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Procedia Computer Science 102 (2016) 570 – 577

Procedia
Computer Science

12th International Conference on Application of Fuzzy Systems and Soft Computing, ICAFS 2016, 29-30 August 2016, Vienna, Austria

Modeling the dynamics of a changing range genetic algorithm

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Abstract

The paper extends an approach of modeling the dynamics of the genetic algorithm that based on the methods from statistical physics. These methods are applied to describe the effect of an adjustment of a search space size of GA according to a power law on the macroscopic statistical properties of population such as the average fitness and the variance fitness of population. An interaction of the various genetic algorithm operators and how these interactions give rise to optimal parameters values is studied. The equations of motion are derived for the one-max problem that expressed the macroscopic statistical properties of population after reproductive genetic operators and an adjustment of a search space size in terms of those prior to the operation. Predictions of the theory are compared with experiments and are shown to predict the average fitness and the variance fitness of the final population accurately.

Peer-review under responsibility of the Organizing Committee of ICAFS 2016

Keywords: genetic algorithms; optimization; statistical mechanics techniques.

1. Introduction

Genetic Algorithm (GA) has become popular tools for search, optimization, machine learning and solving design problem. These algorithms use simulated evolution to search for solutions of a complex problem. A GA is a population-based computational method where the population using randomized processes of selection, crossover, and mutation evolves towards better solutions[1]. To solve efficiently the different complex problems a GA employs a different set of operators that include the common operators of GA like selection, mutation and crossover operators, and the operators which are specific for a particular GA. There are several surveys available[1-5] which discuss in details the implementation of a different set of operators and their advantages and disadvantages.

One way to improve a search strategy is to reduce the search space towards the feasible region where the global optimum is located. These approaches dynamically adjust a search space size and direct GA to the global optimum. These approaches are based on the idea that a parameter-space size adjustment improves accuracy of the discrete sampling in the solution space and significantly reduces the computational time to reach the global optimum[6-10]. Amirjanov[11] analyzed these approaches and employed statistical mechanics techniques to make a mathematical

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Peer-review under responsibility of the Organizing Committee of ICAFS 2016
doi:10.1016/j.procs.2016.09.444

modeling of an adjustment of a search space size. The statistical mechanics approach models an ensemble of populations to find an average of some population statistics. The statistical properties of the ensemble won't fluctuate, even though the members of the populations will. According to this approach to model a changing range genetic algorithm (CRGA) the following equations can be derived to take the population of a CRGA from a generation t to a generation t+1:

$$\begin{pmatrix}\mu(t)\\ \sigma(t)\end{pmatrix} \xrightarrow{selection} \begin{pmatrix}\mu_s(t)\\ \sigma_s(t)\end{pmatrix} \xrightarrow{mutation} \begin{pmatrix}\mu_m(t)\\ \sigma_m(t)\end{pmatrix} \xrightarrow{crossover} \begin{pmatrix}\mu_c(t)\\ \sigma_c(t)\end{pmatrix} \xrightarrow{size\,adjustment} \begin{pmatrix}\mu_a(t)\\ \sigma_a(t)\end{pmatrix} = \begin{pmatrix}\mu(t+1)\\ \sigma(t+1)\end{pmatrix} \tag{1.1}$$

In the paper[11] for modeling a GA with dynamical adjustment of a search space size the one-max problem was considered where each site contributed a different amount to the cost of solution. Every individual of population was defined by L binary variables, $x_i \in \{0,1\}$ with weight J_i, and it was mapped to the interval [u_l, u_u], where u_l is a lower bound and u_u is an upper bound of a specified interval. The problem was to optimize a cost function E over the x's,

$$E_\alpha = u_l + (u_u - u_l)\cdot\sum_{i=0}^{L-1} J_i \cdot x_i^\alpha \tag{1.2}$$

where the J_i are fixed weights at each site.

However, the paper[11] focused only on mathematical description of a size adjustment operator by considering for large selection rates and/or large mutation rate that the population converges rapidly towards its asymptotic limit, where the average fitness and the variance fitness are not changeable by selection, mutation and crossover operators.

This paper will focus on deriving the equations that describe the effect of all CRGA's operators on the macroscopic statistical properties of population which change in time. The full dynamics will be calculated by iterating the sequence in (1.1) starting from the initial population.

2. The genetic algorithm model

3. The goal of the modeling is to assess the evolution in the distribution of fitness of population. It means that, for each GA's operator, the distribution of fitness should be calculated after that operator is applied. In this paper we assume that the distribution of fitness is Gaussian[12]. As a result it is sufficient to consider only $\mu(t)$ and $\sigma^2(t)$.

3.1. Selection dynamics

Selection is the operation whereby more fit strings are increased in the population at the expense of less fit ones. The effect of selection on the distribution of phenotypes within the population is independent of the genotype to phenotype mapping for a particular problem. This is a consequence of the fitness being a function of the phenotype only. It is therefore possible to model selection without reference to a specific problem.

The binary tournament selection is used as a GA selection operator in this paper. In binary tournament selection two members are randomly drawn from the population and the fitter member is copied into the mating pool. Blickle and Thiele[13] obtained the following expressions for infinite population to assess the effect of selection on the average and the variance fitness of population:

$$\mu_s = \mu + \frac{\sigma}{\sqrt{\pi}} \tag{2.1}$$

$$\sigma_s^2 = \left(1 - \frac{1}{\pi}\right)\cdot\sigma^2 \tag{2.2}$$

4. The expressions (2.1, 2.2) were obtained for an infinite population. However, the macroscopic properties of any finite population drawn from the ensemble will differ slightly due to well-known sampling effects[12]. It can be seen that the mean is unchanged, but the variance of a finite population is reduced. Because of a finite population correction the formulae (2.1, 2.2) can be rewritten as follows:

$$\mu_s = \mu + \frac{\sigma}{\sqrt{\pi}} \tag{2.3}$$