

# Parallel Genetic Algorithms with Dynamic Topology using Cluster Computing

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**Abstract**—A parallel genetic algorithm (PGA) conducts a distributed meta-heuristic search by employing genetic algorithms on more than one subpopulation simultaneously. PGAs migrate a number of individuals between subpopulations over generations. The layout that facilitates the interactions of the subpopulations is called the topology. Static migration topologies have been widely incorporated into PGAs. In this article, a PGA with a dynamic migration topology (D-PGA) is proposed. D-PGA generates a new migration topology in every epoch based on the average fitness values of the subpopulations. The D-PGA has been tested against ring and fully connected migration topologies in a Beowulf Cluster. The D-PGA has outperformed the ring migration topology with comparable communication cost and has provided competitive or better results than a fully connected migration topology with significantly lower communication cost. PGA convergence behaviors have been analyzed in terms of the diversities *within* and *between* subpopulations. Conventional diversity can be considered as the diversity within a subpopulation. A new concept of permeability has been introduced to measure the diversity between subpopulations. It is shown that the success of the proposed D-PGA can be attributed to maintaining a high level of permeability while preserving diversity within subpopulations.

**Index Terms**—genetic algorithms, network topology, message passing, parallel architectures, parallel programming.

## I. INTRODUCTION

Genetic algorithms (GAs) are evolutionary algorithms that collect and combine good genes within a population to form better members. The ability of GAs to produce successful results for different types of problems has found widespread use among researchers. Applying a GA in different subpopulations simultaneously is called a Parallel Genetic Algorithm (PGA). PGAs have been accepted by researchers because generating alternative solutions simultaneously makes searching faster, in many cases producing better results than single-population GAs [1]. PGAs are used in many areas, such as multi-objective optimization [2], the traveling salesman problem [3-4], medical image processing [5-6], and determination of control parameters in high-speed vessels [7]. The most important factor of PGAs is considered to be the migration, defined as the transport of specified individuals at specified intervals from one subpopulation to others [8]. Moreover, the migration reduces the risk of converging to local optima [9].

The cluster computing environment gives us the opportunity to add topology to the migration policy.

Therefore, the migration policy adopted in this study is defined as follows:

- *Migration Topology* refers to the interconnection network of subpopulations,
- *Migration Interval and Rate* describe the amount of information to migrate,
- *Migrant Selection and Replacement*
  - Select the information to migrate,
  - Replace the local information with immigrants,
- *Transfer Mode of Migration* indicates the scheme of communicating migrants synchronously or asynchronously.

The above factors directly affect the performance of PGAs. These components of the migration policy are discussed in the following sections.

### A. Migration Topology

The migration topology facilitates the interactions of the subpopulations. The topology supports the propagation of the information discovered between subpopulations. PGAs with a ring migration topology (R-PGAs) have been widely studied in the literature [10] due to their low communication cost and easy implementation. PGAs with a fully connected migration topology (FC-PGAs) interconnect all subpopulations [11-15]. However, this topological structure is costly because it exchanges individuals between all subpopulations. Therefore, the fully connected migration topology has been restricted to use in theoretical studies. In our studies, a PGA without migration, running all subpopulations independently, called simple PGA (S-PGA) was implemented for the experimental comparisons.

### B. Migration Interval and Rate

The main motivation for tuning the migration interval and rate is to enrich the diversity within subpopulations. The migration interval is the number of iterations between two migration steps. The migration occurrences are considered to be essential when the variances within the subpopulations become sufficiently small. The migration rate indicates the number of immigrants in the literature, commonly used as a percent of the subpopulation size. In practical studies, low migration rates are preferred, varying from 1% to 10% [10]. Studies dealing with migration rates and intervals can be found in [1, 8, 11-13, 16-17].

### C. Migrant Selection and Replacement

Migrant selection addresses the selection of the individuals to be transferred to other subpopulations, while

immigrant replacement handles removing individuals to make room for the newcomers. Exchanging the best individuals with the least fit members of the population is the most widely used selection and replacement [14]. Alba and Troya [1] studied the best and random selections of individuals for migration. In Xiao and Armstrong [2], migrating individuals were selected by the tournaments method. A study has reported that the choice of migrants and replacements affects the convergence time [11].

D. Transfer Mode

The transfer modes are classified as synchronous and asynchronous in PGAs. In the synchronous mode, the migration process is performed simultaneously on subpopulations in each epoch. In each migration step, the required number of GA iterations for all subpopulations is expected to be completed before the migration process starts. The asynchronous mode continues to perform the migration process when a subpopulation reaches the migration step, regardless of other subpopulations. The migrated individuals are incorporated into the target subpopulation, and its GA continues to process subsequent iterations [18].

This paper is organized as follows. In the next section, a new PGA called dynamic migration topology (D-PGA) is described, and the performance results are compared with other commonly used migration topologies in Section III. In Section IV, the concept of diversity and the new concept of permeability, as well as the convergence behaviors of PGAs with different migration topologies, are discussed. The overall discussion and the major contribution of the research are summarized in Section V.

II. PROPOSED DYNAMIC MIGRATION TOPOLOGY PGA

The migration topology determines the propagation velocity of the best individuals among the subpopulations, usually referred to as islands, as illustrated in Fig. 1. In the ring migration topology (R-PGA), transferring an individual from the top to the very end of the ring requires  $(number\ of\ subpopulations - 1)$  migration steps. Thus, an R-PGA transfers

$$[(number\ of\ subpopulations) \times (number\ of\ migrants)]$$

in each epoch (Fig. 1a), whereas an individual in a fully connected migration topology (FC-PGA) can penetrate into all subpopulations in a single migration step at the expense of high communication. An FC-PGA transfers

$$[(number\ of\ subpopulations) \times$$

$$(number\ of\ subpopulations - 1) \times (number\ of\ migrants)]$$

in each epoch (Fig. 1b). In this study, a new migration topology that selects a set of target subpopulations for immigrating the best individuals dynamically is developed. The proposed dynamic migration topology PGA (D-PGA) moves the selected individuals to target subpopulations in a single migration step. The D-PGA transfers

$$[(number\ of\ subpopulations) \times (number\ of\ migrants)]$$

in each epoch (Fig. 1c). Therefore, the number of utilized communication links and the total number of transferred individuals of D-PGA are almost equal to those of an R-PGA but significantly lower than those of an FC-PGA.

The main idea behind our proposed D-PGA is to promote the delivery of “fit individuals” to “fit subpopulations”

within a stochastic scheme.

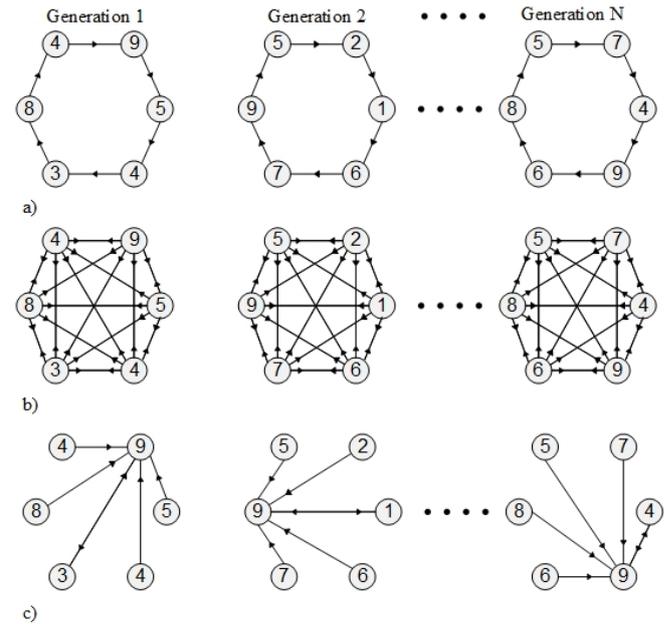


Figure 1. Illustration of communication links of migration topologies a) R-PGA, b) FC-PGA, c) D-PGA

In D-PGA, a subpopulation with high average fitness value has a higher chance of receiving new fit individuals. In each generation, each subpopulation is supposed to select its elites and transfer their duplicates to a single subpopulation of its choice. That chosen subpopulation is called its target subpopulation. A target subpopulation is selected based on the average fitness values of subpopulations via roulette wheel selection in each epoch, as illustrated in Fig. 2. Additionally, the best subpopulation is connected with the inferior subpopulations. The communication links established by this scheme are collectively called the migration topology of that given epoch. Because the migration topology is subject to change in each epoch, this proposed approach is called a dynamic topology.

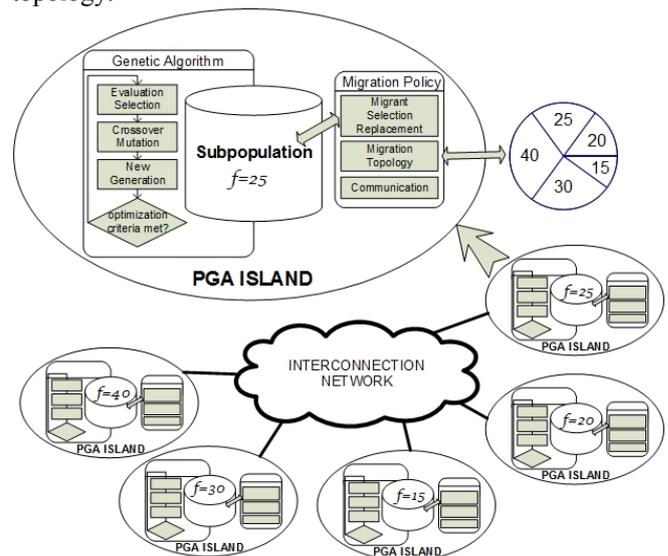


Figure 2. Illustration of D-PGA

Exploration and refinement are the two phases associated with a PGA’s performance. The exploration phase refers to the period starting from the beginning of the search to the turning point of the performance curve. The refinement

phase can be described as the smoothed inclination region of the performance curve following the exploration phase. Our method stimulates the introduction of good schema by delivering the better individuals to the better subpopulations in the exploration phase. Additionally, the inferior subpopulations are supported by the immigrants of the best subpopulation. Thus, D-PGA improves the exploration capability of a PGA by recombining the elite migrated building blocks within a fit subpopulation in earlier iterations.

As observed in Fig. 2, genetic algorithm operations and the migration policy are executed for each subpopulation. Each part of the roulette wheel represents the average fitness value of a subpopulation for a given epoch (Fig. 2). The average fitness values of the  $k^{\text{th}}$  subpopulation  $f_p^k$  are calculated ( $k=1, 2, \dots, p_s$ ) as follows:

$$f_p^k = \frac{\sum_{i=0}^{p_s} f_i}{p_s} \quad p_s = \text{subpopulation size} \quad (1)$$

Each island of a PGA determines a target subpopulation by using the roulette wheel selection with the  $f_p^k$  values. Therefore, those selected fit target subpopulations have a greater probability of receiving fit individuals from multiple subpopulations within the same epoch. This selection may not migrate any immigrants to some inferior subpopulations. To mitigate the further deterioration of inferior subpopulations, the fittest subpopulation of D-PGA transfers its best individuals to the subpopulations with the lowest average fitness. This recovery of low-fitness, likely exhausted, subpopulations are expected to contribute to the overall performance by injecting high-quality building blocks. Concisely, the proposed D-PGA's selection mechanism facilitates two contributing operations. One operation is to transfer the fit individuals to the fit subpopulations. The second operation is to support low-fitness subpopulations with the elite individuals of the current epoch.

### III. ANALYSIS AND RESULTS

In the study, D-PGA, an R-PGA and an FC-PGA (hereafter simply called R-PGA and FC-PGA) have been implemented using the MPI 2.0 library. The PGAs have been executed on the ESOGU Beowulf cluster system with 17 computers. The experimental analyses have been conducted to compare the performance of the proposed D-PGA against R-PGA and FC-PGA. The same number of individuals has been migrated for the PGAs. The three different test functions have been used in comparing the PGAs' performances. Because this study places emphasis on discovering the impact of the migration topologies, the crossover rate, the mutation rate, and the selection method are kept uniform for all experiments.

#### A. Design of the Experiments

For a fair comparison, we offer a new measure of convergence quality that distinguishes a PGA's performance within a range. The motivation for a new measure can be exemplified by using Fig. 3. The convergence curves of two PGAs are given in Fig. 3. In comparing their overall convergence behaviors, a pointwise comparison would be

inconclusive. The convergence curves are divided into three ranges of generations. For each range, the proposed performance measure of a PGA is computed proportionally to the times it has outperformed. These proportional values are represented as percentages in Fig. 3. According to this new measure, the success ratios for PGA1 and PGA2 for the first range (0 to 400 generations) are 33% ( $100 \times 2/6$ ) and 67% ( $100 \times 4/6$ ), respectively (Fig. 3). In the example, it can be observed that PGA2 is better than PGA1 in the first range, while PGA1 is better than PGA2 in the second range. All comparison tables present these outperformance percentages in the following sections.

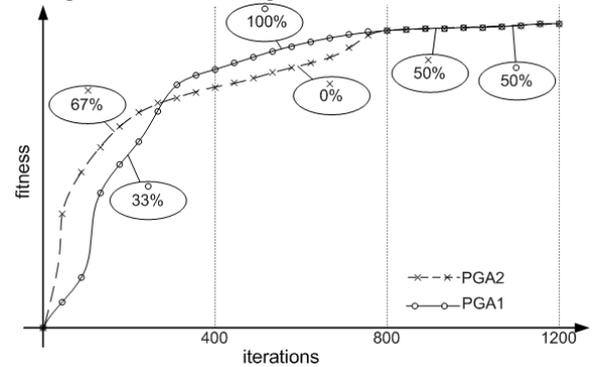


Figure 3. Comparison of the two PGAs over iterations

In Table I, we present the settings and parameters of the PGAs for different migration topologies.

TABLE I. PGA PARAMETERS AND SETTINGS

Name	D-PGA	R-PGA	FC-PGA	S-PGA
<b>Genetic Algorithm Parameters</b>				
Gene length	16 bits	16 bits	16 bits	16 bits
Number of variables	10, 20	10, 20	10, 20	10, 20
Iteration number	1200	1200	1200	1200
Crossover rate	100%	100%	100%	100%
Mutation rate	2%	2%	2%	2%
Selection method	Roulette Wheel	Roulette Wheel	Roulette Wheel	Roulette Wheel
<b>Migration Parameters</b>				
Subpopulation size	80,160, 640	80,160, 640	80,160, 640	80,160, 640
Subpopulation number	16	16	16	16
Migration Rate	7.2%, 14.4%	10%, 20%	1.25%, 2.5%	-
MigrationInterval	20, 80	20, 80	20, 80	-
Selection and Replacement	SB-RW <sup>a</sup>	SB-RW <sup>a</sup>	SB-RW <sup>a</sup>	
Migration Topology	Dynamic	Ring	Fully Connected	Not Connected

a : Send the best individuals, replace with the worst individuals

To evaluate the performance of the different migration topologies, we have selected well-known test problems with multiple local and global optima [8, 17, 19]. They are the Rosenbrock  $f_{Ros}$ , Rastrigin  $f_{Rgn}$ , and Sphere  $f_{Sph}$  functions. Rosenbrock is a non-convex, continuous, inseparable, one-shaped function (2). The number of variables for each function is represented by  $n$ .

$$f_{Ros}(x_i) = \sum_{i=1}^{n-1} \left[ 100 \cdot (x_{i+1} - x_i^2)^2 + (x_i - 1)^2 \right] \quad (2)$$

$$-5.12 \leq x_i \leq 5.12; \quad i = 1 \dots n; \quad n \in \{10, 20\}$$

Rastrigin is a non-convex, continuous, scalable, multi-shaped function (3).

$$f_{Rgn}(x_i) = a \cdot n + \sum_{i=1}^n [x_i^2 - a \cdot \cos(\omega \cdot x_i)] \quad (3)$$

$$-5.12 \leq x_i \leq 5.12; i = 1 \dots n; a = 10; \omega = 2\pi$$

Sphere is a continuous, strictly convex, one-shaped function (4).

$$f_{Sph}(x_i) = \sum_{i=1}^n x_i^2 \quad (4)$$

$$-5.12 \leq x_i \leq 5.12; i = 1 \dots n$$

The experiments have been designed to provide a fair comparison by (i) initiating each PGA with the same population for each trial and (ii) running ten independent random trials for each setting. The performance values are obtained by averaging 10 trials measured at migration points. The outperformance percentages are given for three ranges of 400, 800, and 1200 iterations for all population sizes. The steep and slow exploration phase behaviors of a PGA can be observed within the range of [0-400] and [400-800] for a total of 1200 iterations. The results corresponding to the [800-1200] range show the refinement phase (i.e., the steady-state phase) of PGAs for the test functions. In the following sections, we provide the numerical results first for D-PGA versus R-PGA, and then D-PGA versus FC-PGA.

B. Impact of migration intervals

The migration interval is one of the parameters that may affect the success of a PGA. Therefore, a PGA should be robust in producing good results for different migration intervals. The impact of different migration intervals was investigated for D-PGA and R-PGA performances (Table II). The experiments were performed for the test functions with the migration rate of 10%, the gene number of 10, and the population sizes of 80, 160, and 640.

TABLE II. COMPARATIVE IMPACTS OF MIGRATIONS INTERVALS ON D-PGA AND R-PGA

Migration Interval	Migration Topology	Subpopulation size/Number of GA iterations								
		80			160			640		
		400	800	1200	400	800	1200	400	800	1200
<b>Test Function: Rosenbrock</b>										
20	D-PGA	100	100	100	100	100	100	95	98	98,3
	R-PGA	0	0	0	0	0	0	5	2,5	1,7
80	D-PGA	80	90	93,3	80	90	93,3	100	100	100
	R-PGA	20	10	6,7	20	10	6,7	0	0	0
<b>Test Function: Rastrigin</b>										
20	D-PGA	95	95	96,6	55	78	85	55	68	78,3
	R-PGA	5	5	3,4	45	23	15	45	33	21,7
80	D-PGA	100	100	100	80	90	93,3	80	90	73,3
	R-PGA	0	0	0	20	10	6,7	20	10	26,7
<b>Test Function: Sphere</b>										
20	D-PGA	55	78	85	70	85	90	80	90	93,3
	R-PGA	45	23	15	30	15	10	20	10	6,7
80	D-PGA	60	50	66,6	100	50	40	60	40	33,3
	R-PGA	40	50	33,4	0	50	60	40	60	66,7

D-PGA and R-PGA transfer different numbers of immigrants for a fixed migration interval and a fixed migration rate. In our migration policy, PGAs are allowed to transfer the same number of individuals for a fair comparison throughout the search span. Therefore, the migration rates of 7.2% and 10% were used in D-PGA and R-PGA, respectively. It is observed that D-PGA has produced better results than R-PGA for all cases except one incidence of the Sphere function with a migration interval of 80. However, D-PGA has achieved better performance than R-PGA in the steep exploration phase for even this case.

C. Impact of migration rates

A migration rate determines the number of migrating individuals. Usually, it is expressed as a percentage of the subpopulation size. The experiments considered two settings of the migration rate, 10% and 20%. The results obtained for different migration rates under the same conditions are given in Table III.

It is clearly observed that D-PGA has obtained better results than R-PGA for all test functions, population sizes, and iteration ranges besides two exceptions for the Sphere function.

TABLE III. COMPARATIVE IMPACTS OF MIGRATION RATES ON D-PGA AND R-PGA

Migration Rate %	Migration Topology	Subpopulation size/Number of GA iterations								
		80			160			640		
		400	800	1200	400	800	1200	400	800	1200
<b>Test Function: Rosenbrock</b>										
10	D-PGA	80	90	93,3	80	90	93,3	100	100	100
	R-PGA	20	10	6,7	20	10	6,7	0	0	0
20	D-PGA	100	100	100	80	90	93,3	100	100	100
	R-PGA	0	0	0	20	10	6,7	0	0	0
<b>Test Function: Rastrigin</b>										
10	D-PGA	100	100	100	80	90	93,3	80	90	73,3
	R-PGA	0	0	0	20	10	6,7	20	10	26,7
20	D-PGA	100	100	100	60	80	86,6	60	40	53,3
	R-PGA	0	0	0	40	20	13,4	40	60	46,7
<b>Test Function: Sphere</b>										
10	D-PGA	60	50	66,6	100	50	40	60	40	33,3
	R-PGA	40	50	33,4	0	50	60	40	60	66,7
20	D-PGA	80	90	93,3	60	70	66,6	80	90	93,3
	R-PGA	20	10	6,7	40	30	33,4	20	10	6,7
Migration Interval: 80; Number of Variables: 10										

D. Impact of the number of variables

The chromosomes are composed of genes representing the variables in the test function. The increasing number of variables indicates the complexity level of the optimization problem. In this part of the study, D-PGA vs. R-PGA and D-PGA vs. FC-PGA tests were conducted for the test functions with 10 and 20 variables. The results are given in Tables IV and V.

D-PGA performed significantly better than R-PGA (Table IV). According to the results given in Table IV, D-PGA produced good results on 16 settings, while R-PGA did so

on two settings. The good results of R-PGA on those two exceptional cases may be attributed to the larger population sizes associated with this strictly convex function and single extremum.

TABLE IV. COMPARATIVE IMPACTS OF THE NUMBER OF VARIABLES ON D-PGA AND R-PGA

Number of Variables	Migration Topology	Subpopulation size/Number of GA iterations								
		80			160			640		
		400	800	1200	400	800	1200	400	800	1200
<b>Test Function: Rosenbrock</b>										
n=10	D-PGA	80	90	93,3	80	90	93,3	100	100	100
	R-PGA	20	10	6,7	20	10	6,7	0	0	0
n=20	D-PGA	100	100	100	100	100	100	80	90	80
	R-PGA	0	0	0	0	0	0	20	10	20
<b>Test Function: Rastrigin</b>										
n=10	D-PGA	100	100	100	80	90	93,3	80	90	73,3
	R-PGA	0	0	0	20	10	6,7	20	10	26,7
n=20	D-PGA	80	90	93,3	60	80	86,6	80	70	53,3
	R-PGA	20	10	6,7	40	20	13,4	20	30	46,7
<b>Test Function: Sphere</b>										
n=10	D-PGA	60	50	66,6	100	50	40	60	40	33,3
	R-PGA	40	50	33,4	0	50	60	40	60	66,7
n=20	D-PGA	80	90	93,3	40	70	80	20	10	20
	R-PGA	20	10	6,7	60	30	20	80	90	80
Migration Interval: 80; Migration Rate: 10%										

Table V shows that D-PGA clearly beats FC-PGA for smaller population sizes (i.e. subpopulation size: 80). Having considered the larger subpopulation sizes, D-PGA exhibited a competitive performance against FC-PGA. It can be observed from Table V that the number of variables had no impact on the better performances of D-PGA against FC-PGA with few exceptions.

#### E. Impact of the subpopulation sizes

If a PGA has to operate on smaller subpopulation sizes, the good schema are expected to be explored by different subpopulations. At that point, the performance of the PGA depends on the migration topology to overcome the challenge of diffusing good schema among those smaller subpopulations. Therefore, the impact of the migration topology can be better observed at smaller subpopulation sizes.

The experiments have been designed for small, medium, and large subpopulation sizes. When all the results are examined comparatively, D-PGA outperforms R-PGA and FC-PGA for the smaller subpopulation sizes of 80 in all ranges of iterations (Table II–V). Additionally, D-PGA has produced better performances than R-PGA for medium and large population sizes of 160 and 640 in all ranges of iterations (Table II: 97%, Table III: 89%, Table IV: 80.5%). D-PGA and FC-PGA have produced competitive results for medium and large population sizes.

TABLE V. COMPARATIVE IMPACTS OF THE NUMBER OF VARIABLES ON D-PGA AND FC-PGA

Number of Variables	Migration Topology	Subpopulation size/Number of GA iterations								
		80			160			640		
		400	800	1200	400	800	1200	400	800	1200
<b>Test Function: Rosenbrock</b>										
n=10	D-PGA	100	70	66,6	80	70	46,6	100	100	86,6
	FCPGA	0	30	33,4	20	30	53,4	0	0	13,4
n=20	D-PGA	60	80	86,6	20	10	6,6	0	0	0
	FCPGA	40	20	13,4	80	90	93,4	100	100	100
<b>Test Function: Rastrigin</b>										
n=10	D-PGA	100	100	100	80	90	93,3	60	70	46,6
	FCPGA	0	0	0	20	10	6,7	40	30	53,4
n=20	D-PGA	60	80	80	20	60	73,3	60	60	46,6
	FCPGA	40	20	20	80	40	26,7	40	40	53,4
<b>Test Function: Sphere</b>										
n=10	D-PGA	100	100	100	100	70	60	20	10	6,6
	FCPGA	0	0	0	0	30	40	80	90	93,4
n=20	D-PGA	60	70	60	60	80	86,6	20	10	6,6
	FCPGA	40	30	40	40	20	13,4	80	90	93,4
Migration Interval: 80; Migration Rate: 10%										

#### IV. CONVERGENCE ANALYSIS: DIVERSITY AND PERMEABILITY

The previous section has exhibited the outstanding performance of the proposed D-PGA versus the well-known R-PGA and FC-PGA based on the design settings given in Table I. In this section, these migration topologies will be analyzed in terms of the diversity and a new concept of permeability as the indicators of their underlying search behaviors.

##### A. Diversity

The concept of diversity is an indicator of the similarity of the individuals within a population. Lack of diversity may cause premature convergence [20]. Alternately, higher levels of diversity may result in slower convergence due to random-search-like behavior [21]. Techniques for diversifying a population are typically adopted to reduce selection pressure. A diverse population is able to address multimodal functions and can explore several hills in the fitness landscape simultaneously. Diversity-preserving methods can therefore support global exploration and help to locate several local and global optima. Consequently, a PGA must preserve an adequate level of diversity within its subpopulations over generations. Therefore, numerous researchers have studied the diversity of PGAs [22–25].

The diversity of a PGA can be computed using phenotypic or genotypic methods. Phenotypic methods measure the diversity based on the fitness value assuming that two individuals with similar fitness values also have common features [26]. Genotypic methods calculate the diversity based on the entropy, mostly adopting Hamming pairwise distances of genes [27]. The entropy values are usually computed by counting the sequence of 0s and 1s in the bit positions of all chromosomes [18]. In this study, the

genotypic diversity measure was adopted using bit-entropy values of chromosomes within subpopulations.

### B. Permeability

The diversity is a necessary measure to observe the dispersion within subpopulations. However, this diversity cannot represent the variety and distribution of individuals among subpopulations. The limitations of using the diversity by itself in PGAs may result in significant anomalies in subpopulations, as illustrated in Fig. 4. Fig. 4 represents two pairs of cases, (a-b) and (c-d), which will be classified as the lowest and highest level of diversities, respectively. From the perspective of a PGA, Fig. 4a and 4b should be considered as entirely different cases. While Fig. 4a shows an exhaustion of a PGA, Fig. 4b indicates a lack of diversity within each subpopulation of a PGA with a totally different collective diversity of subpopulations. Fig. 4c and 4d illustrate two distinct distributions with the same highest-level diversity. Fig. 4c indicates high diversity within subpopulations, although the collective diversity of the PGA is reduced to a single subpopulation's diversity. Alternately, Fig. 4d shows high diversity within and between subpopulations simultaneously. In PGAs, the diversity is a necessary measure but not sufficient enough to differentiate (a) from (b) and (c) from (d).

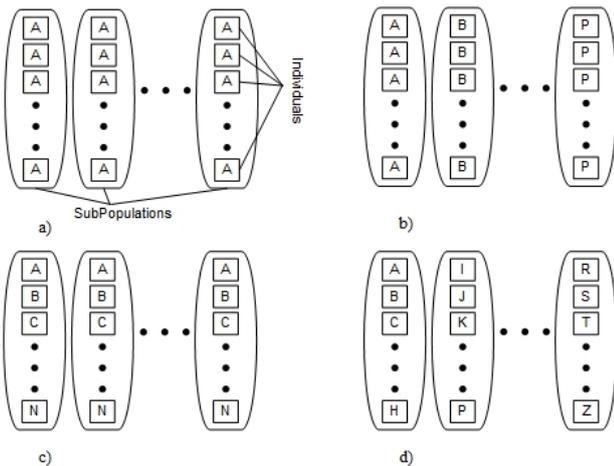


Figure 4. Permeability-diversity relationship (a) low diversity-high permeability, (b) low diversity-low permeability, (c) high diversity-high permeability, (d) high diversity-low permeability

In this study, a new concept called permeability is devised to represent the diversity between subpopulations in addition to the diversity within subpopulations. This new concept of permeability enables PGAs to distinguish the subpopulation distributions of Fig. 4, i.e., (a) from (b) and (c) from (d). The permeability should be considered a complementary measure to the diversity in PGAs. Indeed, the subpopulation distributions of Fig. 4, such as those of (a) and (c) and those of (b) and (d), cannot be distinguished by the permeability itself. The permeability represents the schema-diffusing capability of PGAs between subpopulations, while the diversity addresses the schema distribution within a subpopulation. The permeability is calculated by analyzing the differences between individuals of all subpopulations.

### C. Convergence behaviors in terms of diversity and permeability

The diversity (variety within subpopulations) and

permeability (variety between subpopulations) are both calculated with the entropy based on the Hamming pairwise distances.

The expression for counting the numbers of 0s and 1s in a given bit position is represented in (5). The equation represents the bit positions, chromosome length, and size of a subpopulation as  $i$ ,  $l$  and  $n$ , respectively. If the value at the  $i^{\text{th}}$  bit position of the  $r^{\text{th}}$  individual is equal to  $b$ ,  $c_i^k(r, b)$  is set to 1; otherwise, it is set to 0.  $P_i^k(t, b)$  is the proportion of 0s and 1s at bit position  $i=1..l$  for the subpopulation  $k$ .

$$P_i^k(t, b) = \frac{1}{n} \sum_{r=1}^n c_i^k(r, b), \text{ where} \quad (5)$$

$$c_i^k(r, b) = \begin{cases} 1 & \text{if } c_i^k(r, b) = b, b \in (0,1) \\ 0 & \text{otherwise} \end{cases}$$

The mean entropy of the  $k^{\text{th}}$  population at time  $t$  is defined in (6) [18].

$$H^k[P(t)] = \frac{-1}{l} \sum_{i=1}^l \left[ P_i^k(t, 0) \times \log_2(P_i^k(t, 0)) + P_i^k(t, 1) \times \log_2(P_i^k(t, 1)) \right] \quad (6)$$

The average diversity of PGA,  $\overline{DIV}$ , is calculated based on the average diversity of all subpopulations, as given in (7), where  $p$  represents the number of subpopulations.

$$\overline{DIV} = \frac{1}{p} \sum_{k=1}^p H^k \quad (7)$$

The permeability value of a PGA is also calculated by the mean bit entropy. The expression for counting the numbers of 0s and 1s in a given bit position for all subpopulations is represented in (8). Next, the permeability value of a PGA at time  $t$  is obtained using the mean entropy as formulated in (9).

$$WP_i(t, b) = \frac{1}{p} \sum_{k=1}^p P_i^k(t, b) \quad b \in (0,1) \quad (8)$$

$$\overline{PRM}(t) = \frac{-1}{l} \sum_{i=1}^l \left[ WP_i(t, 0) \times \log_2(WP_i(t, 0)) + WP_i(t, 1) \times \log_2(WP_i(t, 1)) \right] \quad (9)$$

It was shown in Section III that D-PGA has outstanding performance over the considered PGAs. Here, certain tests were carried out to analyze the performances of the migration policies in terms of  $\overline{DIV}$  and  $\overline{PRM}$ . PGAs were implemented using MPI 2.0, and real environment tests were conducted on the ESOGU Beowulf cluster. The impacts of  $\overline{DIV}$  and  $\overline{PRM}$  in maximizing the  $f_{Rgn}$  function were observed for the migration interval of 80, the migration rate of 10%, chromosomes with 10 variables, and the subpopulation size of 160 with 10 independent trials of D-PGA, R-PGA, FC-PGA and S-PGA.  $\overline{DIV}$  and  $\overline{PRM}$  values are collected at the end of each epoch.

Fig. 5a illustrates how the migration policies impact the diversity within subpopulations. The graph shows a steep decline of the diversity within subpopulations as the iterations increased. This decline indicates the propagation of the fit schema at the cost of the diversity loss. Consequently, S-PGA lost the diversity faster than the other PGAs that preserve the diversity depending on the migration

policies designed.

Fig. 5b illustrates the impact of the migration policies on the permeability (diversity between subpopulations) of PGAs. The permeability should be considered a measure of schema similarity between subpopulations. Therefore, S-PGA working on independent subpopulations exhibits the lowest level of permeability over iterations. However, PGAs having different migration policies lead to different levels of permeability. Higher permeability means a higher number of similar schemas distributed in different subpopulations. It is expected that a PGA with higher permeability contains fitter schema than another identical PGA with lower permeability because the schema of highly permeable subpopulations are constructed based on the building blocks of all subpopulations.

Fig. 5c illustrates the performances of PGAs with different migration policies. D-PGA converged to the optimal solution faster than the others. FC-PGA also exhibited close performance to that of D-PGA in the refinement phase. D-PGA and FC-PGA both outperformed R-PGA over all iterations. As expected, S-PGA displayed the weakest performance.

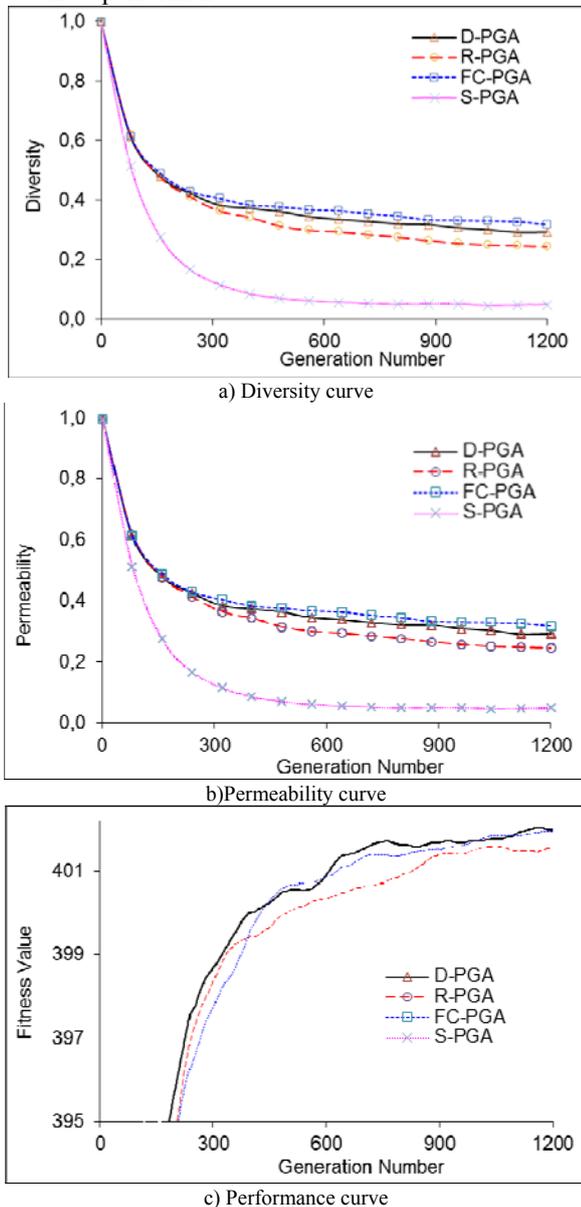


Figure 5. Comparison of D-PGA, R-PGA, FC-PGA, and S-PGA over iterations

Fig. 5 reveals some correlations between the fitness, the diversity, and the permeability of PGAs. The diversity curves of the three PGAs are almost the same, although the performance curves of the PGAs are clearly different from each other. Therefore, an indicator other than the diversity should be addressed in explaining these differences. The permeability, however, shows parallel progression to the fitness curves. This observation allows for consideration of the permeability as the source of these fitness differences. Thus, in the context of the experiment of this section, it can be concluded that the higher permeability is associated with the better performances as conceptually discussed before. Meanwhile, the faster convergence behavior of D-PGA can be attributed to its high permeability supporting faster diffusion of the fit schema while preserving the diversity.

## V. CONCLUSION

There are two main ideas behind this research: (i) each subpopulation must transfer its best individual to the globally best subpopulation in each epoch, and (ii) the global best subpopulation must support inferior subpopulations by transferring its best individuals in each epoch. The implementation of these motivations can only be effectively realized with a dynamic topology because the global best and the inferior subpopulations are subject to change in each epoch. Conventional PGAs are usually designed for static connection topologies due to their dedicated host architectures, such as ring, mesh, tree, and the like. However, PGAs with any connection topology can be programmed by using cluster computing systems. In this article, a dynamic topology for PGAs has been proposed based on the programmable connection capability of cluster computing.

The proposed dynamic topology is defined as a subset of connections among PGA islands subject to change in each epoch. In this context, a connection represents migrating individuals from a source to a selected target subpopulation in D-PGA. Three criteria have been considered in building the topology:

- (i) Each subpopulation must migrate a portion of their best individuals to another subpopulation called the target subpopulation, creating connections equal to the number of subpopulations,  $n$ .
- (ii) A roulette wheel selection picks target subpopulations based on their average fitness values.
- (iii) To leverage inferior subpopulations (with poor fitness values), the best subpopulation migrates a portion of its best individuals to the worst subpopulation, creating one connection.

Thus, these criteria result in  $(n+1)$  connections (almost equal to the  $n$  connections of a ring topology and significantly less than the  $n^2$  connections of a fully connected topology). Because the selected connections are subject to change in each epoch, the topology evolves dynamically over generations, presenting the major contribution of this research to the domain of PGAs.

The performance of the proposed D-PGA has been compared against R-PGAs and FC-PGAs based on a test bed including three test functions and a total of 72 problem settings. The results show that D-PGA has outperformed R-

PGA and has presented comparable performance with FC-PGA. The convergence analysis has revealed that D-PGA has outperformed both R-PGA and FC-PGA in the exploration phase of the genetic search, which might be vital under the pressure of shorter run times.

Also proposed is the new concept of permeability, which, along with the diversity, seems to be a critical indicator in predicting the convergence behaviors of PGAs. Convergence analyses of R-PGA, FC-PGA and D-PGA have been conducted in terms of the diversity and permeability measures. The dynamic topology of D-PGA has maintained relatively high levels of diversity and permeability simultaneously, which may be construed as the underlying factor behind its success. Therefore, the prospect of PGAs having a migration control mechanism to ensure high levels of diversity and permeability simultaneously throughout the PGA search seems to be a promising research area.

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