Coevolutionary Multiagent Systems in multimodal optimization

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Abstract

1 Introduction

Evolutionary algorithms (EA) have been applied with a great deal of success to problems coming from a spectrum of disciplines. A simple EA can be used to search optimum of unimodal functions in a bounded search space. However, in the case of functions characterized by multiple peaks (multimodal functions) both experiments and analysis show that a simple EA will converge to a single solution — even when the best peaks are equally fit [3, 7]. The tendency of convergence to a single solution is caused by the *genetic drift* [2].

There are various real world tasks, however, in which we wish to locate all maxima of a multimodal function because peaks of comparable fitness can provide usefull alternative solutions to the given problem. Examples of such a task include identification of a set of diverse rules that together can be used as the basis of a classifier system [4].

In order to overcome limitations of a simple GA a mechanism that creates and maintains different subpopulations (species) within the search space must be used. Such mechanisms are called "niching methods" [7].

2 Niching methods for evolutionary algorithms

In nature, there exist different subspaces within the environment, which support different types of life (*species*). The number of organisms contained within each niche depends on niche fertility (its *carrying capacity*) and the efficiency at each organism exploits the niche resources. If there are too many organism in a given niche, the least efficient of them will die because of resource shortages. And conversely, if there are too few organisms in a very fertile niche, they will reproduce quickly so as resources of a given niche will be fully exploited.

In case of a multimodal function every peak can be treated as a niche. The number of individuals that live within a niche should be in direct proportion to niche's carying capacity. Carrying capacity in this case means peak's fitness relative to other peaks present in multimodal domain. This is called "niche proportionate population".

The aim of niching methods is to form stable subpopulations (species) in order to:

1. detect all peaks within multimodal domain, and

2. slow down convergence in case when only one solution is needed.

As a result various mechanisms have been proposed to stably maintain species throughout the search process, thereby allowing to identify all peaks of a multimodal function. All these techniques allow niche formation through the implementation of crowding, fitness sharing or some modification of these mechanisms.

Every niching technique can also be classified as *parallel* or *sequential*. Parallel niching methods form and maintains species simultaneously within a single population (regardless of the number of processors used). Sequential niching methods locate multiple peaks temporally, one after another [6].

2.1 Crowding

Crowding based techniques are inspired by an ecological phenomenon. In natural population similar individuals (often of the same species) compete for limited resources. Individuals of different species usually do not compete for resources because they occupy different ecological niches.

One of the first attempts to introduce niching into GA was Cavicchio's "preselection scheme" [1]. The goal of this scheme is to preserve diversity. In preselection scheme children replaces less fit of two parents only when it has higher fitness than parent.

The crowding technique [2] was aimed at preservation of genotype diversity in population. Crowding technique works as follows. Each generation, a proportion of the population G (*generation gap*) is selected (via fitness proportionate selection) for reproduction. For each offspring, a certain number — CF (crowding factor) — of individuals are selected at random. The most similar individual, according to a similarity metric, is then replaced by the offspring. As a similarity metric De Jong used Hamming distance in genotypic space. Crowding does not propote the formation of stable species, but

rather aims at maintaining the diversity of initial population.

Mahfoud developed niching mechanism called "deterministic crowding" [5]. He showed that similarity metrics based upon phenotypes should be prefered to genotype based ones. It was also demonstrated that there was very high probability that the most similar individual to offspring should be searched among its parents. The new offspring is directly compared to their parents. In deterministic crowding parent is replaced only if the children have higher fitness. To determine which of the two possible parent-children pairings should be used in the process of comparing parents to their offspring the total similarities were determined for each possible combination. The pairing that had the highest total similarity (according to some similarity metric) was used.

Probabilistic crowding developed by Mengshoel and Goldberg [8] is based upon Mahfoud's deterministic crowding. The main difference to deterministic crowding is the use of a probabilistic rather than a deterministic acceptance function. This means that stronger individuals win proportionally according to their fitness. The probability of wining the tournament by individual x is

$$P_x = P(x) = \frac{f(x)}{f(x) + f(y)} \tag{1}$$

where f is fitness function.

2.2 Sharing

Fitness sharing was first introduced by Holland [**?**] and further developed by Goldberg and Richardson [**?**]. The main goal was to reduce the fitness of individuals that have highly similar members within the population. This models the ecological fenomenon of competition for limited resources between individuals that occupy the same niche. Fittness sharing technique reduces the fitness of individuals that have highly similar members within the population. Such a mechanism rewards unique individuals and punishes highly similar individuals within the population. The reduced fitness of an individual i is given by

$$f_i' = \frac{f_i}{m_i} \tag{2}$$

where f_i is its raw fitness and m_i is the niche count given by

$$m_i = \sum_{j=1}^{n} sh(d_{ij}) \tag{3}$$

The sharing function is a function of a distance between two individuals of a population. It returns a '1'

$$sh(d) = \begin{cases} 1 - (\frac{d}{\sigma_{sh}})^\alpha & \text{if } d < \sigma_{sh}, \\ 0 & \text{otherwise.} \end{cases} \tag{4}$$

α is commonly set to 1.

3 Niching Coevolutionary Multi-agent Systems

3.1 Evolutionary multiagent systems

3.2 Coevolutionary Multiagent Systems

4 First simulation experiments

4.1 Test functions

4.2 Results

5 Conclusions

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