Survey of Methods to Prevent Premature Convergence in Evolutionary Algorithms

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I. EXTENDED ABSTRACT

Evolutionary algorithms (EA) are general metaheuristic algorithms which have very good characteristics. They are relatively robust and usually generate very good solutions to hard problems [15], [16], [23], [29]. However, they also have many problems with the population converging to a sub-optimal solution instead of an optimal one [27], [28]. This occurrence is called premature convergence, and it is of great importance to develop EAs that consistently avoid it.

Premature convergence is closely related to the diversity of the population. The mutation rate, crossover rate, and selection method of a particular EA reflect the trade-off the algorithm has made between exploration of the search space of the problem and exploitation of the current knowledge [6], [9], [23]. However, the need for diversity within the population is not always constant – in the beginning stages of an EA search, diversity is helpful for finding promising areas of the search space, but in later stages it is essential to exploit the information already known. Each new study using an EA seems to have a new method to prevent premature convergence and it is not clear which works best under what conditions [1], [10], [12], [19], [21], [22], [32]. Therefore, this work will summarize and organize the current methods to prevent premature convergence and the ways to measure their effectiveness.

The methods can be broken down into three main categories – structured populations to lower the transfer rate of genetic material between individuals, selection operators that lower selection pressure or help to retain diversity, and the storage and reintroduction of genetic material [27].

The structured population methods work to avoid premature convergence by separating populations and limiting the rate of genetic transfer between them. This generates diversity through design, as genes do not spread as quickly throughout the population. Some actually separate the populations into large “islands” and periodically migrate an individual between islands [3], [30]. Another popular structured method is to introduce spatial structure to the population, so that individuals may only reproduce with neighbors [14], [18].

One example of selection operators is fitness sharing, which works by emulating niches in normal evolution [8], [15]. In this method, solutions are penalized during the assignment of fitness for occupying closely related portions of the fitness landscape. This encourages further exploration of the solution space of a given problem, however increases the complexity of the calculations for fitness, costing computation time. Other methods such as adapting the probabilities of crossover and mutation, either based on population characteristics or individual fitness, have been used to help prevent convergence [7], [24], [26], [27].

The retention of genetic material for later re-injection into the population is another popular means of retaining diversity [13], [32]. Elitist genetic algorithms that save good solutions from past populations for future re-injection are popular and effective [4], [16]. These methods inject whole individuals into the population to retain genetic diversity. Genetic algorithms which inject random individuals have also been used with good effect in dynamic optimization problems [25]. An interesting alternative is the virus evolutionary genetic algorithm, which uses the analogy of a virus to inject substrings from one member of a population to another [11].

Each of these methods aim to solve the problem of premature convergence by encouraging exploration and less exploitation in the population, though particular methods are often tailored to specific problems. For example, dynamic optimization problems require more exploration to shift the population in response to the environment – the insertion of random individuals acts as to insert new material for crossover in order to permit those shifts [25].

There are few empirical studies of just how well these methods work in their goal, even though many researchers have previously proposed diversity measurements of a population [2], [5], [17], [31]. When looking at the genotypic diversity, entropy and Hamming distance are commonly used [17]. Another alternative is to look at the diversity of the fitness scores [2], [20]. However, it is well known that many diversity measuring methods are inherently linked to either the representation of the problem or to problem space itself [6].

Thus, the problem of premature convergence is a challenging one. As a start, more work needs to be done to clarify the concept and provide a link between diversity and convergence. Once an appropriate measure has been developed (if possible), the different techniques discussed above should be tested empirically for their effectiveness. Perhaps the techniques may only be able to be tested for a small subset of problems, but the field of evolutionary computation can only benefit from the effort.
REFERENCES


