

Differential Evolution with Graph-Based Speciation by Competitive Hebbian Rules

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Abstract—Differential evolution (DE) is an evolutionary algorithm and has been successfully applied to optimization problems including non-linear, non-differentiable, non-convex and multimodal functions. However, it is still difficult to solve hard problems such as multimodal problems and problems with ridge structures. In this study, we propose a new speciation method “graph-based speciation” to keep the diversity of the search points and realize the global search. Also, we utilize the species-best strategy that can realize the global search using speciation and the local search around the seeds of species. It is expected that the efficiency and the robustness of DE can be improved by using the strategy. The advantage of the proposed method is shown by solving some benchmark problems including multimodal problems and problems with ridge structures.

Keywords-differential evolution; speciation; competitive Hebbian rules; Delaunay diagram

I. INTRODUCTION

Optimization problems, especially nonlinear optimization problems, are very important and frequently appear in the real world. There exist many studies on solving optimization problems using evolutionary algorithms (EAs). Differential evolution (DE) is an EA proposed by Storn and Price [1], which is a stochastic direct search method using a population or multiple search points. DE has been successfully applied to optimization problems including non-linear, non-differentiable, non-convex and multimodal functions [2], [3]. It has been shown that DE is a very fast and robust algorithm.

However, it is still difficult to solve hard problems such as multimodal problems and problems with ridge structures. In multimodal problems, search points might converge to a local optimal solution. In problems with ridge structures, search points will move along a narrow path, lost the divergence and might be stopped at a solution that is not optimal. In order to avoid these situations, a global search should be realized by keeping the divergence of the search points. On the other hand, a disadvantage of EAs is that they need a large number of function evaluations before a well acceptable solution can be found. Recently, the size of optimization problems tends to become larger, and the cost of function evaluations becomes higher. It is necessary to develop more efficient optimization algorithms to reduce the number of function evaluations. In order to improve the

efficiency, a local search should be realized by exploring an area near the best search points. Thus, it is important to balance between the global search and the local search.

In this study, we propose a new speciation method “graph-based speciation” to keep the diversity of the search points and realize the global search. Also, we utilize the species-best strategy [4], [5]. In DE, a mutant vector is generated for each parent by using a base vector and one or more difference vectors which are the difference between two individuals. The parent and the mutant vector are recombined by a crossover operation to generate a child, or a trial vector. There are some strategies for selecting the base vector: The best individual is used as the base vector in the best strategy and a randomly selected individual is used in the rand strategy. In the species-best strategy, a population is divided into several species by speciation, and the seed of the species to which the parent belongs is selected as the base vector. The strategy can balance between the global search using speciation and the local search around the seeds of species. It is thought that the efficiency of the species-best strategy is better than the rand strategy and the robustness of the species-best strategy is better than the best strategy. Thus, it is expected that the strategy improves the efficiency and the robustness of the search.

The advantage of the proposed method is shown by solving some benchmark problems including multimodal problems and problems with ridge structures.

In Section II, some studies on speciation are briefly reviewed. In Section III, the graph-based speciation is proposed. DE and DE with speciation are described in Section IV. In Section V, experimental results on some problems are shown. Finally, conclusions are described in Section VI.

II. SPECIATION

Speciation is the evolutionary process to form new biological species by the development of one species into two or more genetically distinct ones. The idea of speciation is mainly used for multimodal optimization where multiple optimal or suboptimal solutions are obtained simultaneously in one run. Each species evolves to find an optimal or suboptimal solution. There exist some types of research using speciation in DE [6] as follows.

Radius-based speciation: A population is sorted in increasing objective value order, first. Then, the best individual in the sorted population becomes a new species seed. The population members that exist within the specified radius from the seed are assigned to the species, and the members are deleted from the population. This process is repeated until the population becomes empty [4], [7], [8].

In this category, it is difficult to select a proper radius, which depends on problems to be optimization and also the search process in the optimization.

Clustering-based speciation: A population is divided into several clusters using a clustering algorithm such as k-means clustering [9] or fuzzy c-means clustering [5], [10]. Each cluster corresponds to a species. An individual that has the best objective value in the species is selected as the seed.

In this category, it is difficult to select a proper number of clusters, which depends on problems and also the search process.

In this study, the graph-based speciation using competitive Hebbian rules is proposed not to solve multimodal optimization but to solve usual optimization for finding one optimal solution and improving the efficiency and the robustness of DE. In the approach, the number of species is dynamically adjusted depending on the function landscape in the search process such as unimodal, multimodal or ridge structures.

III. GRAPH-BASED SPECIATION BY COMPETITIVE HEBBIAN RULES

A. Delaunay diagram

When N vertices $V = \{\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_N\}$ exist in a metric space S , S can be decomposed into N regions, or Voronoi cells $R(\mathbf{x}_i)$, which are the sets of all points in S whose distance to \mathbf{x}_i is not greater than their distance to the other vertices. The Voronoi cells can be defined as follows:

$$R(\mathbf{x}_i) = \{\mathbf{x} \in S \mid d(\mathbf{x}, \mathbf{x}_i) \leq d(\mathbf{x}, \mathbf{x}_j), \forall j \neq i\} \quad (1)$$

where d is a distance function on S .

In Delaunay diagram, two vertices \mathbf{x}_i and \mathbf{x}_j are connected when the regions $R(\mathbf{x}_i)$ and $R(\mathbf{x}_j)$ adjoin each other. Delaunay diagram is the geometric dual of the Voronoi diagram. Proximity graphs such as nearest neighborhood graph, relative neighborhood graph and Gabriel graph are the subgraphs of Delaunay diagram.

B. Competitive Hebbian rules

Martinez et al. [11] proposed a topology representing neural networks which is a subgraph of the Delaunay diagram and is generated by competitive Hebbian rules as follows:

- 1) Set all connection strengths $C_{ij} = 0$.
- 2) Present an input pattern $\mathbf{x} \in S$ with probability $P(\mathbf{x})$.

- 3) Determine the nearest vertex to \mathbf{x} , \mathbf{x}_{i1} and the second nearest vertex \mathbf{x}_{i2} as follows:

$$\begin{aligned} d(\mathbf{x}, \mathbf{x}_{i1}) &\leq d(\mathbf{x}, \mathbf{x}_j), \forall j = 1, 2, \dots, N \\ d(\mathbf{x}, \mathbf{x}_{i2}) &\leq d(\mathbf{x}, \mathbf{x}_j), \forall j \neq i1 \end{aligned} \quad (2)$$

- 4) Strengthen the connection between \mathbf{x}_{i1} and \mathbf{x}_{i2} according to competitive Hebbian rules. If $C_{i1,i2} = 0$, set $C_{i1,i2} > 0$, that is, connect \mathbf{x}_{i1} and \mathbf{x}_{i2} .
- 5) Go back to 2) until termination condition is satisfied.

A subgraph of Delaunay diagram can be generated by the algorithm. If the number of input patterns $M \rightarrow \infty$, Delaunay diagram can be generated.

C. Speciation using proximity graph

In graph-based speciation using proximity graph, the species relation of two points is defined by whether the edge between the points exists or not. Species are formed by a point and the connected points to the points. The seed of the species is defined as follows:

- 1) Create a proximity graph using search points.
- 2) For each point $\mathbf{x}_i, i = 1, 2, \dots, N$,
 - (a) Obtain the points that are connected to \mathbf{x}_i .
 - (b) Form species from \mathbf{x}_i and the points. The best point among the species becomes the seed of the species.

$$seed(\mathbf{x}_i) = \arg \min_{\{l \mid l=i \text{ or } C_{il}>0\}} f(\mathbf{x}_l) \quad (3)$$

IV. SPECIATION-BASED DIFFERENTIAL EVOLUTION USING GRAPHS

A. Optimization Problems

In this study, the following optimization problem (P) with lower bound and upper bound constraints will be discussed.

$$\begin{aligned} \text{(P) minimize} \quad & f(\mathbf{x}) \\ \text{subject to} \quad & l_i \leq x_i \leq u_i, i = 1, \dots, n, \end{aligned} \quad (4)$$

where $\mathbf{x} = (x_1, x_2, \dots, x_n)$ is an n dimensional vector and $f(\mathbf{x})$ is an objective function. The function f is a nonlinear real-valued function. Values l_i and u_i are the lower bound and the upper bound of x_i , respectively. Let the search space in which every point satisfies the lower and upper bound constraints be denoted by \mathcal{S} .

B. Differential Evolution

In DE, initial individuals are randomly generated within the search space and form an initial population. Each individual contains n genes as decision variables or a decision vector. At each generation or iteration, all individuals are selected as parents. Each parent is processed as follows: The mutation process begins by choosing $1 + 2 \text{ num}$ individuals from all individuals except for the parent in the processing. The first individual is a base vector. All subsequent individuals are paired to create num difference vectors. The difference vectors are scaled by a scaling

factor F and added to the base vector. The resulting vector is then recombined with the parent. The probability of recombination at an element is controlled by the crossover rate CR . This crossover process produces a trial vector. Finally, for survivor selection, the trial vector is accepted for the next generation if the trial vector is better than the parent.

Some variants of DE such as DE/best/1/bin and DE/rand/1/exp have been proposed. The variants are classified using the notation DE/base/num/cross. “base” indicates the method of selecting a base vector. For example, DE/rand/num/cross selects the base vector at random from the population. DE/best/num/cross selects the best individual in the population. “num” indicates the number of difference vectors used to perturb the base vector. “cross” indicates the crossover mechanism used to create a trial vector or a child. For example, DE/base/num/bin shows that the crossover is controlled by the binomial crossover using the constant crossover rate. DE/base/num/exp shows that the crossover is controlled by the two-point crossover using exponentially decreasing the crossover rate.

C. Species-based DE with Graph

Some modifications to standard DE are applied for proposed method as follows:

- 1) Species-best strategy for mutation is adopted. The seed of the individual is selected as a base vector.

$$\mathbf{x}' = \mathbf{x}_{seed}(\mathbf{x}_i) + F(\mathbf{x}_{p_2} - \mathbf{x}_{p_3}) \quad (5)$$

where \mathbf{x}' is a mutant vector, $seed(\mathbf{x}_i)$ is the seed of \mathbf{x}_i , p_2 and p_3 are random numbers.

- 2) Continuous generation model is adopted. In this study, when the child is better than the parent, the parent is immediately replaced by the child.

The pseudo-code of SDE-G/species-best/1/exp using competitive Hebbian rules (CHR) is shown in Figure 1.

V. NUMERICAL EXPERIMENTS

A. Test Problems

In this section, benchmark problems including sphere function (f_1), Rosenbrock function (f_2), ill-scaled Rosenbrock function (f_3) and Rastrigin function (f_4) are solved. These functions have various surfaces such as unimodal surface in f_1 , ridge structure in f_2 and f_3 , and multimodal bumpy surfaces. The function definitions and their search spaces, where n is the dimension of the decision vector, are shown in Table I. Table II shows the features of the functions.

All functions are optimized with the dimension of decision vector $n = 30$. Experimental conditions for SDE-G and DE are as follows: Population size is $N = 50$. Scaling factor and crossover rate are generated for each individual.

$$F = 0.7 + N(0, 0.1^2), F \in [0.5, 0.9] \quad (6)$$

$$CR = 0.9 + N(0, 0.1^2), CR \in [0.8, 1] \quad (7)$$

```

SDE-G/CHR/species-best/1/exp()
{
  P=N individuals {x_i} generated randomly in S;
  for(t=1; termination condition is false; t++) {
    Obtain {C_ij} using competitive Hebbian rules;
    Obtain {seed(x_i)} by Speciation using {C_ij};
    for(i=1; i ≤ N; i++) {
      p1=seed(x_i);
      x_p2=Randomly selected from P(p2 ∉ {i, p1});
      x_p3=Randomly selected from P(p3 ∉ {i, p1, p2});
      x_child=x_i;
      j=select randomly from [1, n];
      k=1;
      do {
        x_j^child=x_p1,j+F(x_p2,j - x_p3,j);
        j=(j+1)%n;
        k++;
      } while(k ≤ n && u(0,1) < CR);
      if(f(x_child) ≤ f(x_i))
        x_i=x_child;
    }
  }
}

```

Figure 1. The pseudo-code of SDE-G/CHR, $u(0, 1)$ is a uniform random number in $[0, 1]$.

Table I
BENCHMARK FUNCTIONS

Func.	Definition	Optimum
f_1	$\sum_{i=1}^n x_i^2, -5.12 \leq x_i \leq 5.12$	$(0, 0, \dots, 0)$
f_2	$\sum_{i=2}^n \{100(x_1 - x_i^2)^2 + (x_i - 1)^2\}$ $-2.048 \leq x_i \leq 2.048$	$(1, 1, \dots, 1)$
f_3	$\sum_{i=2}^n \{100(x_1 - (ix_i)^2)^2 + (ix_i - 1)^2\}$ $-2.048/i \leq x_i \leq 2.048/i$	$(1, \frac{1}{2}, \dots, \frac{1}{n})$
f_4	$10n + \sum_{i=1}^n \{x_i^2 - 10 \cos(2\pi x_i)\}$ $-5.12 \leq x_i \leq 5.12$	$(0, 0, \dots, 0)$

The input patterns in competitive Hebbian rules are generated as the middle of random selected two points in the population, and the number of patterns $M = 5N$.

In this paper, 30 independent runs are performed. Each run stops when a near optimal solution is found. In this paper, the difference between the objective value of the near optimal solution and the optimal value is less than 10^{-7} . Algorithms DE/rand (fixed parameters of $F = 0.7$, $CR = 0.9$), DE/rand

Table II
FEATURES OF TEST PROBLEMS

Function	modality	surface	dependency of variables	ill-scale
f_1	unimodal	smooth	—	—
f_2	unimodal	steep	strong	—
f_3	unimodal	steep	strong	strong
f_4	multimodal	bumpy	—	—

(variable parameters according to Eq. (6) and (7)) and SDE-G/species-best are compared.

B. Experimental Results

Table III shows the experimental results. The mean number of FEs until finding a near optimal value and their standard deviation are shown in the top row for each function. Also, the ratio of the mean number of FEs relative to that of the DE with fixed parameters is shown in the bottom row using parentheses. SDE-G can solve the problems f_2 and f_3 within 30% FEs compared with the DE with fixed parameters and in about 60% FEs compared with the DE with variable parameters, solve the problems f_1 in about 50% FEs, and solve the problem f_4 in about 80% FEs. This, SDE-G can reduce a large number of FEs compared with standard DEs.

Table III
RESULTS OF DE AND SDE-G OVER 30 INDEPENDENT RUNS

	DE fixed params.	DE variable params.	SDE-G
f_1	57899.2 ± 1281.1 (1.000)	62902.5 ± 845.8 (1.086)	31091.3 ± 1278.8 (0.537)
f_2	561565.7 ± 17282.9 (1.000)	309062.5 ± 17773.1 (0.550)	127584.9 ± 5273.2 (0.227)
f_3	558257.7 ± 16191.2 (1.000)	307098.4 ± 16518.4 (0.550)	164333.8 ± 9192.4 (0.294)
f_4	160205.0 ± 4865.9 (1.000)	163358.9 ± 3816.8 (1.020)	129007.1 ± 4897.2 (0.805)

Figure 2 shows the number of unique seeds that shows the diversity of the search. In f_1 , the diversity is almost constant. However, in f_2 and f_3 with ridge structures the diversity is high. Also, in f_4 of multimodal problem the diversity is high at the middle search stage (and after finding the optimum and converging to it). It is shown that graph-based speciation can adjust the number of unique seeds and the diversity.

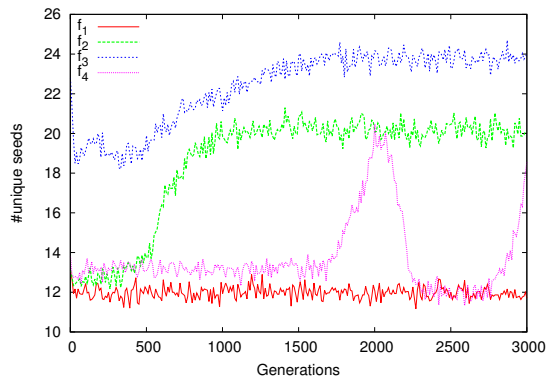


Figure 2. The change of the number of unique seeds over generations

VI. CONCLUSION

We have proposed SDE-G/CHR that utilizes graph-based speciation using competitive Hebbian rules. It is shown that SDE-G/CHR can find optimal solutions stably in unimodal,

multimodal problems and problems with ridge structures. Also, it is shown that SDE-G/CHR can reduce a lot of function evaluations compared with DE. We plan to apply the proposed method to constrained optimization problems.

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