

CONTRASTING TERMINATION CRITERIA FOR GENETIC ALGORITHMS

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Abstract

To find a good termination criterion for genetic algorithms is a difficult and frequently ignored task. In most instances the practitioner stops the algorithm after a predefined number of generations or function evaluations. How this number is established? This stop criteria assume a user's knowledge on the characteristic of the function, which influence the length of the search. But usually it is difficult to say a priori that the total number of generations should be a determined one. Consequently this approach can involve a waste of computational resources, because the genetic algorithm could stagnate at some local or global optimum and no further improvement is achieved in that condition.

This presentation discusses performance results on evolutionary algorithms optimizing four highly multimodal functions (Michalewicz's F1 and F2, Branin's Rcos, Griewank's). The genotypic and phenotypic approaches were implemented using the Grefenstette's *bias b* and the *stability of mean population fitness* as measures of convergence, respectively. Quality of results and speed of convergence are the main performance variables contrasted.

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1. Introduction

According to Michalewicz's report [4], some approaches consider the characteristics of the search for making termination decisions and them can be divided into two categories.

The first category, based on the chromosome structure (genotypic), measures the convergence of the population in terms of the number of converged alleles. Here, an allele is considered converged if some predetermined percentage of the population have the same, or similar, value in this allele.

Grefenstette [3] introduced the *bias* b (called *bias measure*) to define the *population diversity* as follows:

$$b(P(t)) = \frac{1}{l \cdot \mu} \sum_{j=1}^l \max \left(\sum_{\substack{i=1 \\ a'_{i,j}=0}}^{\mu} (1 - a'_{i,j}), \sum_{\substack{i=1 \\ a'_{i,j}=1}}^{\mu} a'_{i,j} \right)$$

where l is the chromosome length and $a'_{i,j}$ denotes the allele value.

The bias b ($0.5 \leq b \leq 1.0$) indicates the average percentage of the most outstanding value in each position of the individuals. Smaller values of b indicate higher genotypic diversity ~~and vice versa. The bias b can be used to formulate an adequate termination criterion.~~

Bäck and Hoffmeister [1], [2] used this concept to establish genotypic diversity.

The second category (phenotypic), based on the 'meaning' of a particular chromosome, measures the progress made by the algorithm in a predefined number of generations and the search is terminated if such progress is smaller than some epsilon. According to this category a genetic algorithm stops if the fitness of the best individual, or the mean population fitness does not change after certain number of generations. Stop criteria which considers characteristics of the search are also known as methods of *improvement probability bound*.

2. Experiments

Two stop criteria were used for testing: the *bias criterion*, a genotypic approach, and the *mean population fitness criterion*, a phenotypic approach.

A hundred series of simple but not canonical genetic algorithm was run, with conventional parameters values, elitism, one point crossover and bit flip mutation.

For the *bias criterion* (b) a value of $b = 0.9$ and a difference $\epsilon = 0.06$ between consecutive generations were used to stop the algorithm.

In the case of the *mean population fitness criterion* (MPF) a difference of $\epsilon = 0.0001$ is used and must be maintained through a given number of consecutive generations to stop the algorithm.

The following testing functions were used.

f1: Michalewicz's multimodal function

$$f(x_1) = 2.0 + x_1 \cdot \sin(10\pi \cdot x_1)$$

$$-1.0 \leq x_1 \leq 2.0$$

estimated maximum value : 3.850274

f2: Michalewicz's highly multimodal function

$$f(x_1, x_2) = 21.5 + x_1 \cdot \sin(4\pi \cdot x_1) + x_2 \cdot \sin(20\pi \cdot x_2), \text{ for } : \\ -3.0 \leq x_1 \leq 12.1, \quad 4.1 \leq x_2 \leq 5.8 \\ \text{estimated maximum value} : 38.850292$$

f5: Branin's Reos Function

$$f_4(x_1, x_2) = \left(x_2 - \frac{5.1}{(4 \cdot \pi^2)} \cdot x_1^2 + \frac{5}{\pi} \cdot x_1 - 6 \right)^2 + 10 \cdot \left(1 - \frac{1}{(8 \cdot \pi)} \right) \cdot \cos(x_1) + 10, \\ x_1 = -5:10, \quad x_2 = 0:15; \\ \text{minimum global value} : 0.397887$$

f6: Griewangk's Function F8

$$f_1(x_i) = 1 + \sum_{i=1}^5 \frac{x_i^2}{40000} - \prod_{i=1}^5 \left(\cos\left(\frac{x_i}{\sqrt{i}}\right) \right), \\ x_i = -6000:6000, \quad i = 1:5, \\ \text{minimum global value} : 0.0$$

As an indication of the performance of the algorithms the following relevant variables were chosen:

$$E_{\text{best}} = (\text{Abs}(\text{opt_val} - \text{best value}) / \text{opt_val}) 100$$

It is the percentile error of the best found individual when compared with the known, or estimated, optimum value *opt_val*. It gives us a measure of how far are we from that *opt_val*.

$$E_{\text{pop}} = (\text{Abs}(\text{opt_val} - \text{pop mean fitness}) / \text{opt_val}) 100$$

It is the percentile error of the population mean fitness when compared with *opt_val*. It tell us how far the mean fitness is from that *opt_val*.

R = (mean fitness/ last generation number). It is a benefit/cost ratio where the benefit is seen as the fitness reached and the cost is seen as the number of generations needed to reach that fitness.

3. Conclusions

Testing functions of diverse complexity were considered and the same genetic algorithm with identical initial population were run to optimize them under different termination criteria.

In general it was determined better quality of results by using the bias criterion and this result is more strongly detected as long as the fitness landscape is more complex. It seems that the method allows to discover more precisely those improvements occurring from one generation to the next.

Nevertheless the mean population fitness criterion is a better criterion than a fixed number of generations and requires less computational effort than the bias criterion.

4. Bibliography

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A COMPARISON OF FITNESS SCALING METHODS IN EVOLUTIONARY ALGORITHMS

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Abstract

Proportional selection (PS), as a selection mechanism for mating (reproduction with emphasis), selects individuals according to their fitness. Consequently the probability of an individual to obtain a number of offspring is directly proportional to its fitness value. This can lead to a loss of selective pressure in the final stages of the evolutionary process degrading the search.

This presentation discusses performance results on evolutionary algorithms optimizing two highly multimodal (Michalewicz's and Griewank's) functions and a hard unimodal (Easom's) function. Experiments were addressed to contrast the behaviour of a simple genetic algorithm against three scaling methods: linear, sigma truncation and recency-weighted-running-average. Diverse measures of performance were used to establish quality of results and convergence speed.

1. Introduction

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