

EXPERIMENTAL COMPARISON OF SELECTED TYPES OF PARALLEL EVOLUTIONARY ALGORITHMS

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Abstract: Parallel evolutionary algorithms are able to improve the performance of simple evolutionary algorithms which use a single population. Their characteristics and performance depend on their architectures and other factors and parameters. In our contribution we present some viewpoints of classification and we demonstrate experimentally the influence of selected factors such as architecture type, migration topology, migration period, number of migrants, numbers of subpopulations, subpopulation size and others on the performance of these algorithms. This experimental study should help to generalise the properties and behaviour of various types of parallel evolutionary algorithms and help to design algorithms for solving hard search/optimisation problems like modelling of bio-medicine processes, optimisation of pharmaceutical dosing, optimisation of large technological and construction tasks etc.

1 INTRODUCTION

Parallel evolutionary algorithms (PEA) or parallel genetic algorithms (PGA) are evolutionary algorithms, which consist at least of two levels of parallelisation. The first level contain most types of evolutionary algorithms thanks their population based nature. Each individual represents a trajectory in the search space. The main drawback of the simple or single-population algorithms is the high computation effort or time needed to find the solution. The next drawback is that simple evolutionary algorithms are often unable to avoid the premature convergence, which is the stagnation in the local optimum. To prevent these drawbacks a next level of parallelisation using multiple populations can be used.

Several authors used various types of PEA and several authors published various classifications of PEA or PGA (Alba, 2002, Cantú-Paz, 1995, Nowostawski, 1999 and others). The PEA, aside from the number of computation units used (processors, computers), bring also other advantages in comparison to simple (single-population) evolutionary algorithms (SEA) or simple genetic algorithms (SGA). These advantages are multi-parallel search in a large, multidimensional search space, higher diversity of the population, better

algorithm control possibilities, higher computation power, etc. If we are able to design efficient architectures of PEA and to find their good parameters, the PEA will reach better solutions, avoid premature convergence and reduce time, which is needed to find the solution in comparison to SEA. Additionally, if using multiple computation units the computation power is growing sub linearly. All together, PEA result in a significant performance increase.

In this contribution some viewpoints of PEA classification are described. But the goal of this paper is an experimental comparison of selected PGA representatives and analysis of the influence of selected PEA parameters on their performance. Our attention was focused to island-based migration-type PGA, island-based overlapping-type PGA and cellular PGA. We analysed the influence of PGA architecture, migration topology, migration period, number of migrants, number of subpopulations, subpopulation size and some other factors on the performance.

2 CLASSIFICATION OF PEA

Let us consider following viewpoints of PEA classification. The first is the number of computation

units used, the second is the granularity or the number of subpopulations and their size and the third viewpoint is the type of information exchange between subpopulations of the PEA.

2.1 Number of Computation Units

The first question is how much computation units are used for the PEA realisation. This is a technical aspect, which influences computation time, but not the algorithm as such or the number of the total fitness function evaluations of the entire PEA needed for finding a good result. Using N-computation units (processors, computers) we are able to speed up the computation power nearly N-times. The use of multiprocessor configurations distributes the computation load to more processing nodes. The simplest computational topology uses only a single population and the algorithm manager distributes the fitness function evaluation (or sometimes also the crossover and mutation) to other free processors. Such topology is called global or master-slave. The only communication is the request for the fitness calculation in one direction and than the computed fitness value in the other direction. This topology can by an extensive way save computation time, but it is not able to decrease the number of fitness function evaluations.

2.2 Granularity of the PEA

The most obvious viewpoint of PEA (PGA) classification is the PEA granularity which divide PEA to coarse-grained and fine-grained ones (Cantú-Paz, 1995).

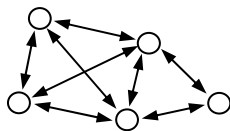


Figure 1: Migration-based coarse-grained PEA.

Coarse-grained PEA consist of relatively small number of relatively large subpopulations (islands) (Fig.1, Fig.2). The use of coarse-grained PEA topologies is advantageous when information combination of individuals from partially isolated subpopulations can produce new perspective search directions or even solutions. Many authors have presented coarse-gained PGA or island models in literature e.g. (Lin, 1994, Whitley, 1999, Cantú-Paz, 1999, Skolicki, 2005) and others.

In case of fine-grained PGA many islands with a small number of individuals are considered. The

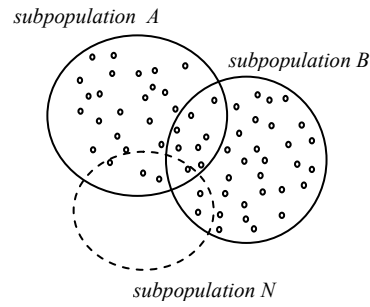


Figure 2: Overlapping-based coarse-grained PEA.

outermost but also the most obvious case is when each island is represented only by a single individual. Such topology is called also cellular (Fig.3) (Giacobini, 2005 and others).

The hybrid topologies are the last case of PEA, which represent various combinations of fine- and coarse-grained PEA.

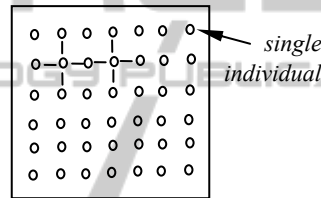


Figure 3: Fine-grained cellular PEA.

2.3 Information Exchange in PGA

The last viewpoint of PGA classification discussed is the information exchange between the subpopulations. Here let us distinguish migration, individual sharing and diffusion. The islands in the coarse-grained PEA interchange the genetic information either using the migration operator or sharing some individuals in overlapping areas of more subpopulations. Migration is performed by copying of selected individuals from the source island to the target island according to defined migration connections (for example as described in Fig.1). The migration is performed in defined periodic time intervals or non-periodically when some predefined conditions are fulfilled. The correct selection of migration periods should ensure that each island has sufficient time for isolated evolution of their individuals and for producing perspective genetic information. Block scheme of such algorithm is in Fig.4. In the overlapping topology, selected number of individuals belongs to more subpopulations; they can be selected as parents and crossed over with individuals of other subpopulations (Fig.2). Finally, in the cellular fine-grained PEA the genetic information is exchanged

due to crossover of each individual of the population with a selected neighbour. The individuals are geometrically organised in a 2-D or 3-D grid. The information motion here imitates diffusion.

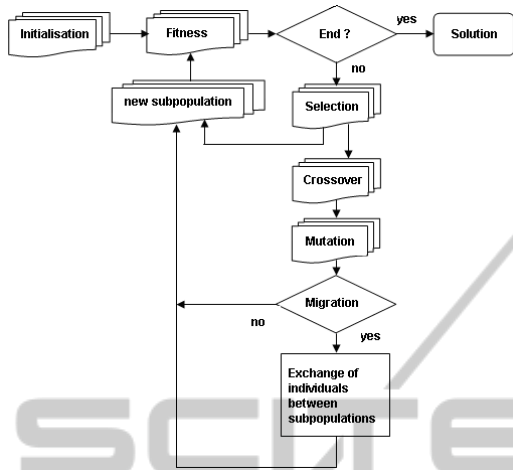


Figure 4: Block scheme of a migration-based PEA with multiple subpopulations and migrations between them.

3 USED PGA CONFIGURATIONS

In our experimental analysis three types of PGA topology have been considered: 1. migration-type coarse-grained, 2. overlapping-type coarse-grained and 3. cellular fine-grained. The influence of selected parameters have been analysed and the performance of selected PGA configurations have been compared on the example of minimisation of the Eggholder function. Note, that during this project other test function has been tested and a very large number of experiments was performed.

3.1 Coarse-grained PGA with Migration

We have used various migration-based PGA topologies with communication between islands according to Fig.5 A-G (Sekaj, 2004, Sekaj, 2007). Each arrow represents a migration direction. When not explicitly indicated, nine islands were used, each island consists of 64 individuals and the number of all individuals in the PGA was $9 \times 64 = 576$. The following genetic algorithm is running in each island:

1. Population initialisation (by random) and fitness calculation.
2. Selection of 4 the best individuals, which are without any change copied into the new population.

Random selection of a group of 20 individuals, which are copied without any change into the new population. Selection of 40 parents using the tournament selection method.

3. Mutation (rate=0.1) and crossover (rate =0.7) of parents.

4. Completion of the new population.

5. Fitness calculation.

6. Test of terminating condition, if not fulfilled, then jump to the Step 2.

The best-random migration policy is used, that is the best individual from the source island is copied and it replaces a randomly selected individual in the target island.

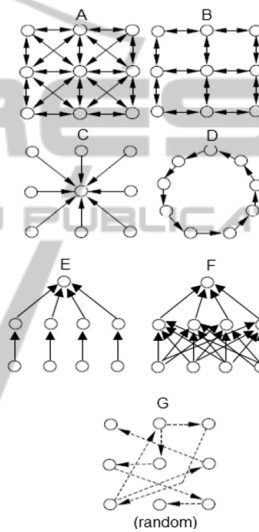


Figure 5: Coarse-grained migration-based PGA topologies used in our experiments.

3.2 Coarse-grained PGA with Overlapping areas

This architecture contains overlapping areas where some individuals belong to more subpopulations and the information interchange between them is provided only by crossover (Fig.6). No migration between islands is provided. However, the evolutionary algorithm used is the same as in the previous architecture.

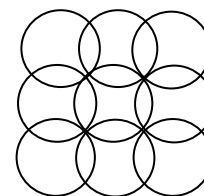


Figure 6: Coarse-grained overlapping-based PGA topology.

3.3 Fine-grained PGA

In the considered fine-grained cellular topologies each node represents a single individual (Sekaj, 2009). There are 24 rows and 24 columns, together 576 individuals (Fig.7). Two types of the fine-grained PGA algorithms have been considered. In each generation we selected one neighbour of 4 or 8 possible neighbour candidates (Fig.7 left and right, respectively) for each original individual of the population using tournament selection. These two individuals are crossed over and two new children are produced. If one of the two children is better than the original individual, it replaces it. But the population is updated (the old individuals are replaced) as late as the last individual of the PGA is crossed over. Two alternatives were used for mutation. In the first case the crossed over children are mutated and then the best individual is chosen to replace the original individual. In the second case all individuals are crossed over, replaced and then the entire population is mutated with the mutation rate 0.1.

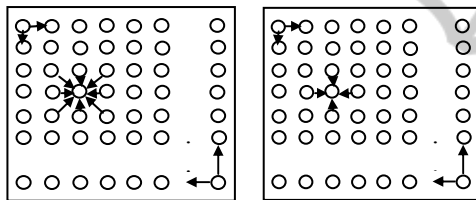


Figure 7: Neighbour selection in cellular PGA topologies. Each island is a single individual.

4 EXPERIMENTAL RESULTS

4.1 Test Function

For all experiments the Eggholder function of 10 variables has been used. It is in form

$$f_1(x) = \sum_{i=1}^{n-1} \left(-x_i \sin \left(\sqrt{|x_i - (x_{i+1} + 47)|} \right) - \sum_{i=1}^{n-1} (x_{i+1} + 47) \sin \left(\sqrt{\left| x_{i+1} + 47 + \frac{x_i}{2} \right|} \right) \right) \quad (1)$$

$$-500 \leq x_i \leq 500$$

The position of the global optimum is unknown. Graph of this function with two variables is in Fig.8

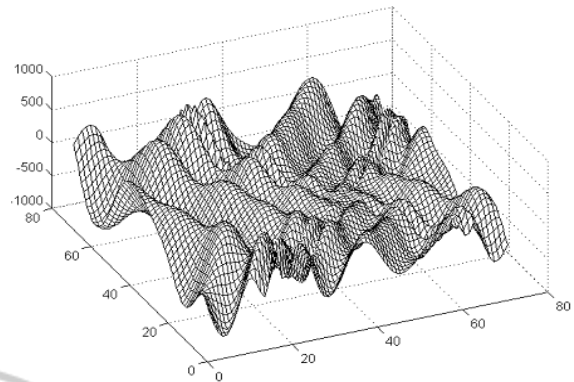


Figure 8: Graph of the Eggholder function with 2 variables.

4.2 Experimental Results

The goal was to perform an experimental analysis of the above described PGA architectures and to find the important factors, which have positive influence on their performance. We have analysed and compared the influence of the PGA type and its topology, migration period length, number of individuals migrated, number of islands and population size on the convergence rate. Each graph in the depicted figures represents the mean value of 30 runs of the corresponding PGA.

In the first experiment the topology B with 9 islands (Fig.5B) is considered. The influence of changing migration period is analyzed (Fig.9). Migration period from 1 to 100 generations has been compared. The best performance was obtained with migration period between 20 and 100 generation. When shorter migration periods, from 1 to 10 generation, were used the PGA starts to behave similar as the single population GA (SGA) because of frequent information exchange between the islands. Such results were worst than the PGA without migration (marked - No migration). In the SGA and in PGA with intensive migration the algorithm is predisposed to premature convergence. This is because the currently best individuals which direct to local optima, can influence the entire population i.e. influence other subpopulations to premature convergence before they are able to evolve perspective genes or building blocs respectively.

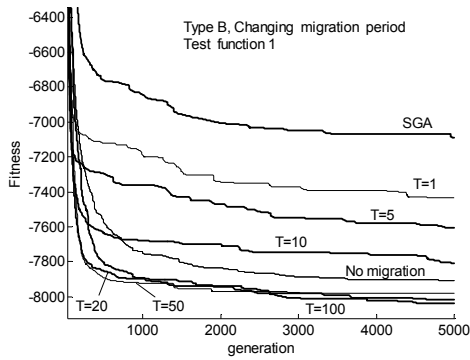


Figure 9: The influence of changing migration period.

Next, the influence of changing the number of islands is compared. Fig.10 depicts results reached with 5 to 25 islands. Number of individuals in each island is 50. The number of all individuals in the PGA is not constant. It is $N \times 50$, where N is the number of islands. For objective comparison the number of fitness function evaluations instead of number of generations is used on the horizontal axes. The best result was obtained with 25 islands. The next experiments (Fig.11 and Fig.12) show that for the Eggholder function with 10 variables the optimal number of islands is between 9 and 25 with subpopulation size from 50 to 100 individuals.

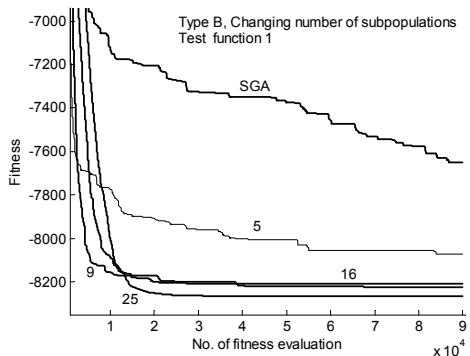


Figure 10: The influence of changing number of islands.

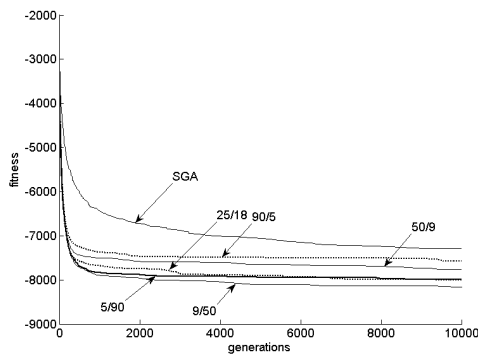


Figure 11: Number of islands / population size.

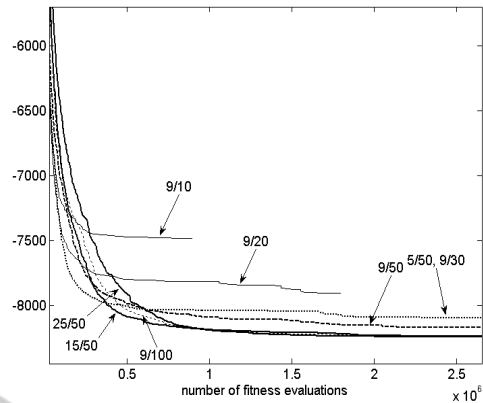


Figure 12: Number of islands / population size.

In Fig.13 various topologies of migration connections (according Fig.5) have been compared. In case of the Eggholder function the topologies A, B and C shows faster convergence rate. However, in general we assume that the migration connection topology has not a significant influence on the PGA performance. Note, that this can change, if we consider PGA with "heterogeneous" structure i.e. when various parameters of GA are used in various islands or regions of the PGA. In such a way it is possible to control the selective pressure and population diversity in the PGA (Sekaj, 2004, Sekaj, 2007). However, this was out of the scope of this paper. In this paper a "homogeneous" PGA structure is considered, where each subpopulation has the same genetic algorithm and its parameters.

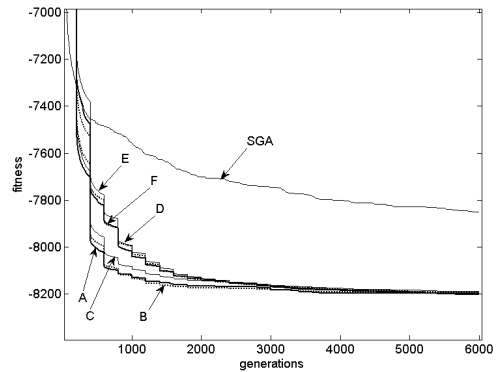


Figure 13: Various topologies of migration-based PGA.

Higher influence than the migration topology has the migration period, number of islands and the subpopulation size. In Fig.14 comparison of changing migration periods vs. changing number of migrants is shown. Here the random migration topology G (Fig.5) has been used. In all cases similar (or even equal) numbers of migrants in a

longer time interval were exchanged. The best performance has been obtained with the migration period between 20 and 100 generations. Lower or higher values of migration periods results in worst performance. Each subpopulation needs time between the migrations for their isolated evolution to produce perspective genes or building blocs, respectively. On the other hand, the number of migrants hasn't a significant influence on the performance (Fig.15).

The next important factor is the population size. In Fig.11 various configurations (number of islands / population size) are compared. In each case the number of individuals in the entire PGA was 450. The best performance results from the configuration 9/50, which has a sufficient number of islands as well as sufficient subpopulation size. In Fig.12 the same factors are considered, but the numbers of individuals in the entire PGA are not equal. Therefore, on the horizontal axes the number of fitness evaluations instead of the number of generations is used. The best performance was obtained with the configurations 15/50, 25/50 and 9/100 where sufficient number of islands and sufficient subpopulation sizes ensures satisfactory conditions, sufficient diversity and relative independence of particular subpopulations.

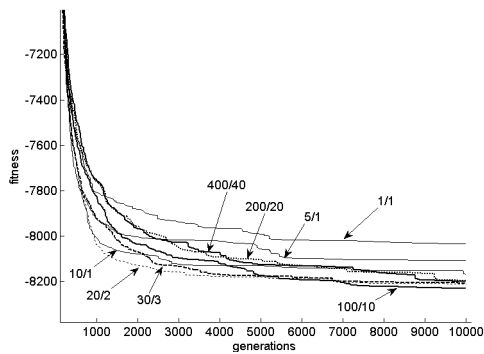


Figure 14: Migration period / number of migrants.

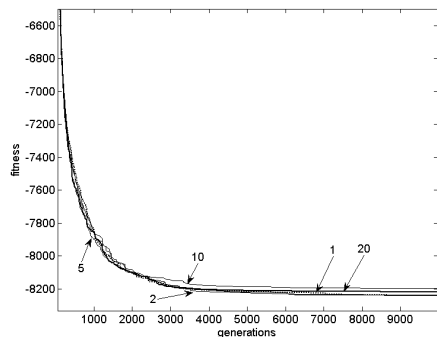


Figure 15: Changing number of migrants, migration period is 100 generations.

In Fig.16 the results of the overlapping-based PGA are compared. We consider the architecture according Fig.6 and Fig.7 with 9 overlapping subpopulations. The number of individuals in the overlapping areas has been changed from 2 to 10 and 16 individuals. The best performance has been obtained with 10 shared individuals between each two subpopulations.

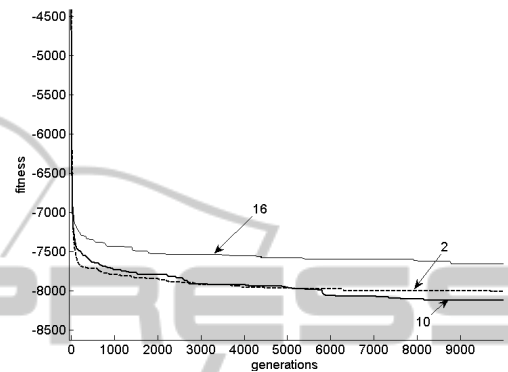


Figure 16: Overlapping PGA, various numbers of shared individuals.

The last mentioned PGA type is the fine-grained or cellular architecture. Four variants of this algorithm are compared in Fig.17. The algorithms are described in the part 3.3. The first two types (1 and 2) perform mutation at the end of the new generation calculation, when all individuals of the population are already crossed over with selected neighbours and replaced by the best offspring. Type 1 selects the partner for crossing over from 8 neighbours (Fig.7 left) and type 2 from 4 neighbours (Fig.7 right). Types 3 and 4 perform the mutation after crossover of both parents. Then the best mutated individual replaces the original individual. Type 3 selects the partner for crossover from 8 neighbours and the type 4 from 4 neighbours.

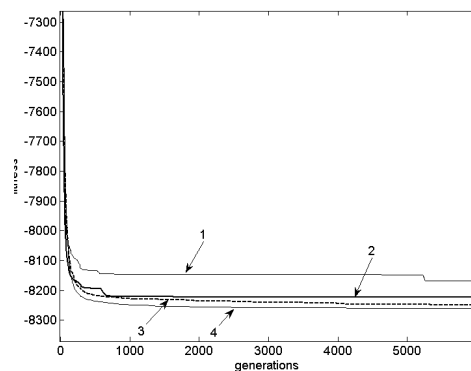


Figure 17: Various types of cellular PGA.

The last figure (Fig.18) depicts the comparison of the best representatives of all PGA architectures. The fastest convergence in case of the Eggholder function has been achieved by the fine-grained (cellular) PGA.

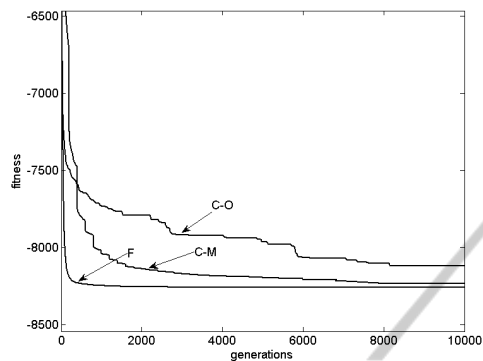


Figure 18: Comparison of various PGA types: Coarse-grained migration-based PGA (C-M), Coarse-grained overlapping-based PGA (C-O), Fine-grained PGA (F).

5 CONCLUSIONS

Selected types of parallel genetic algorithms have been experimentally compared and the influence of some of their parameters analyzed. We have considered various architectures, various topologies of migration connections, influence of changing migration period, population size and number of islands. In our experiments using the Eggholder function the fine-grained PGA performance outperforms the coarse-grained PGA. However, the performance of all PGA types depends on their parameters as well as on the problem to be solved.

In our comparison in each island of the PGA the genetic algorithm with equal parameters has been considered. Such "homogenous" algorithms have the same diversity and selection pressure in all subpopulations. Based on our experiments for such type of PGA (PEA) we can make following conclusions. Changing of migration topology has a small influence on the PGA performance. The main influence on the performance has the migration period, subpopulation size and number of islands. These factors affect the ability of all subpopulations of the PGA to evolve perspective genes and building blocs and effectively to explore the search space. For each problem solved it is important to find a balance between the "independence" of each subpopulation for their evolution and diversity in each subpopulation on the one side and the communication and exchange of perspective genetic information between subpopulations or individuals

on the other side.

The presented experimental study is a part of a project, which should help to generalise the properties and behaviour of various types of parallel evolutionary algorithms and help to design algorithms for solving hard search/optimisation problems like modelling of bio-medicine processes, optimisation of large technological and construction tasks, solving of economical and financial problems etc.

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