

An Attraction Basin Estimating Genetic Algorithm for Multimodal Optimization

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ABSTRACT

Radii-based niching evolutionary algorithms are criticized for the difficulty of the proper choice of the radius parameter. Detect-multimodal method enables the identification of niches without an explicit user-defined radius parameter. Although robust, the detect-multimodal method based algorithms are computationally expensive. We propose a novel algorithm called Attraction Basin Estimating Genetic Algorithm (ABE), which estimates the radius parameter based on the detect-multimodal method and uses the estimated radius to identify niches. Our experiments demonstrate that ABE has a similar ability to solve the multimodal optimization problem as Topological Species Conservation algorithm which is based on the detect-multimodal method, but much more efficiently.

Categories and Subject Descriptors

I.2.8 [Artificial Intelligence]: Problem Solving, Control Methods, and Search—*heuristic methods*

Keywords

Multimodal Optimization, Detect-Multimodal Method

1. INTRODUCTION

Multimodal optimization aims to discover all or most optima (peaks) as opposed to a single best optimum. Evolutionary Algorithm (EA) has a natural advantage in this field, because they are population based. However, a Standard EA tends to converge only to a single optimum.

Niching method tries to maintain the diversity of the population. Most niching methods introduce a radius parameter [1, 4]. A species (subpopulation) is defined as a subset of individuals where the distance between every two members is smaller than the diameter given by the user-defined radius parameter. Each species is built around the best local

individual, called seed. However, it is hard to accurately set the radius parameter. Radii-based methods also assume that the fitness landscape is even.

Detect-multimodal method [6], also called hill-valley detection method [2, 3], has an ability to detect if two individuals track the same optimum. It calculates the fitness of a number of interior points on the line between two individuals. If the fitness of an interior point is lower, in the maximization problem, than that of both the individuals, then the two individuals are considered to track different optima, implying that the two individuals should be separated into different species. This method is robust to irregular landscapes and does not necessitate using radius parameters. However, algorithms based on this method, such as Topological Species Conservation (TSC) [5] and its improved version TSC2 [6], require a large number of fitness evaluations in order to evaluate the interior points, which can be considered inefficient.

In this paper, we propose an algorithm called Attraction Basins Estimating Genetic Algorithm (ABE), which can be considered as a combination of the radii-based method and the detect-multimodal method. The proposed algorithm tries to build a memory called Seed Archive which stores seeds tracking different optima and their corresponding attraction basins. The attraction basin is defined as the biggest hyper-sphere that contains no valleys around a seed. We present a method to estimate the attraction basin for a seed in this paper. Two individuals are considered in the same species simply by testing if they are in the attraction basin of the same seed.

2. METHODOLOGY

We introduce two new variables to a seeds: *lowerbound* and *upperbound*. *Lowerbound* is used as the radius of the hyper-sphere, whereas *upperbound* is an intermediate value used to estimate *lowerbound*. At first, *lowerbound* and *upperbound* are initialized to zero and positive infinity, respectively. We say seed x is covered by y if the fitness of x is smaller than that of y , in addition, the distance between x and y is smaller than the *lowerbound* value of either x or y .

We estimate the attraction basins based on the detect-

Table 1: Criteria value

Tests	peak ratio		peak acc.		dis. acc.	
	ABE	TSC2	ABE	TSC2	ABE	TSC2
F1	0.96	0.97	0.772	0.292	1.363	0.258
F2	0.92	0.68	0.416	0.637	0.408	0.743
F3	1.00	0.97	0.053	66.59	0.016	0.479
F4	0.95	1.00	0.163	0.011	0.187	0.025
F5	0.91	1.00	0.158	0.181	0.026	0.028
F6 2D	0.72	0.17	206	254	0.392	0.081
F6 10D	0.00	0.00	451	562	12.56	12.85
F7	0.80	1.00	0.106	0.124	4.137	0.904

multimodal method. When two seeds x and y are considered to track different optima, the distance between them is calculated and checked if it is smaller than the *upperbound* values for both. If so, the *upperbound* and *lowerbound* values are set to that distance. when x and y are considered to track the same optimum, the *lowerbound* of the seed with better fitness is set to the distance in case it is smaller than the *lowerbound*. Finally, the *lowerbound* is not allowed to be higher than the *upperbound*.

Seed Archive is updated at each generation throughout the following three steps. First, a number of individuals are selected from the population by a standard selection operator. If a selected individual is not covered by any seeds in Seed Archive, then it is stored into Seed Archive as a new seed. Second, the algorithm estimates the attraction basins of a number of the seeds in Seed Archive. When given a seed x , it can be tested with the other seeds around it in order starting from the closest one, or a randomly generated point within its attraction basin. Third, seeds covered by the other seeds in Seed Archive are deleted.

3. EXPERIMENTS

We compare ABE with TSC2 on the benchmark test functions F1,F2,F8,F12,F4,F5,F14 in TSC2[6]. They are renamed as F1-F7 in this paper. We employs peak ratio, peak accuracy, distance accuracy[6] as performance criteria.

The population size is 100, and the crossover rate is 0.6. The mutation rate and mutation strength are manually tuned for each functions. The maximum generation is 3000 for F6 with 10 dimensions and 1000 for other functions. The range of each dimension in genotype is $[-10,10]$, which is mapped to the range of the test functions in the phenotype.

We perform 10 runs for each test function and show the average results in Table 1. F1-F4 aim to test the ability of detecting multiple optima. ABE has similar results as TSC2 on F1, F3 and F4, but significantly better on F2. F5-F7 aim to test the ability to escape the local optima and find the global optimum. TSC2 performs slightly better than ABE on F5 and F7. On F6 with two dimensions, ABE performs significantly better than TSC2. On F6 with 10 dimensions, neither of the two algorithms is able to detect the global optimum. However, ABE achieve a better result for the peak accuracy comparing with TSC2.

In order to compare the computational cost of the two algorithms, we consider the peak ratio for F1-F4, and the peak accuracy for F5-F7 as criteria. For each test function, we separate the range of the criterion averagely into 100 levels and calculate the fractions between the evaluations

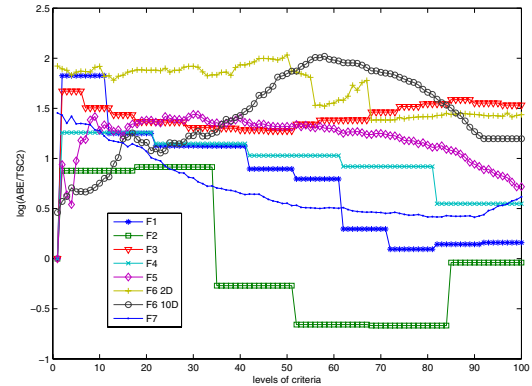


Figure 1: Computational Cost

spent by TSC2 and ABE to reach the same levels. The range of the criterions considered is 0 to 1 for F1-F4, 125 to 0 for F5, 600 to 0 for F6 with 2 dimensions, 1500 to 0 for F6 with 10 dimensions, 0.65 to 0 for F7. As shown in Fig. 1, the x-axis is the fractions which are log 10-transformed, and the y-axis is the levels. Through Fig. 1, it can be clearly seen that TSC2 spends much more evaluations to reach the same level comparing to ABE.

4. CONCLUSION

In the experiments, the abilities to detect multiple optima and to escape from local optima were investigated. The results indicated that ABE has a similar ability to solve the multimodal optimization problem as TSC2. Considering the computational cost, ABE performed much more efficiently than TSC2. Future work is to study more problems and setups.

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