

Optimal parameters selection of the genetic algorithm for global optimization

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Abstract. The aim of this work is to summarize the results of research concerning the application of genetic algorithms, since in solving problems of complex systems optimization, situations are often encountered that make it difficult or impossible to use classical methods. To solve this problem, research was carried out on the functions of Akli, Rastrigin, Shekel, complaints handling functions and Rosenbrock functions. The studies were conducted on three starting point scattering algorithms: LP τ sequence, UDC sequences and universal random variation. As a result of the analysis, the option of initialization, selection, recombination, mutation and coding of this algorithm according to given test functions for the data of the scatter of initial points was chosen. The effective parameters of the genetic algorithm according to the results of research are established.

1. Introduction

To date, the genetic algorithm for global optimization [1 - 4] has many options for the algorithm parameters. When applying this algorithm in practice, we would like to know which options to use in the first place, i.e. what options of parameters give the greatest efficiency, more precisely, what combination of them gives the greatest efficiency on test functions.

The efficiency of the algorithms will be calculated in three directions: by the value of the function, by the number of steps of the algorithm, by the running time of the algorithm. Studies were conducted on Ackley, Rastrigin, Shekel, Grivanka and Rosenbrock functions [2, 5, 6]. LP τ sequence [3, 7], UDC sequence, uniform random scatter - very interesting and effective scatter algorithms of initial points. Recent studies in this area were carried out in the works of the scientist [4, 8, 9].

These studies were applied to specific practical problems, the goal was not to average these parameters, to test for a large number of practical tasks of a test function complex type [1, 10]. LP τ -sequences are an algorithm for scattering points based on a matrix of irreducible Marshal polynomials. UDC sequences are an algorithm for absolutely points uniform distribution over all coordinates in a multidimensional space, regardless of the scatter points number [3, 5, 8]. Uniform random scatter is a stochastic point scatter algorithm using the normal distribution law.

2. Experimental part

Block-scheme of the genetic algorithm, which is on study, is presented on Figure 1. The algorithm is standard and consists of five steps: population initialization, assessment of fitness for each individual in population, selection, recombination and mutation.

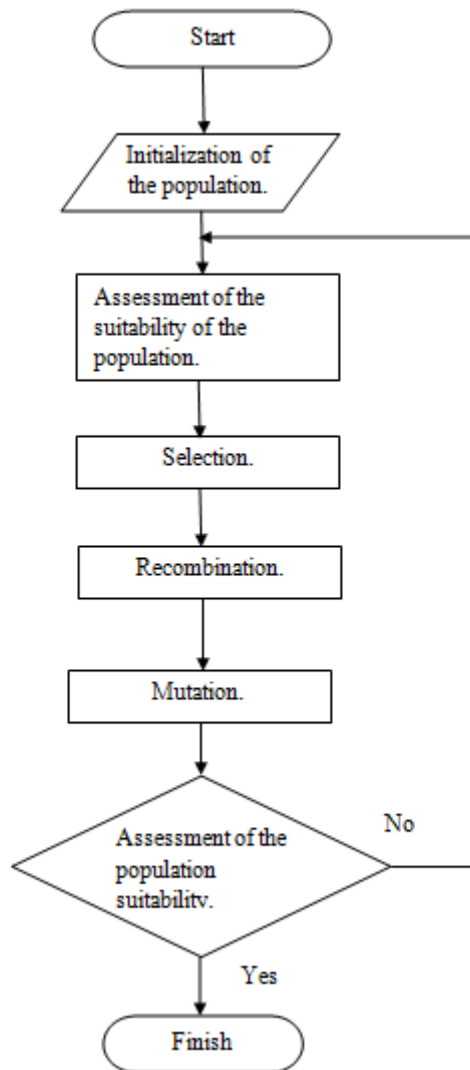


Figure 1. The scheme of the algorithm.

In presented study parameters and intervals of global optimization genetic algorithm parameters were investigated:

- 6 ways to initialize.
- 6 selections: proportional, rank (linear distribution), rank (negative exponential distribution), tournament with 2, 3 and 4 participants.
- 28 recombination methods.

Mutation, in the form of a different probability of mutation:

- The probability of a mutation is 0.001.
- The probability of a mutation is 0.01.
- The probability of mutation is 0.5.
- Probability of a mutation is $1/m$, where m is the number of bits in the chromosome.

Coding information: binary coding and gray coding.

When optimizing a certain function $f(X)$, the genetic algorithm uses points or solutions of a certain length along each space dimension, called individuals, as points or solutions. The value of the decision is the so-called individual fitness. Grouped individuals are called populations. Selection, recombination, and mutation operations are applied to individuals in the population. Breeding consists in the selection of individuals most suitable for crossing (recombination). In the crossing process individuals exchange parts of their chromosomes. As a result, offspring appears, usually the most suitable for further “life”. The offspring mutates with time, i.e. changes some of its “genes”. This continues until an individual is fit enough.

The study was conducted on test functions: the Acley function, the Rastrigin function, the Shekel function, the Grivanka function and Rosenbrock function.

Algorithm inputs:

- The size of the studied patterns space – 2.
- The total scatter points number (boolean strings) and the maximum number of algorithm steps (generations): 10 points and 160 steps; 20 points and 80 steps; 40 points and 40 steps; 80 points and 20 steps; 160 points and 10 steps.
- The accuracy of finding the extremum is 0.01.
- The number of algorithm repeated runs is 100.
- The study area lays in [-45;45] for each coordinate.

At the output, we get arrays of mathematical expectations and standard deviations of the solution quality, as well as arrays of algorithm parameters for different functions, steps-points options and directions of algorithm efficiency. The quality of the decision is the average error in finding the extremum.

3. Results and discussion

As we know, the goal of the optimization algorithm is to find the extremum as accurately as possible, faster and cheaper. Therefore, we should look at the obtained results.

The optimal, in absolute value, parameters of the genetic algorithm (initialization - *Init*, selection - *Sel*, recombination - *Rec*, mutation - *Mut*, coding - *Cod*) were determined, for each test function optimized for each point of view (Tables 1-5).

Table 1. Quality of the solution for function 1.

	Points	Steps	<i>Init</i>	<i>Sel</i>	<i>Rec</i>	<i>Mut</i>	<i>Cod</i>	M	Disp	Time	Calc_ f
FeatureBest (M)	160	10	5	6	15	4	1	1.868710e-02	5.816986e-04	4	1370
Best in algorithm time (Time)	80	20	5	6	1	3	1	2.605533e-02	7.009596e-03	2	746
Best by number of algorithm steps (Calc_f)	160	10	5	6	1	3	1	2.605533e-02	7.009596e-03	2	746

Table 2. Solution quality for function 2.

	Points	Steps	<i>Init</i>	<i>Sel</i>	<i>Rec</i>	<i>Mut</i>	<i>Cod</i>	M	Disp	Time	Calc_ f
FeatureBest (M)	160	10	5	6	17	1	1	6.398188e-03	3.839408e-05	4	1370
Best in algorithm time (Time)	10	160	5	4	6	3	1	4.085319e-01	4.133809e-01	2	746
Best by number of algorithm steps (Calc_f)	160	10	5	6	17	1	1	6.398188e-03	3.839408e-05	2	746

Table 3. Solution quality for function 3.

	Points	Steps	<i>Init</i>	<i>Sel</i>	<i>Rec</i>	<i>Mut</i>	<i>Cod</i>	M	Disp	Time	Calc_f
FeatureBest (M)	160	10	3	5	17	1	1	7.195811e-01	1.367424e-02	17	1600
Best in algorithm time (Time)	10	160	5	5	8	2	1	9.320818e-01	2.061107e-01	3	1600
Best by number of algorithm steps (Calc_f)	10	160	5	5	8	2	1	9.320818e-01	2.061107e-01	3	1600

Table 4. Solution quality for function 4.

	Points	Steps	<i>Init</i>	<i>Sel</i>	<i>Rec</i>	<i>Mut</i>	<i>Cod</i>	M	Disp	Time	Calc_f
FeatureBest (M)	160	10	5	5	15	3	1	1.571134e-02	5.099528e-05	4	1490
Best in algorithm time (Time)	160	10	2	6	4	1	1	2.214829e+04	6.618081e+09	2	1600
Best by number of algorithm steps (Calc_f)	40	40	5	6	17	1	2	4.833150e-01	2.675486e+00	4	1052

Table 5. Solution quality for function 5.

	Points	Steps	<i>Init</i>	<i>Sel</i>	<i>Rec</i>	<i>Mut</i>	<i>Cod</i>	M	Disp	Time	Calc_f
FeatureBest (M)	160	10	5	6	7	1	1	1.669696e-02	7.568911e-04	3	1048
Best in algorithm time (Time)	160	10	5	6	7	1	1	1.669696e-02	7.568911e-04	3	1048
Best by number of algorithm steps (Calc_f)	160	10	5	6	7	1	1	1.669696e-02	7.568911e-04	3	1048

It is not possible to draw conclusions about the optimal, on average, values of the genetic algorithm parameters for all test functions, since the optimal values of each parameter for each test function are different.

To identify the optimal, on average, values of the parameters of the genetic algorithm for all test functions, it is necessary, using new comparison methodology, to identify with a certain level of significance which options of parameters differ significantly from each other, and which do not. Only in this case, it is possible to determine the optimal, on average, parameter values of the genetic algorithm for all test functions.

4. Conclusion

In this study, the genetic algorithm for global optimization was analyzed. The studies were carried out on the Akli, Rastrigin, Shekel, Griwanka and Rosenbrock function. The studies were conducted on three initial point spread algorithms: LP τ sequence, UDC sequence, uniform random variation.

As a result, the best variant of initialization, selection, recombination, mutation, coding of the given algorithm on the given test functions for the given algorithms of the spread of initial points was revealed.

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