A2-4   Research on Diversity Measure Based Fuzzy Adaptive Search Method for Parallel GA

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1   Introduction

GAs are stochastic search algorithms based on principles of natural selection and recombination and have been applied to several types of optimization problems by encoding design variables to individuals. However, GAs have also several issues. For example, the search efficiency of the ordinary GA is not always optimal especially in the early and final stage of the search, because GA parameters (crossover rate, mutation rate and so on) are fixed. The problem of the premature convergence and fall in the local solution also need to be solved.

In our laboratory, we have already proposed Fuzzy Adaptive Search method for Genetic Algorithm (FASGA) as the modified method [1]. In this method, we are able to realize the efficient search by describing fuzzy rules to tune genetic parameters (crossover rate, mutation rate and so on). In other words, the GA parameters are not fixed and varying with the search stage. So FASGA has quick search ability to obtain the best solution than GAs. But FASGA has not very good performance to obtain the higher quality solution, because it could not avoid the premature convergence and fall in the local solution completely.

On the other hand, some GAs in parallel methods were already proposed as the effective method for finding high quality solutions [2]. In parallel methods, the total population is divided into independent subpopulations. There are three kinds of distribution models: 1) master-slave model; 2) coarse-grained model (island model); 3) fine-grained model (cellular model)[3]. In this research, we adopt the island model for avoiding to propagation of local optimum solutions and call it as Parallel Genetic Algorithm (PGA). Because the existence of islands and the operation of migration, the variety of solutions is kept in PGA and higher quality solutions are able to be obtained than GAs. However, PGA is not always effective in using parallel processing because the migration rate of PGA is a constant. In fact, the migration of individuals is not necessarily performed only in case of necessity. To overcome this problem, many researchers have proposed the solved method, such as, a distributed genetic algorithm with the randomized migration rate [4], a parallel genetic algorithm with the distributed environment scheme [5] and so on.

Therefore, in this research, we propose Fuzzy Adaptive Search method for Parallel Genetic Algorithm (FASPGA) combined FASGA with PGA. FASPGA is the genetic algorithm in parallel method with both the quick search and high-quality solutions ability. In this method, parameters tuned by fuzzy rules are not only the crossover rate and mutation rate but also the migration rate. So an efficient migration can be realized in FASPGA. We have proved that FASPGA has better performance than PGA and FASGA in [6].

We have adopted the phenotypic parameters, maximum and average fitness as the inputs of fuzzy rules, but it could be considered that it is not enough to describe the search stage. Therefore, in this paper, as an improvement method for FASPGA, Diversity Measure based Fuzzy Adaptive Search method for Parallel GA (DM-FASPGA) is also proposed. In this method, we introduce the genotypic parameters, such as the hamming distance, into the fuzzy rule. In this paper, the computer simulation is executed to confirm the efficiency of FASPGA and DM-FASPGA and the simulation results also are reported.

2   Fuzzy Adaptive Search Method for Parallel Genetic Algorithms (FASPGA)

In this section, we explain the Fuzzy Adaptive Search method for Parallel Genetic Algorithms (FASPGA). FASPGA not only aims in improving the search performance by using the fuzzy reasoning to tune the genetic parameters, but also plan to obtain the high quality solution depend on tuning the migration rate by fuzzy reasoning.

2.1   Decision of Migration Rate

The migration is an operation that some individuals are selected to move from one island to another. By the migration, the better individuals could be spread in all population quickly, and enhance the precision of the solution. Generally, the migration rate is a constant in PGA. In the other words, the size of individuals migrated are fixed for each island, regardless of the island with the delayed evolutionary condition or with the advanced evolutionary condition. It is obviously disadvantages to convergence of PGA as spreading of individuals in island with the delayed evolutionary condition.

Therefore, for FASPGA proposed in this paper, the migration rate is not constant and is tuned in a range (see Figure 1) by fuzzy reasoning according to states of each island. So the individuals in the island with the advanced evolutionary condition are easy to be spread to whole population. On the contrary, the individuals in the island with the delayed evolutionary condition are difficult to be spread to whole population. In there, the fuzzy rule plays a good role in guiding the evolutional direction to improve the search efficiency.

2.2   Selection of Migration Individuals

We used the roulette wheel selection as the selection method to select migration individuals in FASPGA. Probability of the roulette wheel selection for selecting individuals with high fitness value is used high in the sender island and low in the receiver island as shown in the following equations. In these equation, p means the populations size of island.

Probability of Individual Selection in Sender Island :

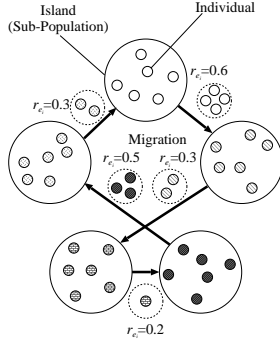$$\frac{f_i}{\sum_{i=0}^{p} f_i} \tag{1}$$

Figure 1. Migration Process in FASPGA

Probability of Individual Selection in Receiver Island :

$$\frac{f_{m_j} - f_j}{\sum_{j=1}^{p} (f_{m_j} - f_j)} \qquad (2)$$

2.3 Fuzzy Reasoning of FASPGA

In FASPGA, the crossover rate r_{c_i}, the mutation rate r_{m_i} and the migration rate r_{e_i} of each island are not fixed (i : island number) and are tuned by the fuzzy reasoning. The IF part of the membership function is composed of the average fitness value f_{a_i} and the difference between the maximum and average fitness value (f_{m_i}-f_{a_i}). And FASPGA adds a parameter called the migration rate in $THEN$ part. The result of output is calculated by the weighted average based on the firing strength. The fuzzy rule and membership functions in IF part and singletons in $THEN$ part are shown in Figure 2.
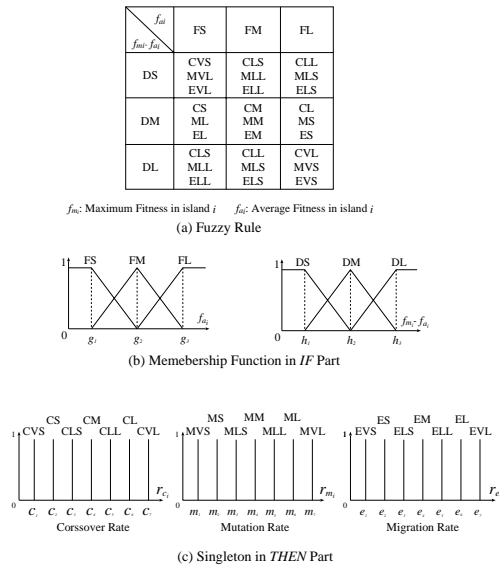

Figure 2. Fuzzy Reasoning of FASPGA

2.4 Algorithm Flow of FASPGA

The algorithm flowchart of FASPGA proposed in this paper is shown in Figure 3. Tuning processes of the crossover rate r_{c_i}, the mutation rate r_{m_i} and the migration rate r_{e_i} in each island by the fuzzy reasoning are executed inside the dotted line area.
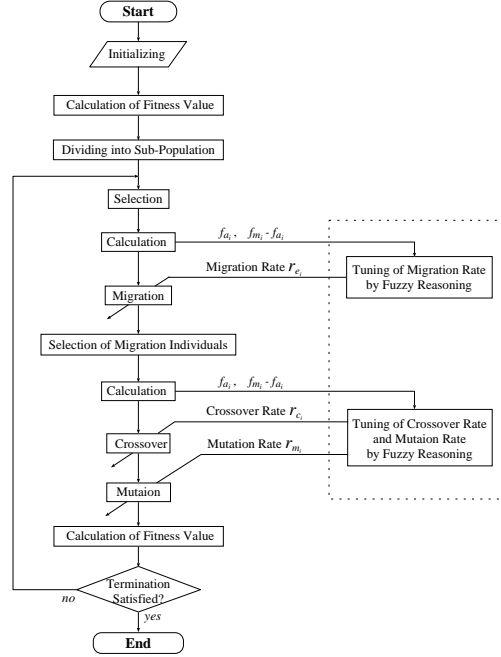

Figure 3. Algorithm Flow of FASPGA

3 Diversity Measure Based Fuzzy Adaptive Search Method for Parallel Genetic Algorithms (DM-FASPGA)

For FASPGA, it could display better search efficiency and higher solution quality than PGA and GA in multi-peaks function such as Rastrigin function. But as for single peak function such as Rosenbrock function, FASPGA certainly cannot display better than PGA, perhaps because the diversity measure by the phenotypic distance doesn't applicable to the fitness evaluation in the function with small change of curvature. Therefore, in this chapter, we propose an improvement method for FASPGA; Diversity Measure based Fuzzy Adaptive Search method for Parallel Genetic Algorithms (DM-FASPGA).

3.1 Diversity Measure

There are many kinds of the diversity measure parameters proposed by the other researchers[7, 8]. Before introduce of the diversity measure parameters used in this research, we must explain that the following calculations for the diversity measure executed in an island, not in whole population.

At first, a genotypic diversity measure parameter based on the Hamming Distances (HD) of the chromosomes between the individual and one individual with average fitness is adopted. Its definition is

$$HD \quad = \quad \frac{\sum_{k=1}^{n} d(I_{aver}, I_k)}{n - 1} \qquad (3)$$

where I_{aver} shows a chromosome with the closest fitness to average one in the island, I_k shows any one chromosome in the island and d(I_{aver}, I_k) means the hamming distance between I_{ave} and I_k. The n means the population size in the island. The range of HD is from 0 to the chromosome's length. If HD is lower, it means more individuals converge on an individual with the average fitness. On the contrary, if HD is higher, it means more individuals diverge from an individual with the average fitness.

There are several variant definitions for the hamming distance shown as follows.

$$HD\ II\ =\ \frac{\sum_{k=1}^{n} d(I_{best}, I_k)}{n-1} \tag{4}$$

$$HD\ III\ =\ \frac{HD\ I - min\{d(I_{aver}, I_k)\}}{max\{d(I_{aver}, I_k)\} - min\{d(I_{aver}, I_k)\}} \tag{5}$$

$$HD\ IV\ =\ \frac{HD\ II - min\{d(I_{best}, I_k)\}}{max\{d(I_{best}, I_k)\} - min\{d(I_{best}, I_k)\}} \tag{6}$$

where I_{best} shows a chromosome with the closest fitness to best one.

In section 2.3, we introduced FASPGA that adopt the Average Fitness (AF) and the Different Fitness between the best fitness and average fitness (DF), which both are the phenotypic diversity measure parameters. These are shown in Equation (7) and (8).

$$AF\ =\ f_{I_{aver}} \tag{7}$$

$$DF\ =\ f_{I_{best}} - f_{I_{aver}} \tag{8}$$

where $f_{I_{best}}$ and $f_{I_{aver}}$ show the best fitness and average fitness value in the island. If DF is samller, it means more individuals converge. On the contrary, if DF is larger, it means more individuals diverge.

There are also several variant definitions for the phenotypic diversity shown as follows.

$$DF\ II\ =\ f_{I_{aver}} - f_{I_{min}} \tag{9}$$

$$DF\ III\ =\ \frac{\sum_{k=1}^{n}(f_{I_{aver}} - f_{I_k})}{n-1} \tag{10}$$

$$DF\ IV\ =\ \frac{\sum_{k=1}^{n}(f_{I_{best}} - f_{I_k})}{n-1} \tag{11}$$

where f_{I_k} show the fitness value of any individual in the island.

At last, we introduce a Relative Phenotypic diversity measure parameter (RP) defined as following.

$$RP\ =\ \frac{f_{I_{best}}}{f_{I_{aver}}} \tag{12}$$

RP values belong to the interval [0,1]. If the value of RP is near to 0, it means that the population is convergence and in final search stage, whereas if it is near to 1, it means that the population is divergence and in early search stage.

4 Simulation

In this simulation, we execute the optimization simulations using Rastrigin and Rosecbrock function with 20 variables. The result of simulations based on maximum fitness value is disscused in this section.

4.1 Parameters Setting

All of the figures in this paper display the maximum fitness on the y-axis, and generations on the x-axis. For the convenience of writing computer programs, we increase one minus sign before the test function. The optimum solution value is 0. In this computer simulation, the population size is 500 and the island size is 10. The inputs of the fuzzy rule of DM-FASPGA are shown in Table 1.

4.2 Simulation Results

In this simulation, we compared the simulation results of methods proposed in this paper with PGA based on the maximum fitness value. In order to obtain stable results, all of the simulation results are the average value of results excuted 10 times.

Table 1. Inputs of Fuzzy Rule

Simulation Mark	Inputs of Fuzzy Rule		Coding
PP1	AF	DF	
PP2	AF	DF II	
PP3	AF	DF III	
PP4	AF	DF IV	
PG1	RP	HD	Binary Coding
PG2	RP	HD II	
PG3	RP	HD III	
PG4	RP	HD IV	
PG5	AF	HD	
Gray-PG1	RP	HD	
Gray-PG2	RP	HD II	
Gray-PG3	RP	HD III	Gray Coding
Gray-PG4	RP	HD IV	
Gray-PG5	AF	HD	

4.3 Remarks

By Figure 4 (a) to (c), we could confirm that PGA has the worst performacne, as the Rastrigin function is test function. PP1 to PP4 which used the phenotypic diversity measure parameters as the inputs of fuzzy rule showed the better performance than PG1 to PG5 which used the genotypic diversity measure parameters. Moreover, Gray-PG1 to Gray-PG5 encoded by the gray code had the best performace. When the Rosenbrock function used as the test function, by Figure 4 (d) and (e), we could find that PGA has the better performance than PP1 both in the early and final search stage, and PP2, PP3, PP4, PG1, PG2, PG3 and PG4 have the better performance than PGA in the early search stage, but there were almost not different nearly in the final stage. From Figure 4 (f), we could find that Gray-PG1, Gray-PG2, Gray-PG3 and Gray-PG4 have the better performance than PGA both in the early and final search stage, while the advantage was tiny in the final stage and PG5 and Gray-PG5 have similar performance to PGA both in the early and final search stage.

From the above-mentioned results, we could find some rules for diversity measure. When the change of curvature of the test function is big, such as Rastrigin function, the phenotypic diversity measure parameter (such as AF, DF) will display the better performance than the genotypic diversity measure paramerter (such as HD). On the contrary, when the change of curvature of the test function is small, such as Rosenbrock function, the genotypic diversity measure parameter will display the better performance than the phenotypic diversity measure parmeter. As this reason, we consider that the change of curvature is bigger, the phenotype distance is bigger, then the phenotypic diversity measure is useful to tune genetic parameters by fuzzy reasoning. On the other hand, the change of curvature is smaller, the phenotype distance is smaller, then the phenotypic diversity measure is unutilizable to tune genetic parameters by fuzzy reasoning. But, in this time, the genotypic diversity measure is useful to tune genetic parameters by fuzzy reasoning.

In addition, we knew that when the inputs of the fuzzy rule include the genotypic diversity measure parameter, the gray coding will show the better performance. The genotypic diversity measure parameter measures the distance in the bit string, and gray coding has closer dependence between the bit string and phenotypic value than the binary coding. Therefore, we considered that the gray coding is useful for evolution of solution when the inputs of the fuzzy rule include the genotypic diversity measure parameter.

5 Conclusions

In this paper, we proposed the Fuzzy Adaptive Search method for Parallel Genetic Algorithm (FASPGA) combined FASGA with a quick search ability and Island model Parallel GA with a high-quality solutions ability. By using the fuzzy reasoning to tune the genetic parameters, FASPGA displayed a good performance in Rastrigin function. However, FASPGA also displayed a bad performance in Rosenbrock function. To improve the performance of FASPGA, we proposed the Diversity Measure based Fuzzy Adaptive Search method for Parallel Genetic Algorithms (DM-FASPGA). A lots of parameter combinations were adopted as the inputs of the fuzzy rule in this paper and the computer simulation was also excuted.

From the simulation results, we confirmed that DM-FASPGA was effective in improving the performance of FASPGA, not noly in Rastrigin function but also in Rosenbrock function. We also confirmed that Hamming Distance (HD) and Relative Phenotypic diversity (RP) were the best parameter combination, when used gray coding.

About the research plan for the future, we would like to introduce other geneotypic diversity measure parameters into the inputs of the fuzzy rule. To confirm the usefulness of the proposed method, the application of the FASPGA method in motion learning experiment of the robot manipulator is also expected.

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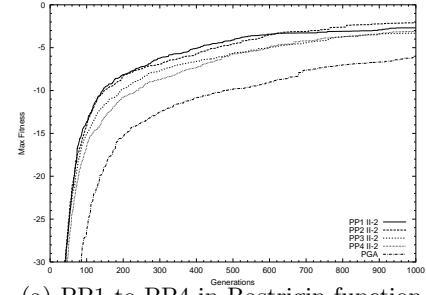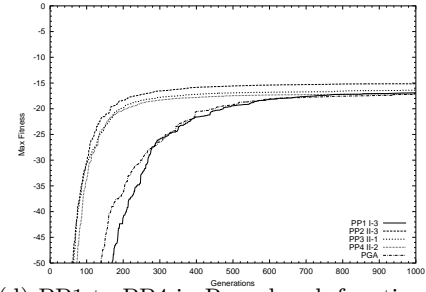
(a) PP1 to PP4 in Rastrigin function
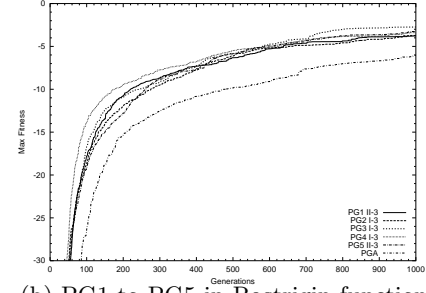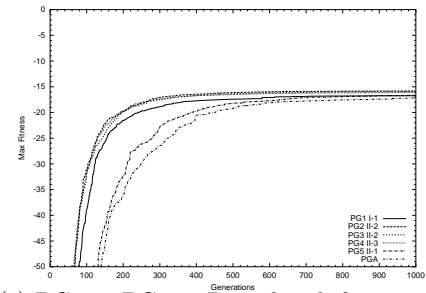

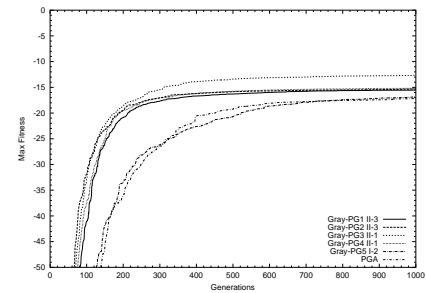(b) PG1 to PG5 in Rastrigin function
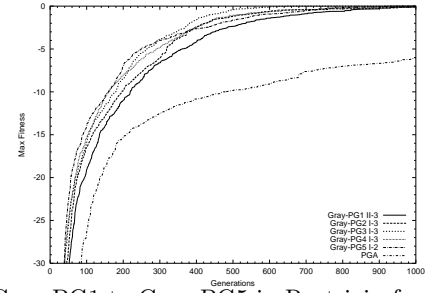
(c) Gray-PG1 to Gray-PG5 in Rastrigin function

(d) PP1 to PP4 in Rosenbrock function

(e) PG1 to PG5 in Rosenbrock function

(f) Gray-PG1 to Gray-PG5 in Rosenbrock function

Figure 4. Simulation Results