

*Dedicated to Professor Iulian Coroian on the occasion of his 70<sup>th</sup> anniversary*

## **Complex dynamics in a collaborative evolutionary search model**

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**ABSTRACT.** The distributed collaborative evolutionary model analyzed in this paper is characterized by structuring the population using a fitness guided topology and by assigning the individuals to three societies characterized by different mating strategies. The membership of offsprings to societies is decided in a probabilistic manner using a dominance probability. The influence of this dominance probability on the dynamics of societies sizes is analyzed both empirically and theoretically. Consequently, values of the dominance probability leading to particular distributions of the population elements in societies are identified. Numerical experiments indicate a good performance of the proposed model.

### 1. INTRODUCTION

Using structured populations in evolutionary algorithms has at least two motivations: improving the algorithm effectiveness in global, multimodal and dynamic optimization and designing efficient implementations based on parallel and/or distributed environments [1].

The model analyzed in this paper is characterized through a particular topology and a mating strategy inspired by the communication processes typical to systems consisting of multiple agents [10]. The particularity of the topology consists in distributing the elements of the population in several layers based on their current fitness. The interaction between elements is based not only on the neighborhood structure defined by layers but also on the distribution of the elements in three different subpopulations characterized by different mating strategies.

A first empirical analysis of the behavior of this distributed model which combines a geometrical fitness guided topology with the existence of societies having different interaction strategies was conducted in [3].

The aim of this paper is to analyze in more depth the dynamics of the societies, especially with respect to the value of the dominance probability. The analysis reveals that societies of individuals form a complex system characterized by an emergent pattern of behavior and a phase transition interval.

Numerical experiments prove the efficiency of the proposed technique, by comparing it with the results obtained by recent evolutionary algorithms for several difficult unimodal and multimodal real-valued functions.

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## 2. THE DISTRIBUTED COLLABORATIVE EVOLUTIONARY ALGORITHM

The distributed evolutionary model analyzed in this paper is characterized by combining two models of structuring the population. On one hand, the population is spatially structured based on a fitness guided topology and on the other hand the population is explicitly divided in three subpopulations having specific collaborative properties. Both methods of structuring the population interfere with the process of selecting mates for recombination and therefore have an influence on the population dynamics.

The main idea of the fitness guided topology is to sort the population with respect to the elements fitness and to distribute the elements in several layers such that elements which have similar values of the fitness are in the same or in neighboring layers while elements which are different with respect to their fitness are usually placed on distant layers.

This topology is used both to decide the order in which the population elements are transformed by applying the evolutionary operators and to restrict the choice of the recombination mates. The restricted mating strategy is related with the existence of three subpopulations, called societies, which are different with respect to the way their elements select and/or accept elements for recombination. The particularities of these societies are described in the following.

- *Local Interaction Agent (LIA) society.* The elements of this society select mates for recombination from their 1-order neighborhood.
- *Far Interaction Agent (FIA) society.* The elements from this society select mates for recombination outside their 1-order neighborhood.
- *Global Interaction Agent (GIA) society.* The GIA elements can select mates for recombination on a global basis from the entire population.

Besides these mating restrictions related with the fitness guided topology there can be introduced restrictions related also to the societies. This means that elements belonging to one society accepts as mates only elements belonging to some prespecified societies and the generated offspring will be assigned to the society corresponding to one of its parents, that which is considered to be dominant. Different variants can be considered here, but we restricted our analysis to the following cases: the elements in LIA (FIA) societies select mates from LIA(FIA) or from GIA society and GIA elements select mates from the entire population (global collaboration); the elements in LIA (FIA) societies select mates from LIA(FIA) or from GIA society, while GIA elements select mates only from the GIA elements (local collaboration).

If both parents belong to the same society the offspring will be assigned to the same society. On the other hand, if a parent belongs to LIA (or FIA) society and the other parent belongs to the GIA society then the offspring will belong to LIA (or FIA) society with probability  $p$  and to the GIA society with probability  $1 - p$ . This means that the dominance relationship between societies is determined in a probabilistic manner, based on the dominance probability,  $p$ . This dominance probability may be viewed as the (probabilistic) membership degree of an offspring to the society LIA (FIA) when one of the parents is a GIA individual. Different values of the dominance probability can lead to different dynamics of the

societies in the population and its influence on the search process is empirically and theoretically analyzed in Sections 3 and 4.

### 3. EMPIRICAL ANALYSIS: INFLUENCE OF DOMINANCE PROBABILITY ON THE SOCIETIES DYNAMICS

The aim of the empirical analysis is twofold: (i) to analyze the influence of the dominance probability on the dynamics of societies; (ii) to analyze the combined effect on the solutions quality of the fitness guided topology and of the restricted mating based on societies. The analysis is conducted for four variants obtained by combining the collaboration variants between societies mentioned in the previous section (global and local collaboration) with two topologies: an ordered one (the fitness guided topology) and an unordered one (the population elements are arbitrarily distributed in layers). The obtained variants are denoted as follows: OG (ordered topology combined with global collaboration), OL (ordered topology combined with local collaboration), UG (unordered topology combined with global collaboration) and UL (unordered topology combined with local collaboration).

For all these variants the underlying evolutionary algorithm is characterized by a population consisting of 64 individuals, convex recombination, a mutation based on additive normal perturbation and a selection of mates based on a tournament of size equal to half of the considered group size.

Since the aim of the empirical analysis is to study the societies dynamics rather than to assess the effectiveness of the evolutionary algorithms in solving optimization problems we limited the results reported here to three classical test functions: shifted Ackley (denoted in the following as  $f_1$ ), shifted Griewank ( $f_2$ ) and shifted Rastrigin ( $f_3$ ) and a small number of functions evaluations.

In order to study the dynamics of societies let us introduce the notion of society diameter,  $d(S) = \text{card}(S)/\text{card}(P)$  which measures the proportion of elements from the population  $P$  which belongs to the society  $S$ . Initially the elements are uniformly distributed to societies, thus their initial sizes are equal and  $d_L(0) = d_F(0) = d_G(0) = 1/3$ . The evolution of the society size is studied against the dominance probability,  $p$ , for all four variants described in the beginning of the section. Figure 1 illustrates the dependence between the societies diameters after  $T \simeq 10000/64$  evolution epochs and  $p$  for test function  $f_1$ . The graph in Figure 1 corresponds to the average of societies diameters, estimated in 10 independent runs, while the error bars illustrate the corresponding standard deviations. Similar results have been obtained for test function  $f_2$ .

In the case of the OG variant, for small values of  $p$  the GIA society manages to quickly dominate the system (all members of the population fall in this society). This is an interesting percolation phenomenon indicating that a society takes global control over the entire population. In the case of the UG variant the GIA society does not take global control. Nevertheless, the vast majority of the individuals fall in this society for small values of the dominance probability. For large values of  $p$  in both cases the LIA and FIA societies become dominant. Thus for the variants based on global collaboration a transition region of the system can

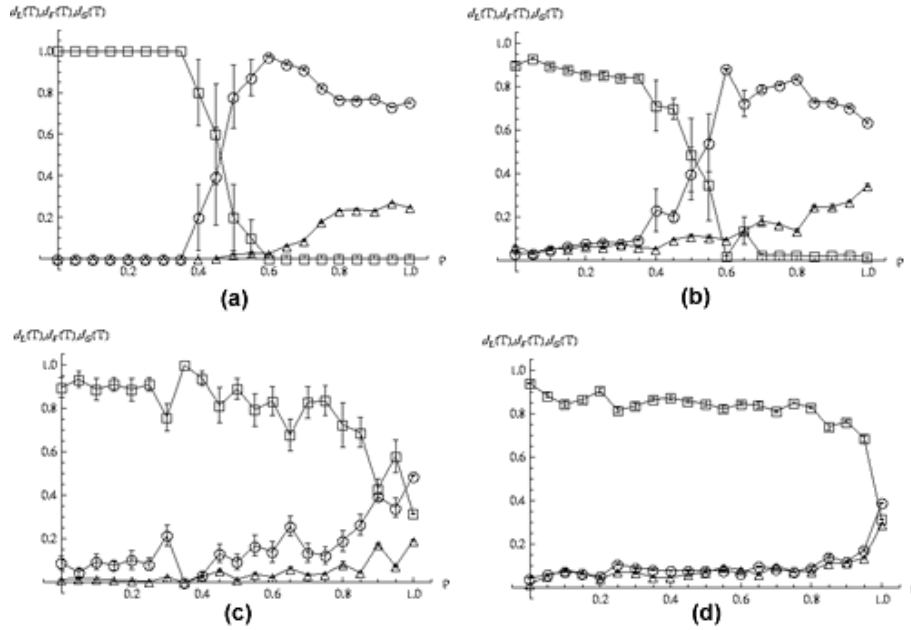


FIGURE 1. Empirical dependence between  $d_L(T)$  (circles),  $d_F(T)$  (triangles),  $d_G(T)$  (squares) and the dominance probability. Test function: shifted Ackley

be detected. This region roughly corresponds to the interval  $[0.35, 0.65]$  indicating the presence of a phenomenon similar to a phase transition.

For the other two variants, namely OL and UL, the dynamics of the three subpopulations does not reveal a similar transition interval for the dominance probability. In these cases, for almost all values of  $p$ , unless those close to 1, the GIA society is dominant. When  $p$  is close to one all societies have almost the same number of elements, arriving to an equilibrium.

Let us analyze now the influence of the dominance probability on the quality of the solution. To evaluate the quality of the solution discovered by the evolutionary algorithm we use the following measure:

$$Q(f) = \exp\left(-\left|\frac{f(x_b) - f(x^*)}{f(x^*)}\right|\right),$$

where  $x^*$  is the true optimum,  $x_b$  is the best element in the population obtained at the end of the evolutionary process and  $f$  is the objective function (for all test functions  $f(x^*) \neq 0$ ). As  $Q$  is closer to 0 as the estimated solution is worse and as it is closer to 1 the estimated solution is better. Figure 2 presents the dependence between  $Q$  and  $p$  for the first test function and for all four variants (OG,OL,UG,UL). As the graphs illustrate there is a significant difference between the behavior of the variants based on fitness guided topology and those based on unordered topologies. On the other hand  $p$  seems to have almost no influence on the solution quality except for the OG variant for which a slight improvement

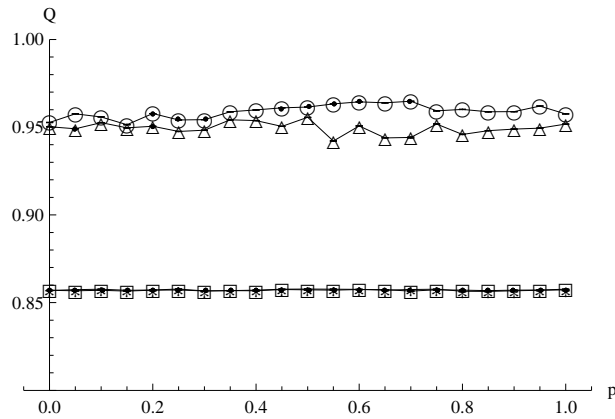


FIGURE 2. Influence of the dominance probability on the quality of solutions. Variants: OG - circles, OL - triangles, UG - squares, UL - stars

can be observed for values of  $p$  inside the transition region previously detected. A closer look to the results obtained for all three test functions (Table 1) suggest that there is a slight improvement for values of  $p$  larger than 0.4.

TABLE 1. Influence of the dominance probability,  $p$ , on the solution quality,  $Q$ , in the case of OG variant (all test functions)

$p$	$Q(f_1)$	$Q(f_2)$	$Q(f_3)$
0	0.952	0.986	0.876
	$\pm 5 \cdot 10^{-5}$	$\pm 5 \cdot 10^{-6}$	$\pm 3 \cdot 10^{-4}$
0.1	0.955	0.983	0.876
	$\pm 3 \cdot 10^{-5}$	$\pm 4 \cdot 10^{-6}$	$\pm 5 \cdot 10^{-4}$
0.2	0.957	0.984	0.872
	$\pm 2 \cdot 10^{-5}$	$\pm 7 \cdot 10^{-6}$	$\pm 5 \cdot 10^{-4}$
0.3	0.954	0.986	0.872
	$\pm 3 \cdot 10^{-5}$	$\pm 5 \cdot 10^{-6}$	$\pm 3 \cdot 10^{-4}$
0.4	0.952	0.985	0.890
	$\pm 2 \cdot 10^{-5}$	$\pm 6 \cdot 10^{-6}$	$\pm 7 \cdot 10^{-4}$
0.5	0.961	0.989	0.901
	$\pm 2 \cdot 10^{-5}$	$\pm 1 \cdot 10^{-5}$	$\pm 3 \cdot 10^{-4}$
0.6	0.964	0.988	0.913
	$\pm 2 \cdot 10^{-5}$	$\pm 1 \cdot 10^{-5}$	$\pm 3 \cdot 10^{-4}$
0.7	0.964	0.987	0.899
	$\pm 3 \cdot 10^{-5}$	$\pm 6 \cdot 10^{-6}$	$\pm 3 \cdot 10^{-4}$
0.8	0.960	0.984	0.904
	$\pm 8 \cdot 10^{-5}$	$\pm 1 \cdot 10^{-5}$	$\pm 1 \cdot 10^{-3}$
0.9	0.958	0.986	0.899
	$\pm 4 \cdot 10^{-5}$	$\pm 1 \cdot 10^{-5}$	$\pm 3 \cdot 10^{-4}$
1	0.957	0.985	0.886
	$\pm 2 \cdot 10^{-5}$	$\pm 2 \cdot 10^{-5}$	$\pm 7 \cdot 10^{-4}$

#### 4. THEORETICAL ANALYSIS: A SIMPLE PROBABILISTIC MODEL FOR THE SOCIETIES DYNAMICS

The aim of this section is to show that the societies dynamics empirically analyzed in the previous section can be modelled by a rather simple probabilistic model which describes the dependence between the proportion of elements in each society after a given number of generations and the dominance probability,  $p$ . The notion of generation is used here to denote  $m$  offspring construction steps,  $m$  being the population size. Despite the fact that the evolutionary process described in the previous sections is an asynchronous one, the probabilistic model is constructed based on the simplifying assumption that the new elements are introduced in the current population only after all of them were generated. Another simplifying assumption is that the fitness guided topology is not explicitly taken into account and the mates selection is uniformly random over the corresponding mating subpopulation. However, with all these simplifying assumptions, the theoretical model explains most of the influence of the dominance probability on the societies dynamics.

In order to describe the probabilistic model let us first introduce some notations. At each generation  $t$ ,  $n_L(t)$  denotes the average number of elements of the local interaction society,  $n_F(t)$  denotes the average number of elements of the far interaction society while  $n_G(t)$  denotes the average size of the global interaction society. The average proportions of societies in the population are denoted by  $p_L(t)$ ,  $p_F(t)$  and  $p_G(t)$  respectively and they correspond to the societies diameters from the empirical analysis. The dynamics of the societies is influenced by the probability of an offspring to be accepted into the population. Therefore we shall consider the following probabilities:  $q_{LG}$  (the acceptance probability of an offspring generated by recombining a first parent from LIA society with a mate from the GIA society),  $q_{FG}$  (the acceptance probability of an offspring generated by recombining a first parent from FIA society with a mate from the GIA society),  $q_{GL}$  and  $q_{GF}$  (acceptance probabilities of offsprings generated by parents from GIA and LIA or FIA societies, respectively).

The main result of this section is the following proposition which allows to describe the dynamics of societies.

**Proposition 4.1.** *The average number of elements in each society satisfy the following recurrence relations:*

$$n_L(t+1) = \left(1 - (1-p)q_{LG} \frac{n_G(t)}{n_L(t)+n_G(t)}\right) n_L(t) + pq_{GL}p_L(t)n_G(t) \quad (4.1)$$

$$n_F(t+1) = \left(1 - (1-p)q_{FG} \frac{n_G(t)}{n_F(t)+n_G(t)}\right) n_F(t) + pq_{GF}p_F(t)n_G(t) \quad (4.2)$$

$$n_G(t+1) = m - n_L(t+1) - n_F(t+1) \quad (4.3)$$

where  $p_L(t) = n_L(t)/m$ ,  $p_F(t) = n_F(t)/m$  and  $p_G(t) = n_G(t)/m$  denote the average proportion of elements in each society.

*Proof.* Since the recurrence relationships for  $n_L$  and  $n_F$  are similar it suffices to prove the first one. There are two processes which influence the number of elements in LIA society. The first one corresponds to the situation when an element from LIA is replaced with an offspring obtained by recombining a LIA with a GIA element and which is assigned to GIA society. This process leads to a decrease of the number of elements in LIA with  $(1-p)q_{LG}n_L(t)n_G(t)/(n_L(t)+n_G(t))$ . This number is derived by taking into consideration that three independent events occur, each one having its probability: (i) a mate is selected from the GIA society with the probability  $n_G(t)/(n_L(t)+n_G(t))$ ; (ii) the offspring is accepted with probability  $q_{LG}$ ; (iii) the offspring is assigned to GIA society with probability  $(1-p)$ . Thus the average number of elements in LIA which are replaced with offsprings belonging to GIA is obtained by multiplying these three probabilities with the current size of LIA society,  $n_L(t)$ .

The second process which influences the size of LIA society correspond to the case when elements from GIA select mates from LIA and the offspring is accepted in LIA, leading to an increase of the number of elements in LIA society. The number of elements added to LIA is also derived based on the probabilities of three independent events: (i) a mate for a GIA element is selected from the LIA society with a probability equal to the proportion of elements in the LIA society,  $p_L(t)$ ; (ii) the offspring is accepted with the corresponding acceptance probability,  $q_{GL}$ ; (iii) the offspring is assigned to LIA society with probability  $p$ . Therefore the number of new elements in LIA is  $pq_{GL}p_L(t)n_G(t)$ . The new number of elements in LIA,  $n_L(t+1)$ , is obtained by subtracted from  $n_L(t)$  the number of elements assigned to GIA and by adding the number of new elements obtained by mating a GIA with a LIA element. The recurrence relation for  $n_F(t)$  is obtained in a similar way, while the number of GIA elements,  $n_G(t)$ , is just the difference between the population size and the number of elements in the other two societies.  $\square$

In order to analyze if this probabilistic model captures the dynamics of the societies illustrated by the empirical analysis we tried first to estimate the values of acceptance probabilities ( $q_{LG}, q_{FG}, q_{GL}, q_{GF}$ ) which lead to a similar dependence between the proportion of societies after a given number of generations,  $T$ , and the dominance probability,  $p$ . As a dissimilarity measure between the empirical and the theoretical dependence we used a simple mean squared difference:

$$D = \frac{1}{N} \sum_{p \in P} ((p_L(T, p) - d_L(T, p))^2 + (p_F(T, p) - d_F(T, p))^2 + (p_G(T, p) - d_G(T, p))^2)$$

where  $P = \{0, 0.05, 0.1, 0.15, \dots, 1\}$ ,  $N = 3\text{card}(P)$ ,  $p_L(T, p)$  ( $p_F(T, p)$ ,  $p_G(T, p)$ ) denotes the theoretical proportion of elements in LIA (FIA and GIA, respectively) corresponding to generation  $T$  and dominance probability  $p$ .  $d_L(T, p)$  ( $d_F(T, p)$ ,  $d_G(T, p)$ ) denotes the corresponding empirical proportions of the societies. The acceptance probabilities were estimated by just choosing for each variant and each test function the quadruple  $(q_{LG}, q_{FG}, q_{GL}, q_{GF}) \in \{0, 0.1, \dots, 0.9, 1\}^4$  which minimizes the mean squared difference,  $D$ . The obtained acceptance probabilities and the corresponding value of  $D$  are presented in Table 2.

By taking a look at Figure 1(a,b,c) one can see that the probabilistic model captures the dependence between the societies proportions and the dominance probability, despite the simplifying assumptions on which it is based. The values in Table 2 confirm the empirical observation that for all test functions the distribution of elements in societies follows similar patterns. For instance in the case of the OG variant for all test functions the acceptance probabilities satisfy the same relationship:  $0 = q_{GF} < q_{FG} < q_{LG} < q_{GL}$ . This suggests that an offspring which has at least one LIA parent has a higher chance to be accepted in the population than an offspring obtained from FIA parents. The lowest acceptance probability corresponds to the offsprings obtained by combining a GIA individual (as first parent) with a FIA individual (as mate). On the other hand it is worth to be mentioned that the probabilistic model accurately describes both the global and the local collaboration variants. In the case of local collaboration the estimated acceptance probabilities  $q_{GL}$  and  $q_{GF}$  are always 0, meaning that none offspring obtained by combining a GIA first parent with a LIA (or FIA) mate is accepted. This fully corresponds to the local collaboration variant which is characterized by the fact that GIA elements select mates only from their society. Another local collaboration strategy would be that characterized through the fact that LIA and FIA elements chose only mates from their society but accept to be mates for elements from GIA. This situation corresponds to the case when  $q_{LG} = q_{FG} = 0$  (see Figure 3(d)).

TABLE 2. Acceptance probabilities estimated based on empirical results

Function/ variant	$q_{LG}$	$q_{FG}$	$q_{GL}$	$q_{GF}$	$D$
$f_1/OG$	0.4	0.3	0.5	0	0.0036
$f_1/OL$	0.1	0.1	0	0	0.0128
$f_1/UG$	0.1	0.2	0.1	0	0.0117
$f_1/UL$	0.1	0.1	0	0	0.0089
$f_2/OG$	0.8	0.3	1	0	0.0033
$f_2/OL$	0	0.1	0	0	0.0223
$f_2/UG$	0.1	0.1	0.1	0	0.0126
$f_2/UL$	0.1	0.1	0	0	0.0060
$f_3/OG$	0.4	0.3	0.5	0	0.0049
$f_3/OL$	0.1	0.1	0	0	0.0177
$f_3/UG$	0.1	0.1	0.1	0	0.0112
$f_3/UL$	0.1	0.1	0	0	0.0075

## 5. NUMERICAL EXPERIMENTS

The OG instance of the proposed model (OGA) is engaged in set of numerical experiments and compared to some of the most recently proposed evolutionary algorithms that can be found in the literature. In order to show the generality of the method, numerical experiments are performed on a different set of unimodal and multimodal benchmark functions [8, 9]:  $h_1$  - Shifted Sphere Function,  $h_2$  -



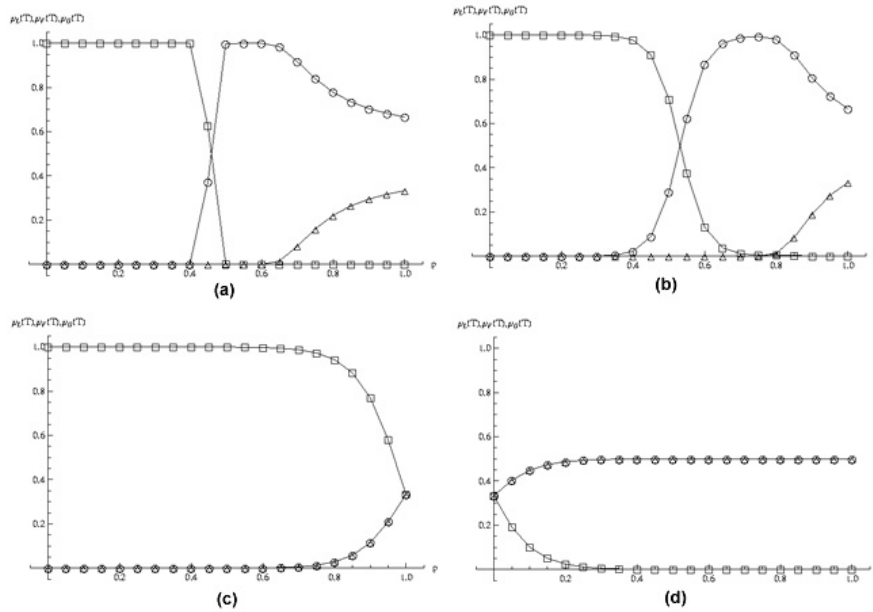


FIGURE 3. Theoretical dependence between the proportion of societies and the dominance probability for different values of the acceptance probabilities: (a):  $q_{LG} = 0.4, q_{FG} = 0.3, q_{GL} = 0.5, q_{GF} = 0$ ; (b):  $q_{LG} = 0.1, q_{FG} = 0.2, q_{GL} = 0.1, q_{GF} = 0$ ; (c):  $q_{LG} = 0.1, q_{FG} = 0.1, q_{GL} = 0, q_{GF} = 0$ ; (d):  $q_{LG} = 0, q_{FG} = 0, q_{GL} = 0.1, q_{GF} = 0.1$

Shifted Rosenbrocks Function,  $h_3$  - Shifted Rotated Ackleys Function with Global Optimum on Bounds,  $h_4$  - Shifted Rastrigins Function,  $h_5$  - Shifted Rotated Rastrigins Function,  $h_6$  - Shifted Rotated Weierstrass Function.

The proposed algorithm uses the following parameters: a population consists of  $8 \times 8$  (64) individuals, the mutation probability is 0.2, the tournament size is of the considered group of individuals. Convex recombination is used.

The OG model has been compared to the following five evolutionary algorithms: Real-Coded Genetic Algorithm (RCGA) [4], Guided Differential Evolution Algorithm (GDEA) [2], Estimation of Distribution Algorithm (EDA) [11], Self-adaptive Differential Evolution Algorithm (SaDEA) [7] and Evolutionary Strategy Algorithm (ESA) [6].

The error values  $h(x) - h(x^*)$  where  $x^*$  is the real optimum, are presented in Table 3. Each column corresponds to a method used for comparison. The best and the average error values have been recorded after  $1E+3$  function evaluations (FEs), after 25 runs of each algorithm for each function with dimension  $D = 10$ . The obtained standard deviations are also presented in these tables. Numerical results indicate a competitive performance of the OG algorithm. A better

TABLE 3. Error values achieved in 25 runs for functions  $h_1 - h_6$  with  $D = 10$  after  $1E+3$  FEs

		OGA	RCGA	GDEA	EDA	SaDEA	ESA
$h_1$	Best	7.26E+02	1.55E+04	7.81E+02	2.90E+03	8.14E+02	1.74E+03
	Mean	1.74E+03	4.03E+03	4.14E+03	5.72E+03	1.98E+03	4.63E+03
	Avg	7.27E+02	1.20E+03	1.57E+03	1.63E+03	6.51E+02	2.35E+03
$h_2$	Best	4.40E+06	7.89E+07	3.61E+07	4.52E+07	1.71E+07	3.81E+07
	Mean	8.25E+07	2.70E+08	2.28E+08	3.90E+08	5.63E+07	5.21E+08
	Avg	7.55E+07	1.28E+08	1.41E+08	2.78E+08	3.45E+07	3.23E+08
$h_3$	Best	2.042E+01	2.03E+01	2.05E+01	2.043E+01	2.04E+01	2.03E+01
	Mean	2.07E+01	2.069E+01	2.069E+01	2.07E+01	2.07E+01	2.06E+01
	Avg	1.33E-01	1.76E-01	1.24E-01	1.09E-01	1.70E-01	1.43E-01
$h_4$	Best	1.64E+01	5.43E+01	5.18E+01	5.70E+01	3.69E+01	4.08E+01
	Mean	3.28E+01	7.17E+01	6.93E+01	8.20E+01	5.44E+01	7.08E+01
	Avg	1.12E+01	9.36E+00	7.70E+00	9.96E+00	7.58E+00	1.63E+01
$h_5$	Best	2.81E+01	6.24E+01	7.74E+01	8.03E+01	4.52E+01	5.80E+01
	Mean	5.67E+01	8.99E+01	9.41E+01	1.01E+02	7.58E+01	9.37E+01
	Avg	1.34E+01	1.02E+01	9.02E+00	9.49E+00	1.17E+01	2.08E+01
$h_6$	Best	6.30E+00	9.97E+00	9.71E+00	9.24E+00	8.94E+00	8.13E+00
	Mean	9.28E+00	1.15E+01	1.14E+01	1.19E+01	1.14E+01	1.13E+01
	Avg	1.23E+00	6.42E-01	8.22E-01	8.18E-01	9.54E-01	1.20E+00

TABLE 4. Statistical analysis for all considered algorithms on the average results obtained in 25 runs for the functions  $h_1 - h_6$  with  $D = 10$ , after  $1E+3$  FEs.

	OGA	RCGA	GDEA	EDA	SaDEA	ESA
<i>eu f</i>	398.13	392.95	394.25	388.61	398.75	382.33
<i>rank</i>	2	4	3	5	1	6

solution is reported by OGA in roughly 90% of the considered cases. Furthermore, the best performance of the proposed OGA is obtained for difficult highly multimodal functions. For these functions OGA clearly outperforms most rival methods considered. Results obtained after  $1E+4$  FEs indicates a slightly weaker performance of the algorithm, which indicate that the proposed algorithm is able to perform an efficient search especially in the first stages of the algorithm. A mechanism for fine tuning and improving local search will be investigated as future work. A statistical analysis is performed using the expected utility approach [5] to determine the most accurate algorithm. The results of the statistical analysis test are presented in Table 4. The proposed OG algorithm obtains Rank 2 after  $1E+3$  FEs, being surpassed only by SaDEA.

## 6. CONCLUSIONS

Despite the simplifying assumptions used in developing the probabilistic model it captures rather accurately the dependence between the sizes of the different societies and the dominance probability. Both the empirical and the theoretical analysis reveal the existence of a range of values for the dominance probability which correspond to changes in the distribution of elements in the societies

and in the same time lead to slight improvements in the ability of the algorithm to identify the global optimum. On the other hand the obtained results suggest that the fitness guided topology does not influence the dynamics of the societies sizes. However it has a significant impact on the effectiveness of the evolutionary algorithm, leading to significantly better results than the variant based on a topology which does not take into account the fitness of elements, at least in the first stages of the evolution.

The performance of the obtained algorithm has been tested against several existing methods for optimizing difficult unimodal and multimodal functions. The obtained results are an indicator of the proposed algorithm efficiency.

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