

The Differences of Parallel Efficiency between the Two Models of Parallel Genetic Algorithms on PC Cluster Systems

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Abstract

In this paper, the characteristics of the typical two models of parallel genetic algorithms are compared. Those models are the coarse grained model and the micro grained model. Especially, the parallel efficiency and the total calculation time on PC clusters that are build with commodity hardware are examined. The characteristics are examined through the numerical examples. There are two major characteristics in the coarse grained model. One of them is the network cost is very small. The other is the fact that the necessary number of iteration is smaller than that of the model of the micro grained model. On the other hand, in the micro grained model, the ideal parallel efficiency cannot be reached to 100 %. Therefore, it is concluded the coarse grained model is suitable for PC cluster systems.

1 Introduction

A Genetic algorithm (GA) [3] is one of the powerful tools for optimization problem. GAs are stochastic searching methods with multi points and GAs can find optimum solutions not only in a continuous space but also in a discrete space. It is said that GA can find optimum solutions even when there are several peaks in objective functions. The utility of GAs, however, suffers from the number of iterations required to find a solution. One of the solutions is to perform GAs on parallel computers.

There are several studies discussed GAs on parallel computers [6, 5]. It is reported that there are several models of parallel GAs. Among them, the micro grained model and the coarse grained model are the typical models of parallel GAs. Those names are come from the size of the network data. The micro grained

model and the coarse grained models are so called the master slave model and the island model respectively.

There are several studies that are concerned with these models. However, there is a few studies that related the comparison of the characteristics of the two models. Therefore, it is difficult for users to decide which model should be used.

In this study, the characteristics of the two models on PC clusters are made cleared. The characteristics are examined through the numerical test function. The result of the examination suggests that the coarse grain model is suitable for PC cluster from the view point of calculation cost and parallel efficiency.

2 Coarse grained model and micro grained model of genetic algorithms

2.1 Genetic algorithms

The genetic algorithm (GA) is an optimization method that derives its behavior from a metaphor of same of the mechanisms of evolution in nature. There are some evolutionary operation; those are crossover, mutation, selection and so on. Because the GA is a multi point searching algorithm, there are several ways to perform GAs in parallel. Among them, the coarse grained model and the micro grained model are typical.

2.2 Coarse grained model

The coarse grained model is so called an island model. In this model, the population is divided into sub populations. Those populations are called islands. In each island, simple GA is operated. Usually, each GA is performed on one processor. After some iterations, some of genes are chosen and those genes are moved to the other islands. This operation is called migration. The flow of this model is shown in figure 1.

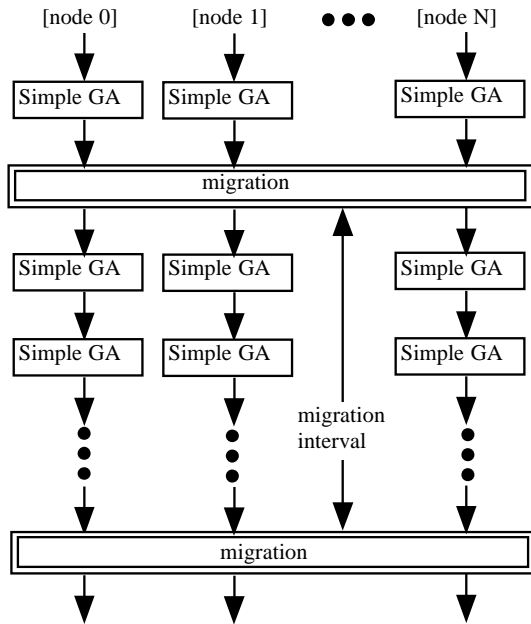


Figure 1. The flow of coarse grained model

Because simple GAs are performed in each island for several iterations, the network traffic is not heavy. This is one of the reasons that this model is suitable for PC cluster systems. Basically, the program coding is not complicated. Migration and terminal parts are the additional to the simple GAs. In this study, when all islands satisfy the simulation is terminated when all islands satisfy the terminal condition. Therefore, it is sometimes happen that the excess synchronous operations are needed.

2.3 Fine grained model

In GAs, the operation of evaluation occupies the most calculation time of total time. It is very simple way to perform the evaluation part in parallel. The micro grained model is the master and slave model. In this model, simple GA except the evaluation operation is performed in the master processor and transfer the data to the slave processors. The master transfers the data of one gene to one processor and the slave evaluate the fitness of the gene and return the data to the master. Just after the master receive the data from the slave, the master send the data of new gene. This algorithm is summarized in Figure 2.

There are some studies using this model. For example, PGA pack [1] is the free software of this model. Forgy et al. [2] reported that this model is very effective when the number of population size is huge. Maruyama et al. [4] developed the efficient program of

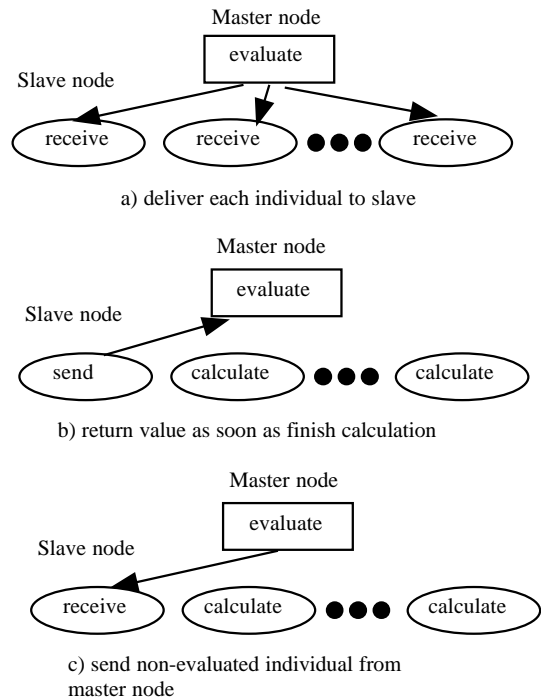


Figure 2. The flow of fine grained model

this model.

The advantage of this model is that the program coding is very simple. Even when there are huge number of genes, users need not to change the programs. The other advantage is that it can be easy to keep the load balance.

On the other hand, the parallel efficiency does not become 100 % because of the existence of the master CPU. Therefore, when there are not so many processors, it is a very big disadvantage.

3 Comparative simulation of micro and coarse grained models of genetic algorithms

In the former section, two typical models of genetic algorithms in parallel are explained. In this chapter, through the numerical example, the characteristics of each model is examined and discussed.

3.1 Cluster system

In this study, the simulation is performed on the PC cluster that is constructed with 16 PCs. The detail speck of this PC cluster system is shown in Table 1.

Table 1. Spec of 16 PC cluster system

CPU	Pentium II (Deschutes, 400MHz)× 16
Memory	128MB
OS	Linux2.2.10
Network	FastEthernet TCP/IP
Communication library	MPICH1.1.2

Table 2. Used parameters of GA

gene length	design variable* 10
coding	gray coding
crossover	one point crossover
crossover rate	0.6
mutation	0>>1 1>>0
mutation rate	1/gene length
topology of migration	ring that is constructed random at every migration chance
migration interval	5
migration rate	0.15

3.2 Test function

To find the characteristics of coarse and fine grained model, the micro grained model and the coarse grained model are applied to maximize the values of the Rastrigin function. The Rastrigin function can be written in the following way,

$$f = -10n - \sum_{i=1}^n (x_i^2 - 10 \cos(2\pi x_i)). \quad (1)$$

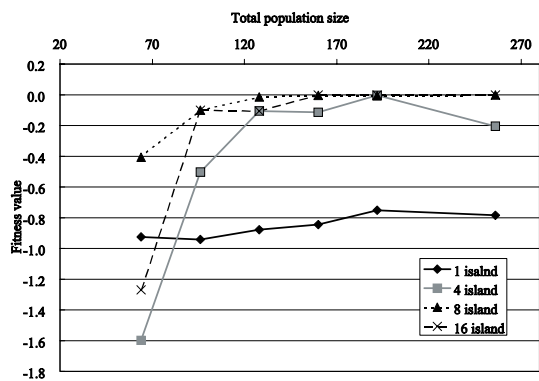
In the numerical example, the iterations of calculation of the values of the Rastrigin function are performed when the function is called. The number of iterations are 4, 40, 400 and 4000. Because of this iteration operation, it takes 0.00001[s], 0.0001[s], 0.001[s] and 0.01[s] to derive the value of the Rastrigin function. This operation changes the rate of the calculation cost and the network cost.

In Table 2, the used parameters of GA are summarized.

3.3 Necessary population size

In Figure 3, there is a relation between the population size and the derived fitness values are shown. Figure3 is the result of 400 iterations. All the results are the mean of 30 trials. There are the results of 1, 4, 8 and 16 islands. The results of the micro grained model are the same as the island model.

When there is enough population size, the coarse grained model can derive the solutions. On the other

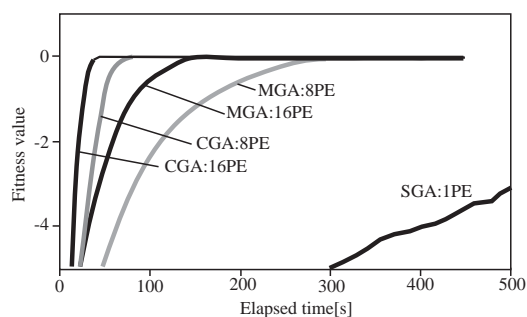
**Figure 3. Population size and fitness value (400 iterations)**

hand, the micro grained model can not find the solution, even when there is a huge size of population.

From Figure 3, it can be said that the necessary population size becomes small, when the number of islands becomes bigger. This result leads that the calculation cost itself is reduced in the coarse grained model. On the other hand, the calculation cost is not changed in the micro grained model.

3.4 Calculation time and fitness value

In Figure 4, the transition of the fitness values with respect to the elapsed time is shown. This is the result of 400 iteration problem. In this figure, the result of simple GA (1 PE), the results of the micro grained model (MGA, 8PEs and 16PEs) and the results of the coarse grained model (CGA, 8PEs and 16PEs) are shown.

**Figure 4. Elapsed time and fitness value (400 iterations)**

From Figure 4, it is obvious that the coarse grained model can derive the better solutions quickly than

those of the micro grained model. Especially, the results of the coarse grained model with 8PEs are better than those of the micro grained model with 16PEs.

Therefore, from the point of the view of the quickness to find the solutions, users may use the coarse grained model.

3.5 Speedup

Figure 5 and 6 are the results of speed up of the coarse grained model and the micro grained model respectively. Speed up is the ratio of the times of one PE and multiple PEs.

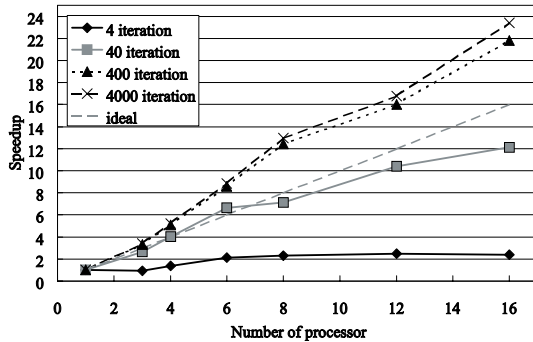


Figure 5. Speed Up (Coarse grained model)

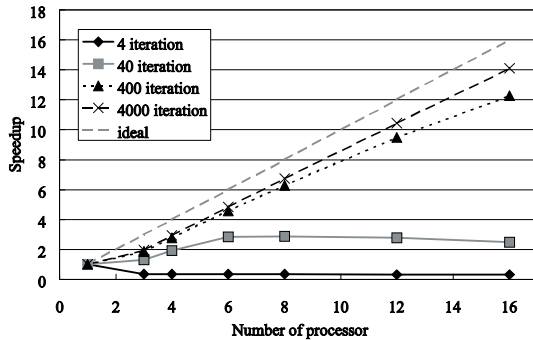


Figure 6. Speed Up (Micro grained model)

When the number of iteration is 4, the speed up is not good in both models because the network cost is high. On the other hand, when the number of iteration is 4000, the speed up is beyond the linear relation in the coarse grained model. This happens from the reasons that the network cost is small and the calculation cost also becomes small in the Coarse grained model. In the micro grained model, because the network cost is relatively high and calculation does not change, a good result cannot get it easily.

4 Conclusions

In this study, the coarse and micro grained models are focused for parallel genetic algorithms. The characteristics of these models are examined and discussed through the numerical examples. In the numerical examples, PC cluster that is constructed of 16 PCs are used.

It is concluded that the micro grained model is not suitable for this kind of cluster model. When it does not take much time to derive fitness value, the derived speed up is very low. When it takes much time to derive fitness value, the parallel efficiency does not become 100 % because of the existence of the master CPU.

It can be said that the coarse grained model is suitable for this type of cluster system. In the coarse grained model, the data is not transferred frequently. More than that, in the coarse grained model, the calculation cost is smaller than that of the micro grained model. Therefore, in the coarse grained model, the very good speed up is derived when the ratio of the network cost becomes low.

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