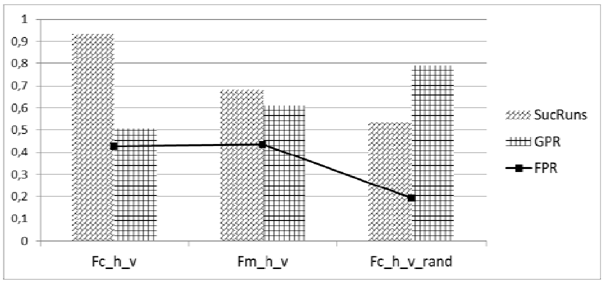

Figure 4 – Histogram with criteria values obtained for MNGA using different HVFs, test suite T2

From the stated above it can be concluded that MNGA$^{n}_{m\_h\_v}$ performance is either close to the performance of MNGA$^{n}_{c\_h\_v}$ or is better in terms of *PR*; at the same time improvements in *PR* are accompanied by the decrease of *SucRuns* for some functions. This is also the case for the MNGA$^{n}_{m\_h\_v\_rand}$, though MNGA$^{n}_{m\_h\_v\_rand}$ often gives worse results than the MNGA$^{n}_{m\_h\_v}$, especially in terms of convergence.

By analyzing data from Table 7 providing benchmarking results for functions F_1–F_4 we can state that generally all kinds of MNGA studied in this research are unacceptable for practical use as far as they are characterized either by low value of convergence criterion (that is less than 90%) or by low ratio of real peaks and high ratio of fake peaks found by the algorithm. This is also true for other test functions. As for F_9, there are observed *SucRuns*=100% and *GPR* value close to 1 for all kinds of MNGA. This can be explained by the specific surface of F_9: the function curve is a plateau with four peaks close to each other. Such a surface is a challenge for most optimization algorithms but turned to be solvable for MNGA.

Note that all experiments in our study are conducted for test functions of small dimensions ($1 \le n \le 3$). The reason is the long algorithm execution time caused by a number of factors including the low convergence percentage. For example, the MNGA$^{n}_{m\_h\_v}$, MNGA$^{w}_{m\_h\_v}$, MNGA$^{m}_{m\_h\_v}$ running time to find optimums of F_5–F_9 took about 48 hours. The computer configuration used to run these algorithms was the following: processor Intel(R) Core(TM) i5-7200U CPU @ 2.50GHz 2.71 GHz; 8.00 GB RAM (7.88 GB available); 64-bit Windows 10 operating system, x64 processor, 2 cores, 4 logic processors.

CONCLUSIONS

In this paper, the MNGA parameter tuning was carried out and experimental analysis of the MNGA performance was conducted. Two modifications of the HVF used to determine the relative position of individuals were proposed. Benchmarking of MNGA with classic HVF and with its modifications was carried out. Experiments showed that proposed modifications had increased the number of real extrema found by the algorithm for most test functions. Stated above determines the **scientific novelty** of the obtained results.

The practical significance of the obtained results lies in the following statements.

– First, as HVF modifications produce less number of wrong basin identifications in comparison with classic HVF, it is recommended to use $F_{m\_h\_v}$, $F_{m\_h\_v\_rand}$ in other GAs using HVF [16–25].

– Secondly, as the overall performance of MNGA is poor in comparison with other known GAs, the MNGA is not recommended for practical use.

Indeed, GAs solving multimodal optimization problems, i.e. the problems of finding several optimums, contribute to grouping individuals of final population into species so that the best individual of each species represents one of the sought optimums. Obviously, it is worthwhile to analyze groups of individuals only in case of GA convergence. Generally, the number and location of function optimums are not known a priory for practical problems. It is known, that individuals of the GA final population may be located in the neighborhoods of function peaks as well as far from them, clustering on peak slopes or even in the valleys. Therefore, to choose an algorithm to solve practical MMOPs, in particular problems of finding global and local peaks, it is important to analyze criteria representing number of real peaks found by the algorithm as well as number of fake species formed by the algorithm. These are the *PR, GPR, LPR* and *FPR* criteria.

Experimental analysis of the MNGA with both classic HVF and its modifications has revealed the unacceptably low value of the convergence criterion (*SucRuns*<90%) and unacceptable for practical use values of the quality criteria, i.e. small values of *PR*, *GPR*, *LPR* accompanied by the high value of the *FPR*. Generally, depending on algorithm parameter values there is observed either improvement of quality criteria values accompanied by the worse algorithm convergence or higher convergence percentage accompanied by deterioration of quality criteria values. Note that quality parameter values of the SCGA algorithm developed for farther hybridization [16, 17] with MNGA are also poor. Let us remark that in [28] there was proposed TCGM_S2 algorithm; criterion values computed in [28] for this algorithm are given in Table 7. It is readily seen that this algorithm provides better criterion values in terms of convergence percentage as well as in terms of quality of the solutions found. Thus it is reasonable to say that it is impractical to use MNGA to find global and local optima of a multimodal function. On the other hand, hybridizations of MNGA with other algorithms could be an option.

Let us remark that there still exist situations when $F_{m\_h\_v}$, $F_{m\_h\_v\_rand}$ return wrong values. Let us consider function F_1 and sample array *gr*=[0.02, 0.25, 0.5, 0.75, 0.98] from [15]. Points 0.0 and 1.0 are wrongly attributed to the same basin of attraction by both $F_{c\_h\_v}$ and $F_{m\_h\_v}$; return value of $F_{m\_h\_v\_rand}$ is wrong with a certain probability. To overcome this, modifications of $F_{m\_h\_v}$ can be proposed. Modifications regarding a method to construct sequences of sample points are an option. Several of these were proposed in [18–20, 24, 30], e.g. replacement of equidistant test points by a golden section search or changing quantity of test points dependent on the distance between individuals.

In [14] it is stated that MNGA forms only one subpopulation in the neighborhood of every peak. Preliminary experiments have shown that using HVF to determine species (niches) formed by the final population instead of the algorithm used in this research (the algorithm from [28]) gives better results in terms of *FPR*. At the same time *SucRuns*, *PR*, *GPR* and *LPR* criteria values obviously stay the same. We believe it is worth to conduct benchmarking of different niching GAs using HVF or its modifications as the algorithm to determine species (or, equivalently, as a post-processing step for every algorithm after its convergence).

Thus, we see two main **directions for further research:** improvements of the HVF and using HVF as a post-processing step for other niching GAs. This will be the object of another paper.

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ЕКСПЕРИМЕНТАЛЬНИЙ АНАЛІЗ БАГАТОНАЦІОНАЛЬНОГО ГЕНЕТИЧНОГО АЛГОРИТМУ ТА ЙОГО МОДИФІКАЦІЙ

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АНОТАЦІЯ

Актуальність. Генетичні алгоритми утворення ніш є одним з найпоширеніших підходів до розв'язання задач багатоекстремальної оптимізації. При проведенні класифікації цих алгоритмів можна виділити алгоритми, що ґрунтуються на явному аналізі топографії ландшафту функції пристосованості. Одним з ранніх прикладів таких алгоритмів є багатонаціональний генетичний алгоритм.

Мета. Розробка та аналіз багатонаціонального генетичного алгоритму та його модифікацій. Алгоритм застосовується для розв'язання задачі пошуку всіх максимумів багатоекстремальної функції.

Метод. Виконано експериментальний аналіз алгоритмів. Проведено численні прогони алгоритмів на відомих тестових задачах та обчислено критерії ефективності роботи алгоритмів, а саме, відсоток збіжності, частка реальних (глобальних, локальних) та хибних піків; зауважимо, що частки піків обчислюються тільки в разі збіжності алгоритму.

Результати. Виконано програмну реалізацію багатонаціонального генетичного алгоритму та проведено експериментальне налаштування його параметрів. Запропоновано дві модифікації функції долин і пагорбів, яка використовується в алгоритмі для визначення взаємного розташування особин. Проведено експериментальний аналіз багатонаціонального генетичного алгоритму з класичного функцією долин і пагорбів та з її модифікаціями.

Висновки. Наукова новизна роботи полягає в тому, що були запропоновані модифікації функції долин і пагорбів, які продукують меншу кількість помилкових ідентифікацій зон притягання порівняно з класичним варіантом цієї функції. Як наслідок, використання цих модифікацій призводить до покращення продуктивності багатонаціонального генетичного алгоритму для низки тестових задач. Втім, для деяких тестових задач поліпшення критеріїв якості супроводжується зменшенням відсотка збіжності. Загалом, відсоток збіжності та значення критеріїв якості, продемонстровані дослідженим алгоритмом, є недостатніми для практичного використання багатонаціонального генетичного алгоритму у порівнянні з іншими відомими алгоритмами. У той же час, використання модифікованих функцій долин і пагорбів як етапу постобробки в інших алгоритмах утворення ніш видається перспективним підходом до покращення роботи цих алгоритмів.

КЛЮЧОВІ СЛОВА: задача багатоекстремальної оптимізації, генетичні алгоритми утворення ніш, багатонаціональний генетичний алгоритм, функція долин і пагорбів, збіжність генетичного алгоритму, частка реальних піків, частка хибних піків.

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ЭКСПЕРИМЕНТАЛЬНЫЙ АНАЛИЗ МНОГОНАЦИОНАЛЬНОГО ГЕНЕТИЧЕСКОГО АЛГОРИТМА И ЕГО МОДИФИКАЦИЙ

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АННОТАЦИЯ

Актуальность. Генетические алгоритмы образования ниш являются одним из самых распространенных подходов к решению задач многоэкстремальной оптимизации. При проведении классификации генетических алгоритмов образования ниш можно выделить алгоритмы, основанные на явном анализе топографии ландшафта функции приспособленности. Многонациональный генетический алгоритм является одним из ранних примеров таких алгоритмов.

Цель. Разработка и анализ многонационального генетического алгоритма и его модификаций. Алгоритм применяется для решения задачи поиска всех максимумов многоэкстремальной функции.

Метод. Выполнен экспериментальный анализ алгоритмов. Проведены многочисленные прогоны алгоритмов на известных тестовых задачах и вычислены критерии эффективности работы алгоритмов, а именно, процент сходимости, доля реальных (глобальных, локальных) и ложных пиков; отметим, что доля пиков вычисляется только в случае сходимости алгоритма.

Результаты. Выполнена программная реализация многонационального генетического алгоритма и проведена экспериментальная настройка его параметров. Предложены две модификации функции холмов и долин, используемой в алгоритме для определения взаимного расположения особей. Выполнен экспериментальный анализ многонационального генетического алгоритма с классической функцией холмов и долин и с ее модификациями.

Выводы. Научная новизна работы состоит в том, что были предложены модификации функции холмов и долин, приводящие к меньшему количеству неправильных определений зон притяжения по сравнению с классическим вариантом этой функции. Как следствие, использование этих модификаций приводит к повышению производительности многонационального генетического алгоритма для ряда тестовых задач. Однако для некоторых тестовых задач улучшение критериев качества сопровождается уменьшением процента сходимости. В целом, процент сходимости и значения критериев качества, продемонстрированные исследуемым алгоритмом, недостаточны для практического использования многонационального генетического алгоритма по сравнению с другими известными алгоритмами. В то же время, использование модифицированных функций холмов и долин в качестве шага постобработки в других алгоритмах образования ниш представляется многообещающим подходом к улучшению производительности этих алгоритмов.

КЛЮЧЕВЫЕ СЛОВА: задача многоэкстремальной оптимизации, генетические алгоритмы образования ниш, многонациональный генетический алгоритм, функция холмов и долин, сходимость генетического алгоритма, доля реальных пиков, доля ложных пиков.

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