The Effects of Varying Population Density in a Fine-grained Parallel Genetic Algorithm

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Abstract - This paper introduces a new method for controlling selection pressure in fine-grained parallel GAs. Our model, inspired by percolation theory, employs a "seeding" mechanism, which provides a means of systematically increasing the population size until the carrying capacity of the lattice is reached. Initially, a relatively small number of individuals (solutions) occupy small isolated patches (demes). As time goes by, additional randomly generated individuals are added to the lattice. As the density increases, the small isolated demes gradually merge to form larger connected demes. This "percolation process" helps to balance the interplay between genetic and population forces. The implications of alternative migration schemes between demes are also investigated in terms of the population diversity, selection pressure and consequently algorithm performance. Experimental results using benchmark optimisation problems confirm that the "step-wise" increase in the population density does affect the quality of the solutions found in a given trial.

1. INTRODUCTION

Genetic algorithms (GA) are abstract implementations of natural evolutionary processes used to solve search and optimisation problems [1][2]. Recently, there has been increased interest in parallel versions of the algorithms, in particular where the population has a spatial structure [3]-[5]. The most common implementations are the coarse-grained (or island) model and the fine-grained (or grid) model. In a coarse-grained model, the GA population is divided into multiple subpopulations (or demes). Each subpopulation evolves independently, with only occasional exchanges of individuals between subpopulations. This isolation promotes diversity, thereby helping to prevent premature convergence across the population as a whole. In a fine-grained model, individuals are commonly mapped onto a 2-dimensional lattice, with one individual per node [6]. Fitness evaluation of individuals is carried out in parallel using discrete time steps. Selection and crossover occurs locally within small, overlapping neighbourhoods. Subsequently, good genes slowly diffuse across the lattice.

The benefits of isolating subpopulation have long been known in the field of evolutionary algorithms [7]-[9]. Parallel GAs are known to handle difficult multimodal functions more efficiently than serial GAs [10]. However, both the course and fine-grained models are artificially constrained. The quality of the search and efficiency of the algorithms can be severely affected by the parallel parameter settings [11]. For example in the coarse-grained model, one has to decide the number and size of subpopulations, migration frequency, the number of migrating individuals and migration topology. Currently most of these parameters are determined empirically and there is no generally accepted agreement on how to choose them [12]. Empirical studies of coarse-grained parallel GAs and various specifications of subpopulation size and number and migration policies can be found in a number of papers [7][10][13]. In the case of the fine-grained model, much of the research has concentrated on the effects of neighbour size and shape [14]. Sarma and De Jong found that the ratio of the radius of the local neighbourhood to the lattice size could be used as an adjustable parameter to control the selective pressure [14]. In previous work, we have examined the effects of introducing ecological features (eg. disturbances, metapopulation concepts) into the fine-grained model [15][16]. An important feature of these models was the "extinction-colonisation" cycle, which provided a mechanism for continuously varying the size and structure of the evolving population, thereby allowing previously suppressed individuals the opportunity to survive and reproduce.

In this paper, we introduce another form of spatial separation in addition to the "isolation-by-distance" that already exists in a fine-grained parallel GA. The proposed model employs a "seeding" method that provides a means of varying the population density across the 2-dimensional lattice. Here, individuals are added to the lattice based on a specified probability and time interval. Initially, a large number of small demes are formed. As the run progresses, the demes slowly merge. This process allows a natural formation of demes, eliminating the need for pre-specifying the size and number of demes. The selection pressure can be also adjusted via the seeding method and migration schemes. Our model is a hybrid parallel GA combining the features of both coarse-grained and a fine-grained algorithms [3][5][15]. The motivation for this approach is derived from "percolation theory", where the effects of density and formation of clusters on the global behaviour of a system have been the subject of study [17]. In this research, we examine the effects of varying population density on the performance of a density-based fine-grained PGA model.

The remainder of the paper is organised as follows. In Section 2, we provide a brief outline of percolation theory and discuss the motivation for this research. Section 3 presents a description of our model. The experiments and results follow this. In Section 5, we discuss the implications of the results. Finally we give our conclusion.

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2. WHAT IS PERCOLATION?

Percolation theory is the study of connectivity in stochastically generated structures [17]. Consider a 2-dimensional lattice in which cells of the lattice are occupied with probability *p* and are left unoccupied with probability 1 - *p*. A standard mathematical result in lattice percolation is the emergence of a large "spanning cluster" at a critical probability p_{crit}. The value of p_{crit} is determined by the connectivity rules. If connections between adjacent, occupied lattice cells are restricted to occur only in north, south, east, and west directions, then the p_{crit} is equal to 0.5928 for a 2-dimensional lattice[17]. That is, if the proportion of occupied cells is greater than or equal to this value, there is a higher probability of spanning the lattice (Fig 1b). Other critical probabilities can be obtained by changing the connectivity rule, for example, by allowing connections to run diagonally (northeast, southwest, etc.) between occupied cells.

This basic idea is best illustrated using a simple example given in Fig. 1. Assume that occupation of the cells on a 2-dimensional lattice is at random, i.e., the state of each cell (occupied or empty) is independent of status of its neighbours. In Fig. 1a, note that some cells are filled, whereas others are left empty. We can define a cluster (deme) as a group of neighbouring cells with a common side (i.e., nearest neighbour sites). There are two such demes shown Fig. 1a. We consider all sites within a deme to be connected to each other by one "unbroken chain". Fig. 1b shows that when density of occupied cells increases, there is a greater chance that a deme will contain an "unbroken chain" that spans from one boundary of the lattice to another.

In this paper, we combine percolation theory and fine-grained parallel GAs to create a hybrid algorithm where the size of the evolving population slowly increases (until the carrying capacity is reached). The rationale for this approach is that if we control the rate of diffuse of genetic material across the lattice, population diversity will be maintained and high quality solutions (i.e., fitter individuals) will slowly spread across the lattice. In our model, the need to specify the number and size of demes in the parallel GA has been removed. As the density of occupied cells slowly increases, small demes merge with other small demes creating larger demes. This will eventually lead to the formation of spanning clusters and eventually all cells in the lattice will be occupied.

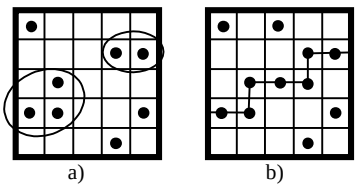


Figure 1. Demes formed by "connected nearest neighbours". a) two small demes have formed; b) a percolating cluster has formed spanning from one boundary of the lattice to another.

3. DESCRIPTION OF THE MODEL

3.1 Fine-grained Model Parameters

Individuals of the GA population are distributed randomly across the 2-dimensional lattice. The probability of a cell being occupied is *p*, mimicking the percolation phenomenon described in the previous section. It is important to note that the status of a particular cell is independent of the status of its surrounding neighbours.

Two types of local neighbourhoods are considered here: the 4 -cell Von Neumann neighbourhood (north, south, east and west) and the 8-cell Moore neighbourhood (Von Neumann set plus four diagonal neighbours). Selection is based on a form of tournament selection where the best individual from the local neighbourhood is selected as the mate. The offspring generated then compete with their parent to occupy the current cell. In this form of *crowding*, only the fittest offspring replace their parent.

3.2 Percolation Model Parameters

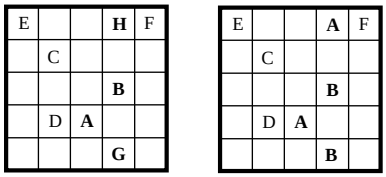
Two new parameters are used to control the density of the population: *seeding interval* and *seeding probability*. After a fixed number of generations have elapsed (the seeding interval) the lattice is scanned and new individuals may be introduced into the population. If a cell is currently occupied the individual occupying the cell simply continues to occupy the cell. However, if the cell is currently empty, the probability of a new randomly generated individual occupying the cell is determined by the seeding probability. This seeding mechanism provides a way of gradually increasing population density as time progresses (see Fig. 2).

In the early stages of a trial run, many small demes will exist. As a consequence of the local neighbourhood restrictions, each deme will evolve independently perhaps converging. However, genetic diversity as a whole will be preserved across the lattice [18]. These isolated demes can be considered as being equivalent to the subpopulations in a typical "island model". Empty cells act as barriers preventing interaction between different demes. As population density increases, more and more empty cells are taken over by newly arrived individuals. The newly occupied cells provide a "link in the chain". The resulting aggregation of demes allows for the slow diffusion of genetic material across the lattice.

3.3 Migration schemes

The rate at which the fragmented demes merge is controlled by the seeding mechanism. However, the introduction of fitter individuals into an isolated deme may also enhance the search process [4]. Consider the scenario described in Figure 3. Here, all individuals are ranked based on their fitness values (A has the best fitness - H the worst fitness value). Fitter individuals (eg. A and B) can be selected to replace G and H respectively. This migration mechanism provides an

Figure 2 : Snapshots of the evolving population with a seeding probability of 0.2 and a seeding interval of 40. Greyscale of the cells on the lattice refers to levels of fitness of individuals. Lighter colours to indicate higher fitness values. Black cells indicate empty sites.



a) b)

Figure 3. a) before migration; b) after migration.

additional means of controlling selection pressure across the population as a whole.

Two alternative migration mechanisms are examined in this paper. In the first method (M1), a culling process is applied to the evolving population. Here, a fixed percentage of the least-fit individuals are removed and replaced with the best individuals from the remaining population. In the second method (M2), rather than using the best individuals to replace the least-fit individuals, we use the individuals selected as a result of running tournament of size of two from the remaining fitter population. These selected individuals will then be used to replace the least-fit ones. The introduction of clones of "good" individuals to diverse areas of the lattice (depending on where these least fit individuals are located) is similar to the periodical migration among sub-populations in a typical "island model". M1 should provide the greatest selection pressure. The selective pressure of M2 will be somewhat less than M1, however, it will be stronger than no migration (NM) at all.

4. EXPERIMENTS AND RESULTS

4.1 Test functions

To evaluate the performance of our density-based parallel GA we use the following benchmark functions, which are all considered to be difficult multimodal functions. Each function is defined such that its global minimum is 0.0:

***Rastrigin function*:** $f(\vec{x}) = 10n + \sum_{i=1}^{n} x_i^2 - 10 \cdot \cos(2\pi x_i)$

where n = 20 and $-5.12 \le x_i \le 5.12$;

***Griewangk function*:** $f(\vec{x}) = 1 + \sum_{i=1}^{n} \frac{x_i^2}{4000} - \prod_{i=1}^{n} \cos(\frac{x_i}{\sqrt{i}})$

where n = 10 and $-600 \le x_i \le 600$;

***MMDP*:** *(Massively multimodal deceptive problem*)

$$f_{MMDP}(\vec{x}) = \sum_{i=1}^{k} unitation(x_i)$$

where k = 40 and unitation values given in Table 1 below. MMDP is made up of k subproblems with 6 bits each. Every subproblem contributes to the fitness according to its unitation given in the Table 1. The optimum has a value of k, but for consistency with other test functions used here, we turn this maximization into a minimization problem with a global minimum of 0.0.

4.2 Model Parameters

Table 2 lists the model parameters used. All individuals are encoded using a binary chromosome. Two-point crossover is used with bit-flipping mutation. Two different local neighbourhood sizes are examined (4 cell and 8 cell nearest neighbours).

To effectively explore the impact of the seeding mechanism it is necessary to employ a reasonably large lattice. Here we set the carrying capacity of the lattice to be 1600 individuals (40x40 square lattice). We restrict the total

Table 1: Unitation values for the 6-bit deception problem MMDP.

Unitation	Subproblem value
0	1.0
1	0.0
2	0.360384
3	0.640576
4	0.360384
5	0.0
6	1.0

Table 2: Density based fine-grained parallel GA configuration

Fine-grained parallel GA standard parameters	
Representation	binary 16 bits per function variable
Crossover	rate =1.0, two-point binary mode
Mutation	rate =0.001, bit-flipping
Population size	maximum of 1600 (40x40 lattice)
Local selection	tournament in local neighbourhood
Termination	maximum of 250 generations
Update	only fitter offspring replace parent

Additional parameters for the density-based model	
Seeding	probability =0.2, 0.4, 0.6, 0.8 and 1.0 interval = every 10 generations
Migration	rate = 0.01, every 5 generations NM or M1 or M2

Table 3: MBF and SD (4-cell neighbourhood).

Seeding probability		0.2	0.4	0.6	0.8	1.0
Rastrigin	NM	3.98E-01±3.45E-01	1.99E-01±4.52E-02	2.30E-01±1.80E-01	1.92E-01±3.82E-02	1.91E-01±2.81E-02
	M1	1.79E+00±1.15E+00	1.03E+00±7.83E-01	6.81E-01±7.99E-01	7.05E-01±7.65E-01	4.28E-01±4.49E-01
	M2	5.64E-01±5.32E-01	2.08E-01±6.50E-02	2.07E-01±1.82E-01	2.07E-01±1.94E-01	1.74E-01±2.83E-02
Griewangk	NM	3.82E-01±8.55E-02	3.29E-01±5.91E-02	3.48E-01±1.16E-01	3.12E-01±5.84E-02	3.39E-01±8.38E-02
	M1	3.12E-01±7.26E-02	2.74E-01±7.68E-02	2.77E-01±6.09E-02	2.69E-01±6.48E-02	2.51E-01±8.44E-02
	M2	3.89E-01±9.26E-02	3.63E-01±8.45E-02	3.26E-01±8.77E-02	3.33E-01±9.29E-02	3.04E-01±7.94E-02
MMDP	NM	5.99E-02±1.36E-01	1.20E-02±6.56E-02	0.00E+00±0.0E+00	1.20E-02±6.56E-02	0.00E+00±0.0E+00
	M1	1.51E+00±6.65E-01	8.51E-01±5.21E-01	5.39E-01±3.63E-01	3.45E-01±4.43E-01	2.64E-01±3.39E-01
	M2	2.04E-01±2.62E-01	3.59E-02±1.10E-01	0.00E+00±0.0E+00	1.20E-02±6.56E-02	1.20E-02±6.56E-02

Table 4: MBF and SD (8- cell neighbourhood).

Seeding probability		0.2	0.4	0.6	0.8	1.0
Rastrigin	NM	4.59E-01±4.96E-01	3.06E-01±3.91E-01	1.82E-01±4.73E-02	2.44E-01±2.52E-01	1.75E-01±3.61E-02
	M1	2.20E+00±1.83E+00	1.33E+00±1.04E+00	1.07E+00±9.47E-01	8.35E-01±6.94E-01	4.20E-01±4.20E-01
	M2	3.93E-01±4.10E-01	2.58E-01±2.54E-01	2.39E-01±2.69E-01	1.81E-01±3.33E-02	2.45E-01±2.57E-01
Griewangk	NM	3.62E-01±9.52E-02	3.41E-01±8.04E-02	3.36E-01±8.30E-02	3.21E-01±7.03E-02	2.94E-01±7.16E-02
	M1	3.30E-01±9.14E-02	2.95E-01±6.81E-02	2.79E-01±6.91E-02	2.73E-01±6.48E-02	2.33E-01±7.35E-02
	M2	3.85E-01±1.52E-01	3.39E-01±7.80E-02	3.44E-01±9.65E-02	3.30E-01±7.53E-02	3.09E-01±6.80E-02
MMDP	NM	1.25E+01±6.03E-01	6.71E+00±9.41E-01	1.99E+00±8.69E-01	9.17E-01±6.07E-01	3.12E-01±4.50E-01
	M1	1.72E+00±8.04E-01	1.03E+00±8.16E-01	6.32E-01±6.49E-01	4.65E-01±6.34E-01	3.95E-01±3.45E-01
	M2	2.28E-01±3.33E-01	7.19E-02±1.74E-01	0.00E+00±0.0E+00	3.59E-02±1.10E-01	0.00E+00±0.0E+00

number of evaluations for a fully occupied lattice (density = 1.0) to be 400,000 or a maximum of 250 generations. We systematically vary the seeding probability from 0.2 up to 1.0 in steps of 0.2. Note that in the case of density value of 1.0, the model is equivalent to a typical fine-grained parallel GA.

For all trials, the seeding interval was kept constant (every 10 generations). Fig. 4 plots the population density *vs* time for a typical run. When a smaller seeding probability is used there will be fewer fitness evaluations. When the migration option was turned on, the migration interval was set to every 5 generations. It is important to note that we do not use local optimisations techniques (eg., hill-climbing) as our objective is to focus on the effectiveness of the seeding method and the migration schemes used**.**

Each configuration was executed thirty times. The mean best fitness (MBF) and standard deviation (SD) over the independent trials are the performance metrics reported (see Table 3 and 4).

4.3 Population diversity

We are also interested in determining the impact of population density on diversity. To do this, we focus on the frequency of specific alleles (bit values). A GA population may be perceived as a form of memory, storing information in the form of allele frequencies. Its ability to adapt depends critically on allelic diversity. Allelic diversity of a GA population can be measured by the observed allele frequencies as compared with the allele frequencies of a maximally diverse population. For example, if we consider loci with exactly 2 alleles, then the maximum diversity is obtained when each allele frequency is 0.5. The diversity of alleles of a GA population at locus (bit position) *i* can be defined as

$$D_i = 1 - 4(0.5 - observed\_freq_i)^2 \qquad \textbf{(1)}$$

where $observed\_freq_i$ is the frequency of the 0 allele at locus *i* [19]. Note that D_i may range from 0.0 to 1.0. D_i being 0.0 indicates complete fixation (convergence), while 1.0 indicates the maximum possible genetic diversity. The genetic

diversity of the population for the entire chromosome (individual) *S*, can be given by:

$$D = \frac{\sum D_i}{|S|} \qquad \textbf{(2)}$$

The above *D* also ranges from 0.0 (fixation) to 1.0 (maximal diversity).

Figure 5 and 6 plot the change in allele frequency for each configuration examined using the MMDP with NM.

5. DISCUSSION

The ability to control selection pressure is often seen as a critical performance parameter in parallel GAs. Here, we show that changes in the structural complexity of the spatially distributed population do have an impact on the selection pressure and subsequently the diversity of the evolving population. An important feature of our model is the gradual increase in the density of occupied cells in the lattice. The starting point is usually an empty lattice with a small number of individuals. As time increases, new individuals are added to the lattice. The aggregation of small, isolated demes eventually results in the emergence of a "spanning" or "percolation cluster". Initially, the flow of genetic material is restricted to the fragmented patches. However, as the density of the occupied cells increases, genetic material diffuses slowly across the lattice.

Tables 3 and 4 show the results for each of the parameter settings examined. In Table 3 the results for the 4-cell local neighbourhood are reported. Table 4 records the 8-cell local neighbourhood results. Each table illustrates the impact of increasing the population density on the best solution found averaged over 30 independent trails.

In Table 3, there is a general degradation in performance within each migration category as the density value decreases from 1.0 to 0.2, for each of the test functions. The spatial separation introduced by the seeding method alone (i.e., without using migration) does not really improve the performance on the Rastrigin and Griewangk functions, however, there is improved performance on the MMDP. This result is in agreement with the results reported by Whitley *et. al* using a "island model" [10], in which they claimed that increasing parallelism, (the use of more demes) does not help when solving the Rastrigin function, but does help on the deceptive function. The optima was found in all 30 runs for the MMDP with NM or M2 + a seeding probability of 0.6. Using the NM + seeding probability of 1.0 settings, we were also able to find the optima in all 30 runs, however this configuration uses more evaluations. If we compare the results obtained between NM, M1 and M2, it is interesting to see that the combination of a migration scheme and seeding method does in fact lead to improved performance. For the Rastrigin function, M2 + seeding probability of 1.0 leads to a better result than NM + seeding probability of 1.0. For the Griewangk function, it is even more obvious that M1, using all the seeding probability values, are equal or better than all the results obtained using NM. In the case of the MMDP function, both migration NM and M2 used with a seeding

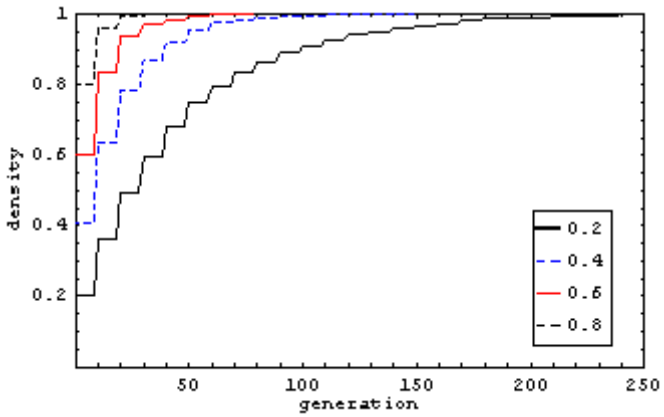


Figure 4. The proportion of individuals increases as a result of the seeding mechanism. Note the "stair-case" effect as time increases.

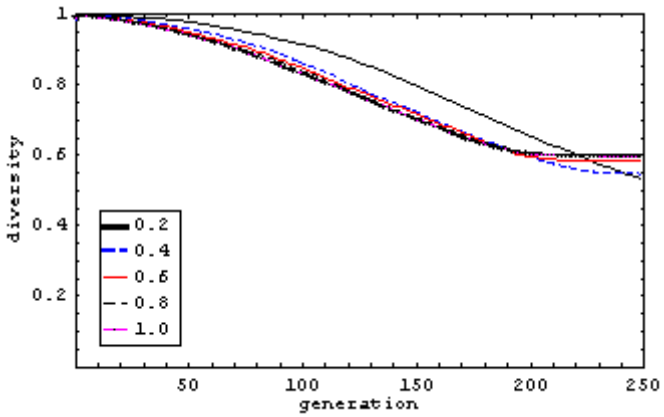


Figure 5. Diversity *vs* generation for the MMDP function: 4-cell local neighbourhood, migration option turned off.

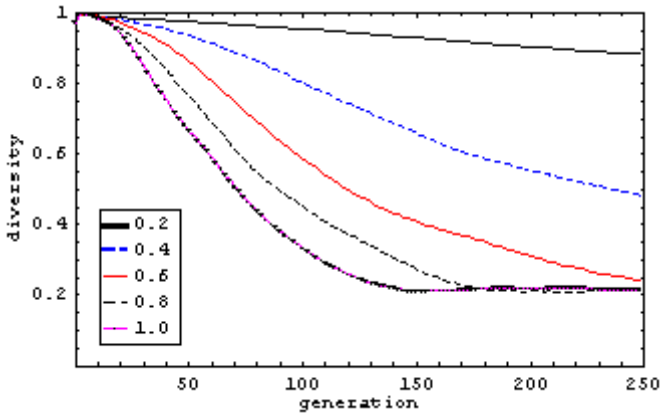


Figure 6. Diversity *vs* generation for the MMDP function: 8-cell local neighbourhood, migration option turned off.

probability of 0.6 results in the optima being found in all 30 runs. This indicates that spatial separation introduced by using the seeding method can be effective if used in conjunction with migration schemes. However, when the M1 migration method was used, the increased selection pressure resulted in a drop off in performance.

The results for the Rastrigin and Griewangk functions using the 8-cell local neighbourhood (Table 4) are very similar to the smaller neighbourhood listed in Table 3. For the MMDP function, we can observe that the increased local selection pressure limits the ability of the algorithm to find the optimal solution. Once again, migration scheme M2 combined with a seeding probability of 0.6 leads to the best results.

An important aspect of this study was to examine the relationships between population density, diversity, and the quality of solution found. Plots of population diversity (measured by allelic diversity) versus time for the MMDP function can be seen in Fig. 5 and 6. In the smaller 4-cell local neighbourhood (Fig. 5) greater levels of diversity are evident as compared to the larger neighbourhood (Fig. 6). Of interest here is the clustering of the plots when the 4-cell neighbourhood is used and the migration option is turned off (NM). This can be attributed to weaker selection inherent in this model. However, when the seeding method is used in conjunction with M1 or M2, differences are evident in the diversity curves. The migration schemes effectively reintroduces the best (using M1) or fitter (using M2) individuals into the population, thereby increasing selection pressure. In the case of the 8-cell local neighbourhood, the impact of the seeding method are more pronounced.

6. CONCLUSION

In this paper, we have described a method to adjust selection pressure in a fine-grained parallel GA by varying population density. This method does not require a pre-determined specification of the number and size of demes. Instead, the formation of demes occurs naturally by using a seeding method that periodically injects new individuals onto the 2-dimensional lattice. There is no fixed migration topology. Migration of "fit" individuals to different demes can be carried out without explicitly specifying which demes they are assigned to. Preliminary experiments have been conducted and the results show that the seeding method and migration schemes can induce a range of different selection pressure. In conclusion, we make the following observations:

- It is possible to adjust selection pressure in fine-grained parallel GAs by controlling the density of the population;
- The use of small, isolated demes in the preliminary stages of a run helps to foster genetic diversity across the population as a whole;
- The coalescing of demes, as a result of increased density, combined with suitable migration schemes can produce results comparable to those by a purely fine-grained PGA;
- Spatial separation, introduced by the seeding method, is most effective when dealing with functions that favour increased parallelism such as the MMDP; whereas for other functions, varying density alone might not be sufficient, and it often has to be used in conjunction with migration schemes.

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