A Parallel Genetic Algorithm with Distributed Environment Scheme

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Abstract

This research deals with the effect of crossover and mutation rates in parallel distributed GA, and introduces an alternative approach to relieving the task of choosing optimal mutation and crossover rates with distributed environments. It is shown that the best mutation and crossover rates depend on the population sizes and the problems, and those are different between a single and multiple populations. The proposed distributed-environment GA uses various combination of the parameters as the fixed values in the subpopulations. The excellent performance of the new scheme is recognized for several standard test functions. It is concluded that the distributed-environment GA is the fastest way to gain the best solution under the given population size unless the appropriate crossover and mutation rates are known.

1 GA with Distributed Environments

We propose a new PDGA (Parallel Distributed GA) with a distributed environment scheme, where a whole population is divided into several subpopulations, and the GA parameters such as the mutation rate and the crossover rate in each subpopulation are different from each other, as shown in Figure 1, where the thermometers represent the mutation ratse and the heart symbols represent the crossover rates. High temperature means a high mutation rate and the big heart symbol means a high crossover rate. This scheme is called the PDGA/DE (PDGA/Distributed Environment). With PDGA/DE, it can be expected that the various building blocks of an optimum solutions for a particular problem are evolved in various subpopulations, and migration provides the global optimum. The tuning of GA parameters is not necessary with PDGA/DE since many combinations of such GA parameters are used in many subpopulations.

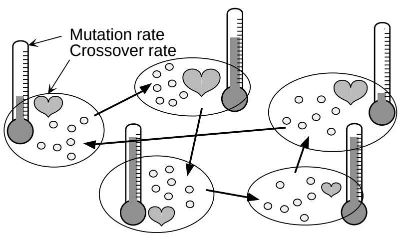

Figure 1: PDGA/DE (Distributed Environment)

2 Effectiveness of PDGA/DE

To demonstrate the effectiveness of the proposed scheme, a PDGA/DE with 9 subpopulations was performed. The combination of the crossover rates of 0.3, 0.6 and 1.0, and the mutation rates of 0.1/L, 1/L and 10/L, where L is the length of the chromosome, are used. The computer used is a parallel computer, nCUBE2, and one processor is assigned to one subpopulation. The optimization problems used here are the minimization of standard test functions.

The performance of PDGA/DE can be seen in Figure 2 for the overall population size of 180 and 1620, where the fitness value at 1000 generations are compared. These results show the performance of PDGA/DE compared with the results obtained by CGA (Canonical GA) and PDGA/CE (Constant Environment). The advantage of PDGA/DE is clear from the results. Consequently, PDGA/DE is the fastest way to gain a good solution under the given population size unless appropriate crossover and mutation rates are known.

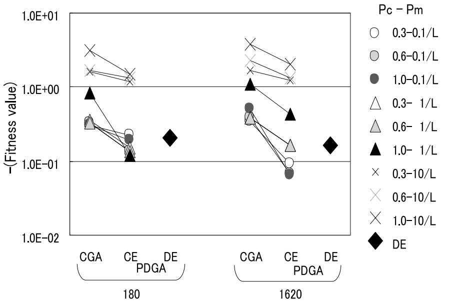

Figure 2: Comparison of the performance of DEGA with CGA and PDGA (Griewank function)