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PARALLEL MUTATION BASED GENETIC CHROMODYNAMICS

ANCA GOG AND D. DUMITRESCU

Abstract. Genetic Chromodynamics is a strategy for preventing premature convergence and detecting multiple optimal solutions. A new technique of applying genetic operators is proposed. The Parallel Mutation Based Genetic Chromodynamics (PMGC) improves the local search from the standard approach and combines it with the global search, by using an appropriate mutation strategy.

Keywords: Evolutionary Computation, Genetic Operators, Genetic Chromodynamics

1. Introduction

Genetic Chromodynamics is an evolutionary technique for multimodal optimization. The main idea of Genetic Chromodynamics is to force the formation and maintenance of stable sub-populations. This aim is achieved by using a local interaction scheme ensuring sub-population stabilization in the early search stages. One of the Genetic Chromodynamics principles is the stepping stone search mechanism, every solution being involved in a search process by means of recombination or mutation operators.

A new technique of applying genetic operators is proposed. This method preserves the benefits of local interaction scheme from the standard approach of Genetic Chromodynamics and improves it by means of recombination followed by a small rate mutation, and is also making the exploration of the solutions space by means of a large step mutation. These two operators are simultaneously applied, and the two obtained offspring compete for survival only if they belong to the same optimal region and after they compete with the parents. If they belong to regions of different optimal points, both of them will be kept in the next generation. The enlargement of the population is not a problem, because of the merging operator that is fusing similar individuals. This way the population size will be reduced.

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For the small rate mutation, the Gaussian strategy is applied. The Cauchy mutation strategy is applied for the large step mutation. The experimental results show an improvement of the existing technique, by applying the proposed method on several benchmark multimodal functions. The proposed model is called *Parallel Mutation Based Genetic Chromodynamics* (PMGC).

The paper is organized as follows: Section 2 presents an overview of the Standard Genetic Chromodynamics (SGC) approach. The new technique of applying genetic operators is presented in Section 3. Section 4 describes the two mutation strategies used in the new approach. Experimental results prove the efficiency of the proposed model in Section 5. There are also conclusions presented in Section 6.

2. Genetic Chromodynamics

Many evolutionary techniques for solving multimodal optimization problems have been proposed. Genetic Chromodynamics is a non-niching strategy that maintains population diversity and detects multiple optima. The main principles of Genetic Chromodynamics are:

1. population size is variable;

2. sub-population structure is not predefined, but emergent;

3. each individual within the current population is considered to be a stepping-stone for the search process;

4. a new operator for merging very close individuals is considered;

5. at convergence, the number of sub-populations represents the number of optimal solutions.

In the standard Genetic Chromodynamics approach, every solution is involved either in recombination or mutation. The best between the dominant parent and the offspring created by recombination or mutation will be kept in the next generation. In this approach, the offspring obtained by mutation will be unconditionally accepted if it is better than its parent. Thus, this strategy can be useful in the first generations of the search process, but in the later stages could cause some optima extinction. To prevent this situation, the mutation will always create offspring belonging to the interaction range, by choosing an appropriate value of the standard deviation parameter [4].

3. Parallel Mutation for Genetic Chromodynamics

We may consider a new recombination – mutation scheme, depicted in Figure 1. This scheme may be viewed as a new composed search operator. Recombination followed by mutation can be considered as a unique search operator. It will be called RM. We also consider another mutation operator, called M, which acts independently. In the proposed model, the difference between the two mutation operators is made. M1 has a small rate of mutation, and M2 has a higher step.

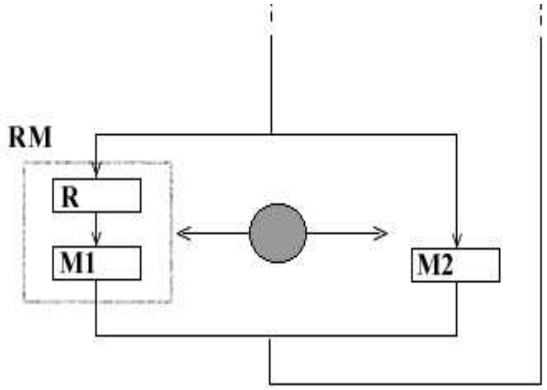

FIGURE 1. PMGC model

The proposed search model applies the two operators simultaneously and is called Parallel Mutation Based Genetic Chromodynamics (PMGC). Both genetic operators will create offspring that will compete for survival first with their parents. After this, the best of them will survive if the two obtained offspring belong to the region of the same local optimum. If they belong to regions of different local optima, both of them will survive. This approach will not affect the local interaction scheme and will improve the exploration of the solutions space.

The role of the very small rate mutation (operator M1) is to avoid the interference between recombination and high mutation. If the offspring obtained after recombination is a good solution for the problem, we do not want to loose this descendent by applying a high mutation rate [1]. The proposed strategy is the Gaussian one, which ensures a small mutation rate.

Larger mutation step (operator M2) ensures the exploration of the solutions' space. Also, when recombination cannot be made anymore, this mutation will attend faster the optimal points. Using a Cauchy mutation strategy ensures the larger step (see Section 4).

The reason why both descendents survive if they belong to different regions of optimal points is to avoid the extinction of useful potential optima. This situation can interfere if the offspring obtained by M has a higher fitness that the fitness obtained by RM and it belongs to a region corresponding to a different optimum point. This way, a useful optimum point represented by the RM offspring is lost.

In order to keep all useful solutions, distance between the offspring is taken into account. If the two possible solutions belong to different regions (the second does not belong to the interaction range of the first one) then both of them will be kept.

4. Gaussian and Cauchy mutation strategies

Gaussian mutation strategy accomplishes the request of a small mutation rate that follows the recombination. Cauchy strategy is used for the mutation that acts simultaneously to it. The two mutation strategies are described in the following paragraphs:

4.1. **Gauss mutation strategy.** Let us consider the following chromosome:

$$\{x_1, x_2, \ldots, x_m\}$$

If the element x_k is selected for mutation, $k = 1, \ldots, m$, the result will be:

$$\{x_1, \ldots, x'_k, \ldots, x_m\}$$

Gaussian mutation has two parameters: a mean value and a standard deviation. In this mutation approach, the following relation transforms the element x_k into x'_k:

$$x'_k = x_k + \eta N_k(0,1), \tag{1}$$

where the correction step η is the standard deviation for Gaussian mutations. $N_k(0,1)$ denotes a normally distributed one-dimensional random number with mean 0 and standard deviation 1. This random number is generated anew for each value of k, $k = 1, \ldots, m$ [3].

4.2. **Cauchy mutation strategy.** Cauchy mutation can perform longer jumps with high probability. The search step size is much larger than the search step of the Gaussian mutation. The shape of Cauchy density function is similar to that of the Gaussian density function but approaches the axis so slowly that an expectation does not exist [7]. As a result, the variance of the Cauchy distribution is infinite. Figure 2 shows the difference between Cauchy and Gaussian density functions.
The one-dimensional Cauchy density function centered at the origin is defined by:

$$f_t(x) = t/\pi(t^2 + x^2), -\infty < x < \infty,$$

where $t > 0$ is a scale parameter. The corresponding Cauchy distribution function is given by:

$$F_t(x) = 1/2 + arctan(x/t)/\pi.$$

In this mutatin strategy, the following relation transforms the element x_k into x'_k:

$$x'_k = x_k + \eta\delta_k, \tag{2}$$

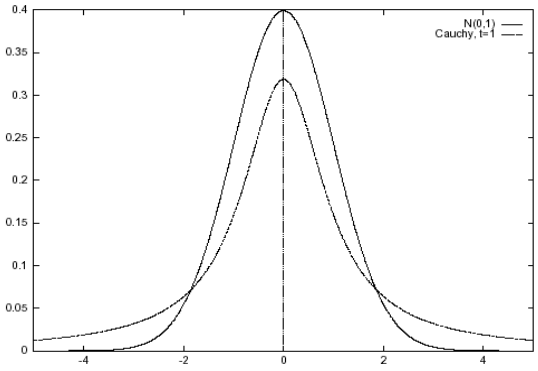

FIGURE 2. Comparison between Cauchy and Gaussian density functions

where δ_k is a Cauchy random variable. The method used to generate Cauchy random numbers is based on the inverse transformation, i.e. the inverse distribution function, and is defined by:

$$\delta_k = ttan[\pi(U(0,1) - 1/2)],$$

where U(0,1) denotes the unit rectangular variate [5].

In the continuous case, the uniform distribution is also called the *rectangular distribution* because of the shape of its probability density function. The *standard uniform distribution* is the continuous uniform distribution with the values of a and b set to 0 and 1 respectively, so that the random variable can take values only between 0 and 1.

Generally t is taken to be 1. δ_k is generated anew for each value of k. Correction step η may have the same value as in correction rule (1).

5. Experimental results

Multimodal functions having local optima are often regarded as being difficult to optimize. The effectiveness of the method is demonstrated on a number of eight multimodal test functions [2], [6]. One-dimensional functions have been chosen for implementation, but the method can be easily extended to n-dimensional functions.

The following eight benchmark functions are used for testing the proposed model:

$$f_1(x) = [0.002 + \sum_{i=1}^{25} 1/(i + (x - a_i)^6)]^{-1}, -1000 \leq x \leq 1000$$
$$f_2(x) = 0.00025(x - 100)^2 - cos(x - 100) + 1, -600 \leq x \leq 600$$

$f_3(x) = -\sum_{i=1}^{5} c_i[exp(-(x-a_i)^2/\pi)cos(\pi(x-a_i)^2)], 0 \leq x \leq 10$
$f_4(x) = 20 - 20exp(-0.2x + e - exp(cos(2x\pi)/n)), 1 \leq x \leq 30$
$f_5(x) = 10 + (x^2 - 10cos(2x\pi)), 1 \leq x \leq 5$
$f_6(x) = 418.9828872724339 - xsin(\sqrt{|x|}), -500 \leq x \leq 300$
$f_7(x) = lnxsin(e^x) + sin(3x), 0.1 \leq x \leq 4$
$f_8(x) = exp(-2ln2((x-0.1)/0.8)^2)sin(5x\pi)^2, 0 \leq x \leq 3$

Remarks:
(i) Coefficients a_i, $i = 1, \ldots, 25$ in function f_1 (Shekel's Foxholes function), are components of the vector a=(-32 -16 0 16 32 -32 ... 0 16 32).
(ii) Coefficients c_i, $i = 1, \ldots, 5$ in function f_3 (Langerman's function), are components of the vector c=(0.806 0.517 1.5 0.908 0.965), and coefficients a_i, $i = 1, \ldots, 5$ are components of the vector a=(9.681 9.4 8.025 2.196 8.074).

Example:
Let us consider the function defined as:

$$f_3(x) = -\sum_{i=1}^{5} c_i[exp(-(x-a_i)^2/\pi)cos(\pi(x-a_i)^2)],$$
$$0 \leq x \leq 10.$$

Algorithm parameters are given in Table 1.

TABLE 1. PMGC parameters for test function f3.

Initial population size	**300**
Interaction (mating) radius	**0.5**
Mutation step size	**0.001**
Merging threshold	**0.1**
Number of epochs before stopping	**10**
Remarks	**The function has one global optimum and seven local optima.**

Results obtained are given in Table 2.

Initial population is depicted in Figure 3. Populations obtained at several intermediate stages (epochs) are depicted in Figures 4 and 5. Final population is depicted in Figure 6. Final population contains only problem optima. All optima are correctly detected.

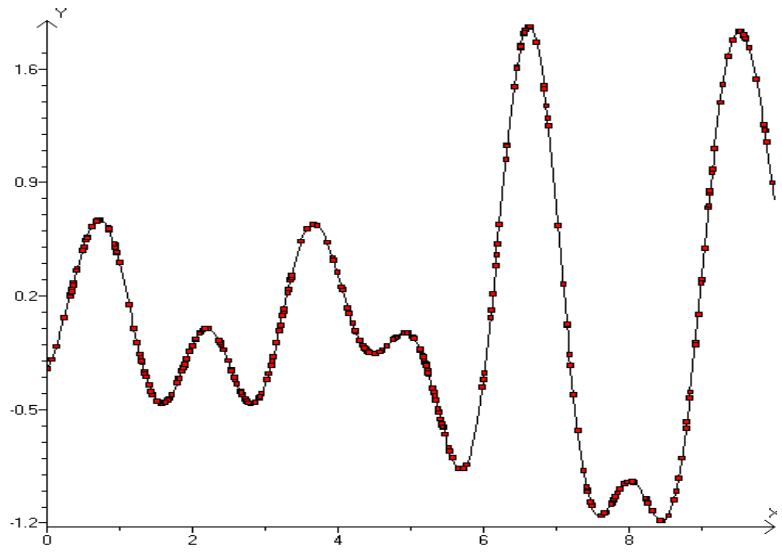

FIGURE 3. Initial 300 members population.

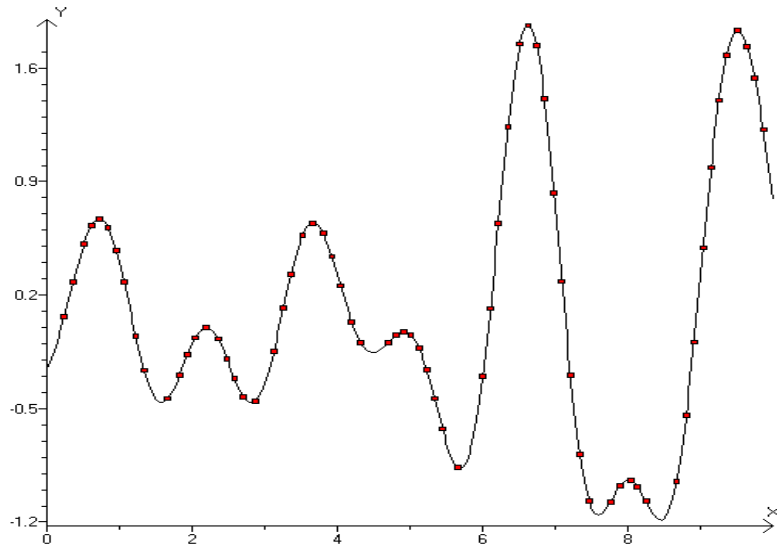

FIGURE 4. PMGC population after 2 epochs. Population has 68 members.

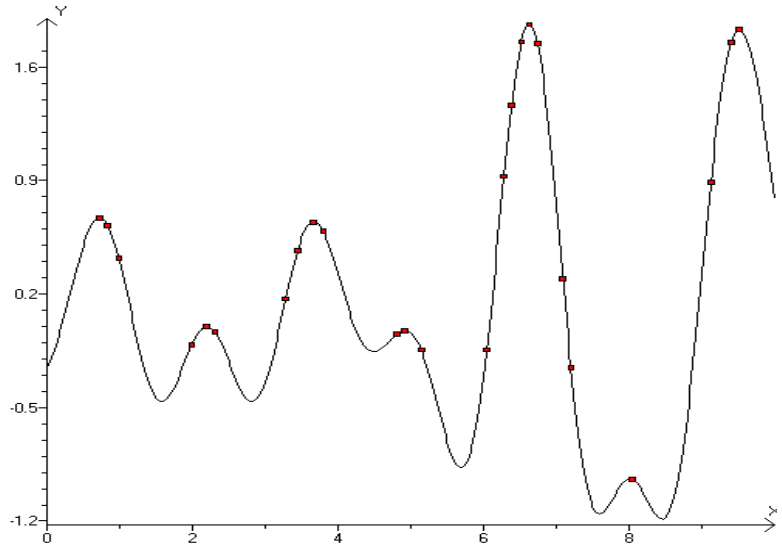

FIGURE 5. PMGC population after 5 epochs. Population has 25 members.

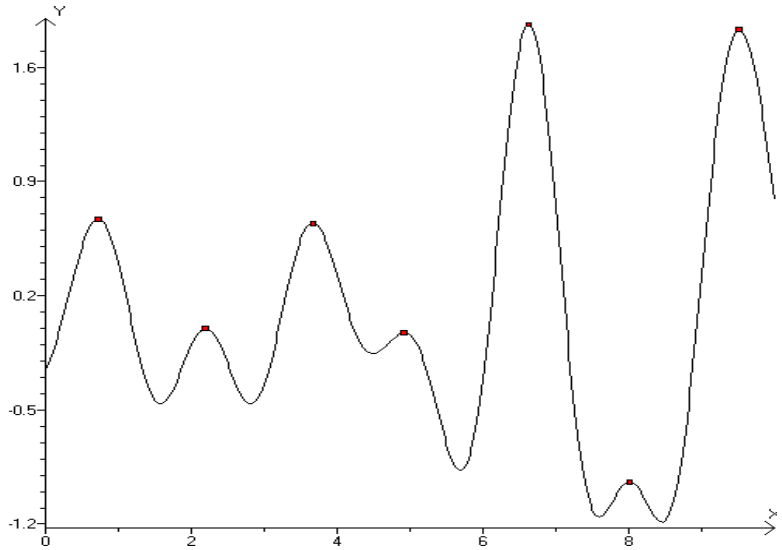

FIGURE 6. PMGC final population obtained after 35 epochs. Population has 7 members representing optimal solutions. All optimal solutions are correctly detected in this run.

TABLE 2. PMGC results obtained for test function f3 with parameters in Table 1.

Number of detected optima	**7**
Number of epochs needed for convergence	**35**
Number of recombinations involved	**232**
Number of mutations involved	**242**

Table 3 summarizes the final results obtained after 100 runs of SGC and PMGC for all considered benchmark functions. It can be seen that PMGC performs better than SGC consistently for these functions. The proposed PMGC model outperforms SGC as regards the number of epochs needed to find the local optimal points. The results regard the average number of generations needed to locate the optimal points in both SGC and PMGC approaches after 100 runs of both algorithms. Also, the best value obtained in both approaches can be seen in Table 3.

TABLE 3. Results obtained after 100 runs of PMGC and SGC; the average and the best number of epochs needed to find the optimal points.

Test function	**Average PMGC**	**Average SGC**	**Best PMGC**	**Best SGC**
f_1	**57**	**83**	**39**	**64**
f_2	**53**	**66**	**32**	**35**
f_3	**71**	**102**	**31**	**60**
f_4	**55**	**99**	**35**	**50**
f_5	**52**	**107**	**34**	**51**
f_6	**53**	**95**	**37**	**52**
f_7	**69**	**792**	**52**	**685**
f_8	**52**	**53**	**35**	**38**

Regarding the number of optimal points detected, PMGC and SGC have similar results. For the considered test functions, in both approaches, in 98% of the cases all the optimal points have been detected.

6. CONCLUSIONS

A new model of applying genetic operators consistently improves the results obtained by the standard approach of Genetic Chromodynamics. The model is based on the parallel action of two genetic operators: recombination followed by small rate mutation and high rate mutation. The obtained offspring will compete

with the parents for survival. The two chromosomes with the higher quality will survive if they belong to regions of different optimal points. The Gaussian mutation strategy is proposed for the mutation that follows recombination and the Cauchy strategy is proposed for the mutation that acts parallel to recombination.

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Babes-Bolyai University of Cluj-Napoca, Faculty of Mathematics and Computer Science, Computer Science Department

E-mail address: {anca,ddumitr}@cs.ubbcluj.ro