Parallel Genetic Algorithms with Distributed-Environment Multiple Population Scheme

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1. Abstract

This paper proposes a new approach where some of the parameters in genetic algorithms are not necessary to be predetermined. The optimization problem is to minimize the volume of truss structures under tensile, buckling, and displacement constraints. The whole population is divided into several subpopulations which are called islands, and a migration scheme which moves some individuals in one island to another island is adopted to mix various individuals. In the proposed approach, different values of the mutation rate and the crossover rate are assigned to different islands, that is, the GA environments of the whole islands are not the same. The distributed environment scheme shows a good performance compared to conventional distributed algorithm. This scheme does not need to predetermine the GA parameters, and it is very useful for many problems where the proper values of those parameters are not known.

2. Keywords

Genetic Algorithms, Parallel Processing, Distributed GA, Distributed Environment

3. Background

Genetic algorithms[1] are one of the most popular optimization approaches for complicated problems, but they have some drawbacks. Firstly, GAs require many iterations of computations, and secondly, they are apt to yield premature convergence. Thirdly, they have some difficulty in determining appropriate values of some parameters such as the crossover rate and the mutation rate. Parallel and distributed genetic algorithms have a possibility of overcoming these disadvantages.

In parallel GAs, global population models have a single large population where one processor is assigned to treat some individuals and each individual has global interaction with each other, while island models have multiple and smaller populations and exchange information among the subpopulations; this exchange is performed by moving some individuals from one population to another and is known as migration. The distributed GAs (DGAs) have another merit in addition to speedup. Tanese showed the ability of finding fitter individuals than the traditional one[2]. Belding extended Tanese's work on DGA to the different fitness functions (the royal road problem) in order to determine whether her results were specific to the Tanese functions[3]. He showed that DGA outperformed canonical GAs (CGAs: single population GAs) for the functions which are not easy for canonical GAs. From these results, we can conclude that DGAs outperforms CGAs in some sense.

On the other hand, the performance of each GA depends on the good choice of the crossover and the mutation rates. However, it is difficult to choose a proper combination of these parameters. Tuson and Ros[4] showed that the most suitable crossover rates also depend upon the problem to be solved. Those results are obtained for canonical GAs with a single population, and researches that deal with the good choice of the crossover and mutation rates in distributed GAs which has multiple populations are very few.

This paper presents a good performance of parallel and distributed genetic algorithms for a structural optimization problem and proposes a new approach where some of the parameters in the algorithms are not necessary to be predetermined.

4. Optimization Problems and GA procedures

To investigate the effect of the mutation rate and the crossover rate, the following structural optimum design problem is considered. The optimization problem here is the minimum volume problem of a 10-member truss under the constraints on the tensile strength, compressive buckling and displacement. The detail of this problem is described in [5].

The fitness function is as follows:

$$\begin{aligned}
&\text{Fittness} = 1 / H, \qquad H = w_{\mathrm{v}} V_{\mathrm{T}} + P_{\mathrm{d}} + P_{\mathrm{t}} + P_{\mathrm{b}} \\
&P_{\mathrm{d}} = w_{\mathrm{d}} d_6^2 \quad \mathit{if}\ d_6 > d_6^* \\
&P_{\mathrm{t}} = \sum_{i=1}^{N_m} P_{it} \quad P_{i\mathrm{t}} = 1 \ \ \mathit{if}\ \sigma_i > \sigma^*, \quad P_{i\mathrm{t}} = 0 \ \ \text{otherwise} \\
&P_{\mathrm{b}} = \sum_{i=1}^{N_m} P_{i\mathrm{b}} \quad P_{i\mathrm{b}} = 1 \ \ \mathit{if}\ L_i > L_i^*, \quad P_{i\mathrm{b}} = 0 \ \ \text{otherwise}
\end{aligned} \tag{1}$$

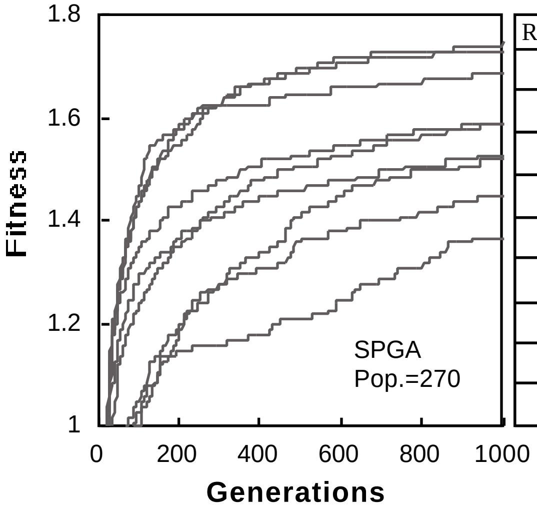
where H is a Lagrange function, V_T is the total volume of the truss structure, P is the penalty function, the subscripts d, t, and b represent the displacement, tensile, and buckling constraints, respectively. W_v represents the weighting factor for the volume and is set to 600 according to the preliminary experiments. σ represents the tensile stress and L represents the buckling load in each truss member.

The design variables are the sectional areas of their members, and they are coded with a 10-bit Gray code yielding chromosomes. The length of the chromosomes is, therefore, 100 bits.

5. Effect of Mutation and Crossover Rates

The effect of crossover and mutation rates on the performance of GAs with a single population (SPGA: Single Population GA) and with a multiple population (MPGA: Multiple Population GA) are described here. Two SPGAs and two MPGAs were conducted with different population sizes, 270 and 2430, respectively. The mutation rates are 0.1/L, 1/L, and 10/L where L is the length of the chromosome, the crossover rates are 0.3, 0.6, and 1, and the combinations of these values are used, thus providing 9 cases for each condition. All the numerical results are the average of 10 trials out of 12 omitting the highest and lowest ones.

At first, a SPGA is performed to investigate the proper values of the crossover and mutation rates. Figure 1 shows the histories of the fitness for SPGA with the population of 270. The table right to the figure shows the performance ranking at 1000 generations and the mutation and crossover rates. It can be found that these GA parameters affect a remarkable difference in the evolution process. The similar result is obtained for SPGA with the population of 2430, where the different combination of the mutation and crossover rates shows a good performance.



Rank	Mutation	Crossover
1	1/L	0.3
2	1/L	0.6
3	1/L	0.1
4	0.1/L	1
5	0.1/L	0.3
6	0.1/L	0.6
7	10/L	0.3
8	10/L	0.6
9	10/L	1

Fig. 1 Evolution process in the single population GA.

Next, two MPGAs were conducted with 9 subpopulations having different subpopulation sizes, 30 and 270, respectively. The overall population sizes are 270 and 2430, respectively, which are the same as those used in the SPGAs. Therefore, the comparison between the SPGA and MPGA can be done for the same overall population sizes. The parallel computer used is nCUBE-2E with 64 processors.

The migration rate is 0.3 and the migration interval is 20 generations, but these values does not have a large sensitivity to the results. The migration scheme used is random-ring, which means that the destination subpopulations are randomly chosen at every migration under the constraint that the migration is performed from one subpopulation to one subpopulation.

The performance of the MPGA is remarkably good compared with the SPGA since the MPGA prevents the premature convergence by maintaining the diversity of individuals due to a certain isolation in the subpopulations. The effect of the mutation and crossover rates is also remarkable like the SPGA, but it has the different tendency.

From these results, it is found that the MPGA outperforms the SPGA, but the appropriate determination of the mutation and the crossover rates is found to be difficult.

6. A New Distributed GA with Distributed Environments

A new approach is proposed in the parallel and distributed algorithm where some GA parameters such as the crossover rate and the mutation rate are not predetermined. In this approach, different values of those parameters are assigned to different islands, that is, the GA environments of whole subpopulations are not the same as shown in Fig. 2. It can be expected that the solutions would find their proper environments for their evolution.

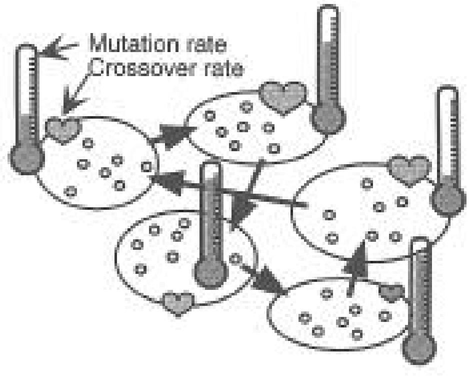


Fig. 2 Distributed-Environment GA.

Figure 3 shows the overall result comparing the fitness at 1000 generations for the SPGA, MPGA, and the DEGA (Distributed Environment GA, shown as DE in the figure). It is clear that the combination of the mutation and crossover rates affects the performance, the MPGA shows remarkably good performance compared to the SPGA, and the DEGA shows a excellent performance compared with all the results. It should be noted that the best mutation and crossover rates can only be determined after performing various experiments, while in the DEGA, such preliminary experiments are not necessary. Therefore, the DEGA can be considered to be the best approach unless a plenty of time is provided.

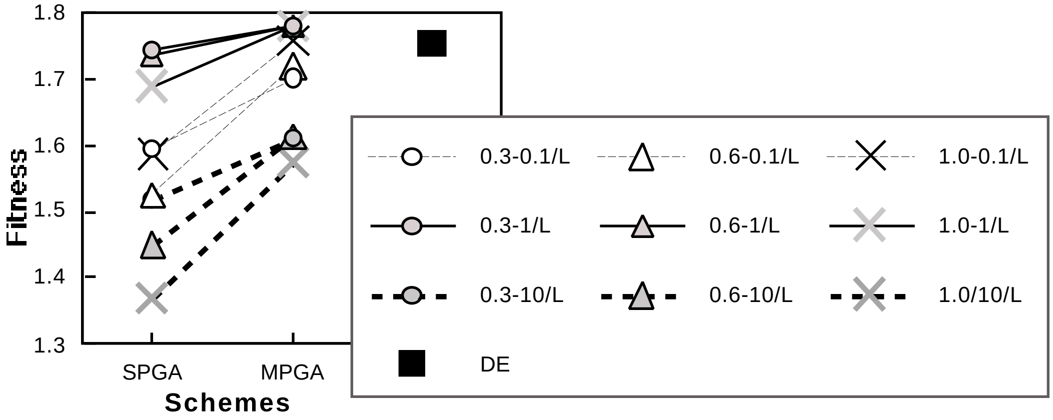


Fig. 3 Overall performance of SPGA, MPGA, and DEGA.

7. Conclusions

The following results were obtained from numerical experiments.

(1) The multiple population GA yields better solutions than the single population GA because the diversity of individuals are maintained in the multiple population GA during the evolutional process.

(2) The distributed environment scheme in the multiple population GA shows a good performance compared to other conventional GAs. This scheme does not need to predetermine the GA parameters, and it is very useful for many problems where the proper values of those parameters are not known.

8. References

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