

New genetic selection strategy for Genetic Parallel Algorithm

Milena N. Karova¹, Vassil J. Smarkov²

Abstract – However, the major disadvantage of GA is that the algorithm uses a tremendous amount of processing time. This paper proposes a method that can reduce the processing time by using Parallel Genetic Algorithm (PGA). The new genetic selection strategies are presented.

Keywords – Parallel Genetic Algorithm, selection, population, crossover, mutation, mutation rate, crossover rate

I. INTRODUCTION

The major disadvantage of GA is that the algorithm uses a very large amount of processing time. A parallel algorithm approach can be applied to the classical GA for reducing processing time. Parallel Genetic Algorithm (PGA) can be classified into three different models: Master-slave PGA, Coarse-grained PGA and Fine-grained PGA.

Master-Slave parallelization is machine dependent [1]. A shared memory multiprocessor computer is not easy available when compared with a clustered computer, which consists of network of workstations. This paper present selection schemes of Grained PGA. The aim is apply Genetic Algorithm to find an optimal solution, which satisfies nontrivial constraints of timetable problem.

II. GENETIC REPRESENTATION

A. Chromosome

Our work use alternative chromosome representation where each position in a chromosome represents the period which the classes take place.

B. Genetic Operators

The genetic operators are defined as follows:

Selection: The selection Scheme use Tournament Selection, random Walk Selection and Spatially Orientated selection.

Crossover: The algorithm proposes 3 variants of crossover: uniform crossover, one point and two point crossover.

Mutation: mutation operator swaps two values at random mutation positions. It is direct mutation (Fig. 1).

Genetic parameters: Table 1 shows the algorithm parameters. The set of constraints are generated as an input file. The node number varies from 1 to 9. The efficiency of Parallel GA is measured in terms of computational effort, defined as the number of individuals that must be processed to

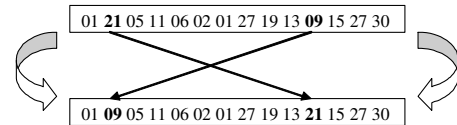


Fig. 1. Direct Mutation

get solution, compared to the serial algorithm. The optimal solution is defined like as solution that satisfied all hard constraints. The good solution is defined like as satisfied 95% of all hard constraints.

Table 1

Population Size	16 (32)
Crossover probability	90%
Mutation probability	0,4%
Migration size	10%
Maximum generation	500

Fitness function: The fitness function (1) is a sum of penalties.

$$f(ch) = \sum_{i=1}^{events} \sum_{j \in C} W_j P_j, \quad (1)$$

where $f(ch)$ is fitness function, events is length of chromosome (number of lectures), C is set of constraints, W_j is weight of constraints j and P_j is function that returns 1 (violated constraint j) and 0 (not violated constraint j). The target value is 0.

III. PARALLEL GENETIC ALGORITHM (PGA)

GA has the ability to be parallelized because an algorithm work with a set of population, not only an individual. The evolution of an individual is separated from each other. The concept of PGA is to divide the task of the classical GA and distributes on different processors. [2, 3] There are three main types of PGA:

Master-Slave PGA: This model uses a single global population and the fitness evaluation is done on different processors. Furthermore, genetic operations may also be done in parallel. The nature of GA is not changed because an algorithm still works with the whole population. A global population is suitable for a shared memory computer.

¹Milena N. Karova is of the Department of Computer Science, Studentska 1, Technical University Varna Email: mkarova@ieee.bg

²Vassil J. Smarkov is with the Department of Computer Science, Studentska 1, Technical University Varna Email: smarkov@ieee.bg

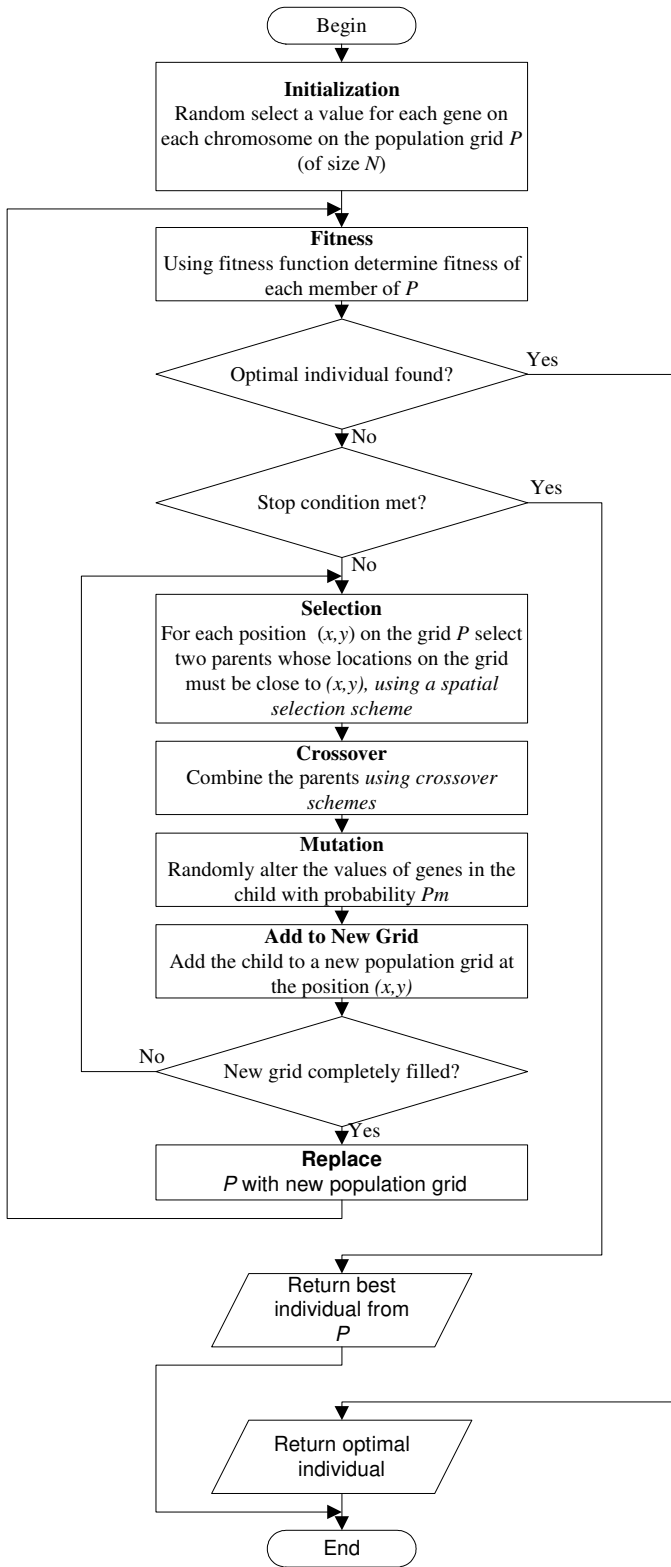


Fig. 2. PGA

Coarse-grained PGA: The population is divided into a few large subpopulations. Each of these subpopulations are maintained by different processors and some selected individuals are exchangeable via a migration operator. The model is known as Island model or distributed PGA and subpopulation

called deme. Island model [4] is a popular and effective parallel genetic algorithm and also reduces probability of premature convergence – finding the local instead of the global optimum.

Fine-grained PGA: The population is separated into a large number of very small subpopulations, which are maintained by different processors. The subpopulation may be only an individual. This model is suitable for massively parallel architectures – machines consisting of a huge number of basic processors and connected with a specific high speed topology. The computer structure limits an interaction between individuals. This model is machine dependent like Master-Slave PGA.

The flowchart of PGA is shown at Figure 2. The population is thought of as occupying a two dimensional grid, each individual occupying its own position on the grid. The grid is taken to be toroidal, which is to say it wraps round itself so that the position to the right of a cell in the last column of the grid is a cell in the first column and the same row.

IV. SELECTION SCHEMES

The question of how parents are selected from the population is fundamental to the operation of genetic algorithms. As with many other aspects of GAs there is no hard and fast rule regarding the choice of selection scheme. Selection schemes must strike a balance between the stochasticity needed to maintain diversity (‘exploration’ in Holland’s analogy) and the determinism needed to propagate fit schemata (‘exploitation’). Some methods are of particular use in granular PGAs as they make use of the spatial orientation of individuals in the population.

A. Random Walk Selection

Random walk is a local selection method for use in granular PGAs. A random path of length k is mapped out starting from the position on the grid for which a parent is needed (Fig. 3). Of the k individuals encountered along this path the fittest is chosen for breeding. The stochasticity of random walk is provided by the random choice of direction:

```

right: currentIndex -= (int) sqrt (POPULATION) - 1
        or currentIndex += 1
left:  currentIndex += (int) sqrt (POPULATION) - 1
        or currentIndex -= 1
up:    currentIndex += POPULATION -
        (int) sqrt (POPULATION)
        or currentIndex =
        (int) sqrt (POPULATION)
down:  currentIndex -= POPULATION -
        (int) sqrt (POPULATION)
        or currentIndex += (int) sqrt (POPULATION)
POPULATION is the size of population.
  
```

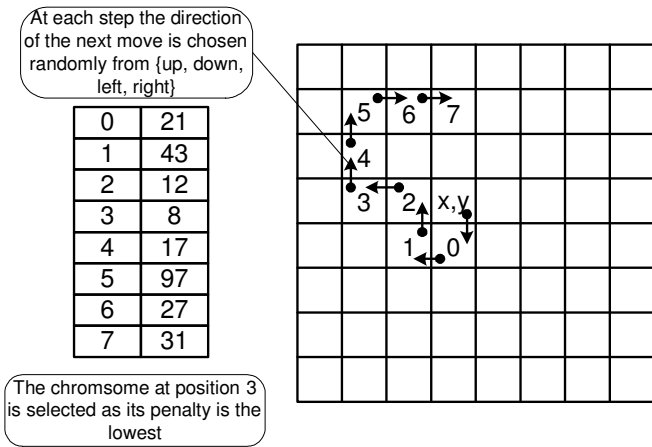


Fig. 3. Random Walk selection

B. Spatially selection

Spatially selection is orientated selection scheme for granular PGAs. Here (Fig. 4) the idea is to move a square ‘window’ or ‘mask’ over the grid such that the position for which parents are sought lies at its centre. The fittest of the chromosomes located at positions within the window is chosen as one parent and the chromosome at the centre of the window as the other.

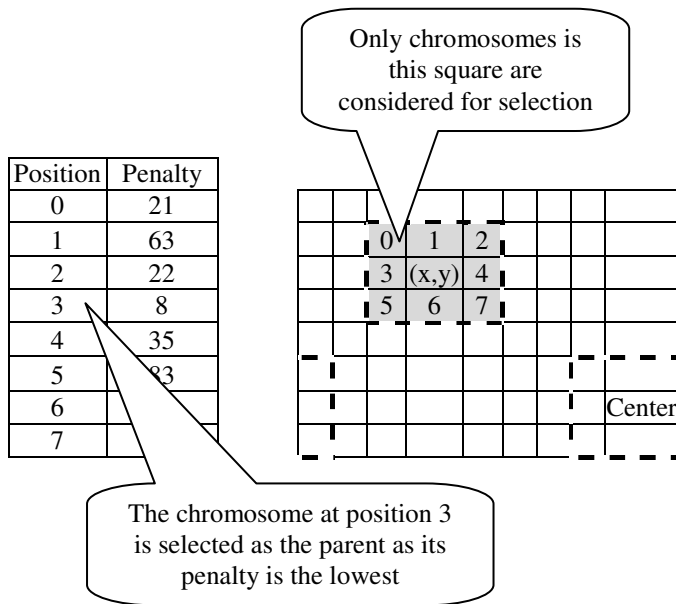


Fig. 4. Spatially Selection

Compared to Random Walk Spatially selection is a more explicitly spatially orientated and local selection scheme. Whereas Random walk may sometimes end up choosing as a parent an individual located at some distance (for example if at each iteration the same direction is chosen) Spatially selection restricts the choice of parents to within a clearly defined area. Spatially selection can implemented with a 3x3 window. The intention was to contrast a highly localised spatial selection method with a less localised one (Random walk).

The comparison of two selection schemes Tournament Selection and Random walk Selection is shown at Figure 5. Evolution process of GA using Random walk selection convergences previously using Tournament selection.

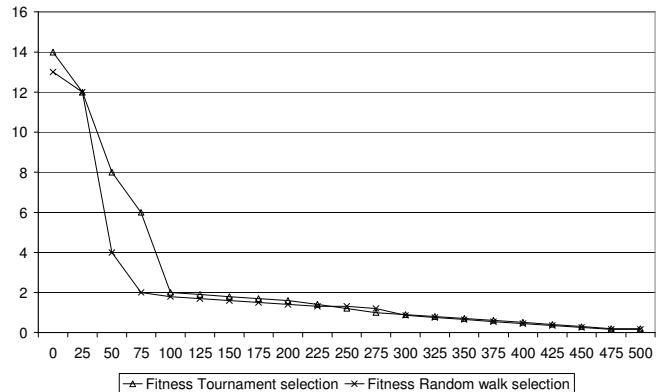


Fig. 5. Comparison of two Selection schemes

V. CONCLUSION

A little effort is needed to converting classical GA to grained PGA [5]. Each processor performs simple GA and periodically exchanges some population by migration operators. Using Random walk selection and Spatially selection provide for fast optimal individual find. Granular PGAs are able to evolve sub-populations in relative isolation possibly leading to improved overall performance. They can be usefully implemented on single processor or serial hardware. The possible efficiencies they offer are not solely related to implementation on parallel hardware. A great deal of further work will be needed to better understand and exploit Spatially selection with different mutation schemes in evolutionary timetabling. Of immediate interest would be a study of transitions in convergence rate over the course of search.

REFERENCES

- [1] Corcoran A.L., A Parallel Island Model Genetic Algorithm for the Multiprocessor Scheduling Problem, Proceeding of the 1994 ACM/SIGAPP Symposium on Applied Computing, ACM Press, March 7-8, 1994, pp.483-487.
- [2] Nowostawski M., Poli R., Parallel genetic algorithm taxonomy, University of Otago, New Zeland, 1999.
- [3] Ross P., Ballinger G., PGA-Parallel Genetic Algorithm Tested, Department of Artificial Intelligence, University of Edinburgh, 1993
- [4] Vertanen K., Genetic adventures in parallel: towards a good island model under PVM, Oregon state university, 1997
- [5] Gong Y., Nakamura M., Tamaki S., Parallel genetic algorithms on line topology of heterogeneous computing resources, GECCO'05, Washington, DC, 2005