

The analysis of the interaction of the migration, diversity and permeability in parallel genetic algorithms

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Abstract: Diversity is an important factor for genetic algorithms to do a successful search. High diversity obtained owing to the migration is one of the most important reasons of generation of successful results by Parallel Genetic Algorithms. While permeability is a new term that analyses the effect of the migration parameters in Parallel Genetic Algorithms. In this study, the effect of changing migration intervals on the permeability and the performance of algorithm has been examined and it has been showed that the migration done in exploration phase has made much more contribution to the performance of the algorithm. In addition to this, for the different migration parameters of the individuals that will migrate the values of diversity and permeability have been calculated and the obtained results have been analysed.

Keywords: Parallel genetic algorithms; migration; diversity; permeability

AMS Classification: 65Y05, 68W10, 80M50.

1. Introduction

Genetic Algorithms (GAs) do search by using individuals that represent different regions of search space. As for Parallel Genetic Algorithms (PGAs), they have been formed by practicing GA on different subpopulations. The most important property that separates PGAs from GAs is the migration that enables the individuals to change places between populations. The migration in PGAs enables the transmission of the required amount of individuals in subpopulations to different subpopulations. Owing to the individuals shared between subpopulations by migration, the risk of being caught at the local bests in PGAs decreases [1]. The migration process by sending good individuals to other subpopulations reduces the possibility of deterioration or loss of these individuals in the big population as a result of GA operations. This result enables PGAs to generate better results than GAs.

The migration method extensively used in PGAs is ring migration method (R_PGA) [2-8]. In addition to this, the random ring method [9, 10], where migration process is carried out to a randomly chosen subpopulation, is another method that is used. The other method to be used is fully-connected migration method (FC_PGA) [3, 4, 11], where all subpopulations are connected to each other. According to this method, all subpopulations exchange individuals among themselves during the migration process. However, since this structure includes too many connections its communication cost is high. Elitist Migration Method (E_PGA) is a migration method that aims at generating good results earlier by transmitting good individuals to the right subpopulations faster. E_PGA by doing goodness evaluation among subpopulations, enables good individual to go to the good subpopulation [12-16].

In PGAs, migration parameters are used in addition to GA parameters. Migration parameters are topology, migration method, number of the migrated individuals, migration interval, the selection method of migration individuals, the method of changing places after migration, subpopulation number, subpopulation size and communication model. The selection of these parameters affects the search success in PGAs. Therefore, the studies and settings done on the migration are important for the algorithm to give faster and more efficient results.

In GAs, diversity is used for the measure of the affinity between the individuals in the population. High diversity values are necessary to obtain more successful search results [17]. However, only the examination of the individuals in the population is not enough to exhibit the relationship between diversity and PGA performance. In this study, the term of permeability is introduced as the diversity measure between populations. Thus, the effects of migration parameters to PGA have been examined with the measures of diversity in subpopulation and diversity between subpopulations.

In the following part of the study, the terms of diversity and permeability have been explained, in part 3 the effect of the migration interval changing linearly and parabolically to the permeability has been examined, in part 4 and 5 the permeability and diversity of the individuals that will migrate have been examined. As for part 6 the obtained findings have been interpreted.

2. Diversity and permeability in parallel genetic algorithms

2.1. Diversity and permeability

GAs are formed of individuals representing different regions of the search space. Owing to this, they can reach the solution in different points at the same time. However, as the iteration steps proceed if the reached solutions are out of the region in which there is the best solution, it becomes difficult to obtain a good result. Therefore, there is a need for a balanced selection pressure which will gather the individuals of the population around the best solution. Besides this, the gathering of the individuals only in a specific region is not a desired situation as well. If the region in which the individuals gathered is not

the right region to do the search, a good solution cannot be caught and the possibility of getting caught to the local bests increases. For this reason, sufficient diversity and selection pressure are needed in order to reach good solutions in GAs [17]. As for PGAs the migrated individuals in them, since they are not same with the individuals in the target subpopulation, they contribute to the formation of the diversity. High diversity in all subpopulations (big population) is shown as the main reason of the PGAs' generation of good results [18].

The diversity in GAs is calculated by two methods considering fitness values or gene structure. The diversity is calculated in the first method by looking at the closeness of fitness values of population individuals with each other and in the second method according to the differences in the gene structures of the individuals. According to the second method the affinity rate between the genes are determined by using Hamming Distance (HD) and the diversity is calculated [19].

Another used gene-based diversity analysis is entropy calculation carried out on bits forming the chromosomes. In this approach, 0 and 1s in bit positions belonging to all chromosomes are counted, the rate being used in entropy expression, is evaluated as the diversity belonging to the result population obtained as chromosome length [2]. Since this approach is completely independent from fitness value and fitness function, it is easy to adapt to structures with different parameters.

As for permeability, it is calculated with the diversity analysis between the individuals by examining the subpopulations as a whole population. Since permeability is obtained by the evaluation of the individuals in all subpopulations together, it is an approach used to determine whether the genes spreaded in the big population correctly, and thus used to interpret the quality of the gene change. When permeability is provided, low permeability values; when it is not provided sufficiently high permeability values are obtained. Since the correct spread of the genes provides a faster convergence to a good solution, it is a desired situation that the permeability takes minimum values. If the migration is not carried out successfully, the permeability value doesn't come close to the minimum. In this case,

subpopulations by being caught to the local best points, do not generate good results.

2.2. The calculation of diversity and permeability by entropy

The used diversity analysis method is the entropy approach calculating the diversity by counting the 0 and 1s on the bit points of chromosomes in subpopulation. In Figure 1 subpopulations in PGA and the gene distribution of the individuals belonging to them are given representatively. In this way, i expresses bit position, l chromosome length, and n expresses the number of individuals in subpopulation. 0 and 1s are counted by using Equation (1) on subpopulations formed by using binary coding and the rate of 0 and 1s in i th bit position is determined. In Equation (2) [2] where l expression represents the chromosome length, diversity value belonging to k th subpopulation is determined by using 0 and 1 rates in all bit positions. A general diversity value is calculated by averaging the diversity values belonging to subpopulations as in Equation (3) [16, 20].

Equation (1) is the expression used to calculate the rate of 0 and 1s in the i th bit position. The summand term $c_i^k(r,t)$ takes its values depending on the value at the i th bit position which belongs to the r th individual of the k th subpopulation. It takes 1 if the corresponding bit value is equal to t and 0 if not.

$$P_i^k(t) = \frac{1}{n} \sum_{r=1}^n c_i^k(r,t)$$

$$c_i^k(r,t) = \begin{cases} 1, & \text{if the value at the } i\text{th bit position belonging to the } r\text{th individual of the } k\text{th subpopulation is equal to } t, t \in (0,1) \\ 0, & \text{if not,} \end{cases} \quad (1)$$

$$H^k [P(t)] = -\frac{1}{l} \sum_{i=1}^l \left(P_i^k(0) \times \log_2 P_i^k(0) + P_i^k(1) \times \log_2 P_i^k(1) \right) \quad (2)$$

	l	2	3	i	$l-2$	$l-1$	l	
Subpopulation 1	1	0	1	1	0	0	1	l
	0	0	0	0	1	1	0	2
	1	1	1	0	0	1	1	3
	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
	0	0	0	1	0	1	0	r
Subpopulation 2	1	0	1	1	1	1	0	$n-2$
	0	1	1	1	1	0	1	$n-1$
	0	1	0	0	0	0	1	n
	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
	0	1	0	1	1	1	0	r
Subpopulation p	0	1	1	0	1	1	0	l
	1	1	1	1	0	1	0	2
	0	1	0	1	1	0	0	3
	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
	1	0	1	0	0	1	1	r
Subpopulation p	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
	1	0	0	1	0	0	0	$n-2$
	1	1	0	0	1	1	1	$n-1$
1	1	1	1	0	1	0	n	

Figure 1. Subpopulation structure

Hence, $P_i^k(t)$ gives the rate of the t values at the i th bit position, which is obtained by summing the $c_i^k(r,t)$ values over all the individuals of the k th subpopulation and normalizing the summation by their total number n [16, 20].

$H^k[P(t)]$ [2] given in Equation (2) is the expression where the entropy value has been calculated by using the rate of 0 and 1s in i th bit position belonging to k th subpopulation.

The expression given in Equation (3) enables to calculate the diversity value (DIV) among all individuals by averaging the diversity values calculated independently in subpopulations. p in Equation (3) and (4) expresses the subpopulation number [16, 20].

$$DIV = \frac{1}{p} \sum_{k=1}^p H^k \quad (3)$$

As for the calculation of permeability in PGAs, when it is wanted, diversity analysis is done by

$$PRM = -\frac{1}{l} \sum_{i=1}^l (WP_i(0) \times \log_2 WP_i(0) + WP_i(1) \times \log_2 WP_i(1)) \quad (5)$$

3. The effect of changing migration interval to permeability and algorithm performance

The optimization process in GAs is carried out in two phases as exploration and exploitation. The exploration phase is the phase where the different regions of solution space are searched, as for the exploitation phase it is a phase in which a better solution has been obtained by using the genes gathered in the region where there are good solutions [21]. The number of the migration and the iteration step in which it has been done, is important in order to obtain a successful PGA. It is obvious that a great number of migration process will increase the cost, but few migrations will not make enough contribution to the performance. Therefore, it is important to carry out the migration process in the correct steps. In this stage of the study, it is put forward that if the migration process in exploration phase is done densely in PGAs, better results are produced. The reason of this, is that there are more genes in the first iteration steps which will enable variety among subpopulations. As for the following iteration steps, since the genes in subpopulations resemble each other, the variety will decrease, the exchange of the individuals among subpopulations will not make enough contribution to the performance.

examining subpopulations as a whole population. First of all, the rates of 0 and 1s in i th bit position within the subpopulations are determined by applying Equation (1) exactly. As for the next step, the rates of 0 and 1s in i th bit position when all populations are considered, are calculated by applying the following Equation (4) [16, 20].

$$WP_i(t) = \frac{1}{p} \sum_{k=1}^p P_i^k(t) \quad t \in (0,1) \quad (4)$$

In Equation (5) given below, permeability (PRM) has been obtained by using the rates of 0 and 1 in i th bit position obtained by using Equation (4).

In this part of the study, the values of performance and permeability of PGAs have been obtained by taking stable migration interval 80 with increasing and decreasing migration intervals as linear and parabolic and the results have been exhibited. E_PGA [12-16] has been used in this analysis. The results obtained from Rastrigin (f_{Ras}) function [10, 22, 23] given in Equation (6), have been given by using subpopulation size 640, migration rate 7.2%. The trials have been carried out by using 8 subpopulations. In these trials, equal number of migrations have been done at the iteration length. In all of the real environment tests done in this study “send the best, replace with the worst in target subpopulation” method which is used widely as the migration policy [24], has been used.

$$f_{Ras}(x_i|_{i=1..n}) = a \cdot n + \sum_{i=1}^n [x_i^2 - a \cdot \cos(\omega \cdot x_i)] \quad (6)$$

$$a = 10, \quad \omega = 2\pi$$

$$-5.12 \leq x_i \leq 5.12$$

3.1. Linear changing migration interval

In this part of the study, the maximum fitness value and permeability results obtained by

migration interval increasing and decreasing linearly are presented. As is seen in Figure 2(a), the approach whose migration interval increases linearly, namely which carries out the majority of the migration at the initial steps, has shown a faster climb and has reached the flexion point earlier. As for the migration interval decreasing linearly, compared with increasing and stable migration interval approach, has converged more slowly and has not produced a good result. When the permeability results in Figure 2(b) are examined, it is seen that increasing migration interval approach has reached lower values faster compared with other models however, at the end of the iteration it has finished at a close value with the decreasing migration interval. The reason of this is that at the increasing migration interval approach migration cannot be carried out towards the end of the iteration and due to this, the result does not change and the obtained permeability value advances horizontally. As for the decreasing migration interval, the migration exhibits a reverse behaviour to increasing approach showing its effect on permeability at the end of the iteration steps.

The real environment tests presented in this part, show that by doing the migration process at initial iterations better results can be reached at early steps. It has been put forward that migration done frequently at initial iterations decrease the permeability quickly. When Figure 2(a) and Figure 2(b) are examined together, it is seen that as the permeability decreases, the performance of the algorithm increases. This result exhibits the effect of the migration process to performance obviously. The reason of increasing migration interval approach to reach good result at early iteration steps is the low possibility of migration individuals to exist in the target subpopulation initially. The sent individual will contribute to the diversity in the target subpopulation, and good results will be able to be obtained with the gathering of good genes. As for the following iterations, since all subpopulations will start to search in the correct regions of the search space, the sent individuals will be similar to the present individuals, and thus a low migration effect will be formed [16].

3.2. Parabolic changing migration interval

As is shown in the previous part, it provides to obtain better results to do the migration process frequently when the iteration has started. In this

part of the study, it has been searched how it will perform when the migration process is more frequent initially, compared with the linear change. Thus, trials have been carried out by using migration intervals changing parabolically.

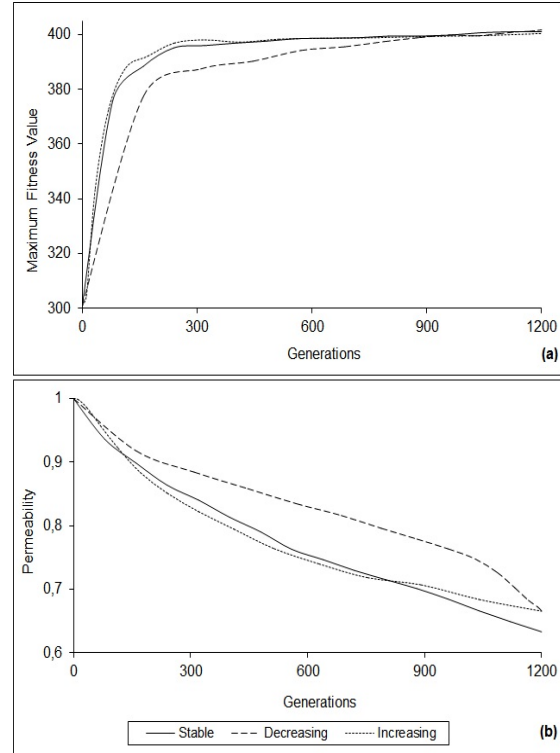


Figure 2. For linear changing intervals (a) maximum fitness value and (b) permeability results

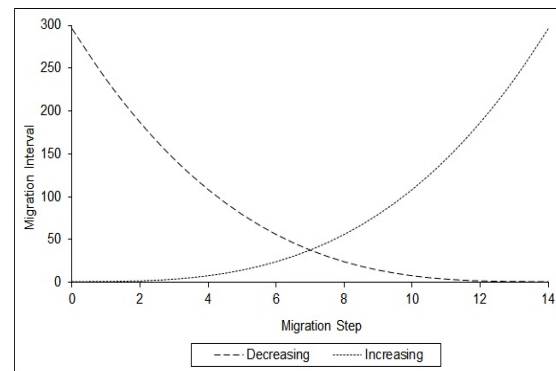


Figure 3. Parabolically changing migration intervals

In Figure 3, migration point-migration interval graphic has been given. By selecting 1200 as total iteration number, the obtained values have been used normalizing with a determined coefficient. As it is understood from Figure 3, in each migration step the process has been done by defining after how many iterations the migration process will be carried out.

The test results for parabolically changing migration interval and the change in permeability values have been given in Figure 4. In parabolically increasing migration interval, initial iterations carry out more migrations. As a result of this, a very fast convergence to flexion point has been obtained. As for parabolically decreasing migration interval, since few migrations are carried out at initial iterations, in all iteration steps it is seen to produce worse results than other methods as is seen in Figure 4(a). As is given in Figure 4(b) the permeability belonging to parabolically increasing migration interval has decreased very quickly at first, but in the latter iteration steps it has not reached low values since it could not carry out migration. As for parabolically decreasing migration interval, the permeability has shown very little change at initial steps in it, but since the migration process increases approaching the last steps, it enters into a fast decrease period [16].

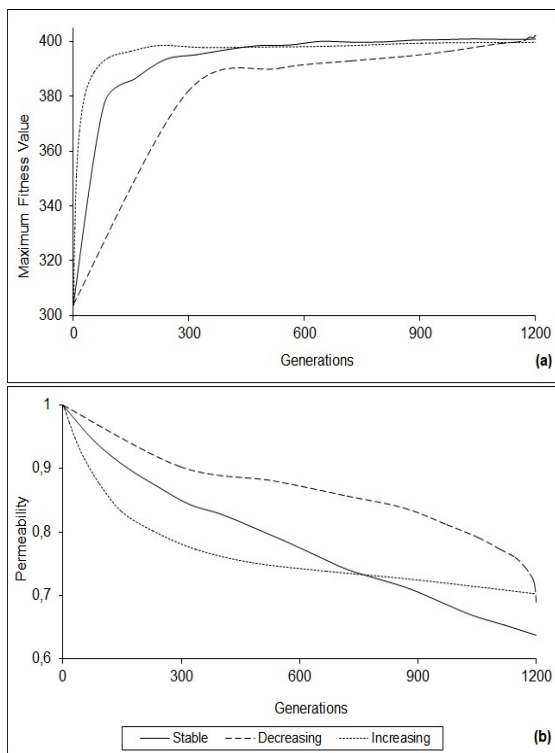


Figure 4. For parabolically changing migration intervals (a) maximum fitness value and (b) permeability results

4. Migration individuals and permeability

New individuals are added to the subpopulations as a result of migration process. The new individuals since they are most probably not the individuals existing in the subpopulation, reform

the space where the search is done. For this reason, the analysis of the individuals that are selected to the migration process is important. The permeability results for migration interval 5, 20, 80, 160 and migration method E_PGA, obtained from the whole of all populations and from the individuals that will migrate are given in Figure 5. In the given graphic permeability has been shown as PRM , permeability belonging to the migration individuals as $mPRM$. As for the migration interval, it is the value presented with this illustration. According to the results, the permeability obtained from the whole of the subpopulations takes bigger values than the permeability obtained only for the individuals that will migrate. The reason of this is the selection of the best individuals for migration and thus sending of the individuals resembling each other. According to the results obtained from the real environment tests, the permeability values obtained for migration interval 160 are very high. Since the migration interval is too much, very few migrations have been done, many GA steps have been carried out between two migration points, and the populations have acted completely independent from each other. For these reasons, the individuals joining the subpopulation by migration have not been effective, the permeability obtained by the evaluation of the whole of the populations and the permeability values obtained from the migration individuals have shown a little difference. When the migration interval is 80, the permeability difference between the population and the migration individuals increases. Since the migration interval decreases, migration individuals take place in the target subpopulations more efficiently. When the migration interval is taken as 5 and 20, the difference between the permeability values belonging to the population and the migration individuals increases quickly. The permeability values belonging to the population and the migration individuals similarly get close to each other in the following iteration steps for migration interval 5 and 160. When the migration interval is taken as 5, because of the migration done very frequently, the majority of the target subpopulation is formed of migration individuals and the whole of the population consists of similar individuals. In the following steps, since both population and the migration individuals are formed with the effect of the migration, the permeability difference between them decreases very much. The other point that must be

considered in this study is that as the migration interval decreases, the permeability value belonging both to the population and to the migration individuals decreases quickly. This

result shows that the permeability term that has been put forward, has analysed the migration effect correctly [16].

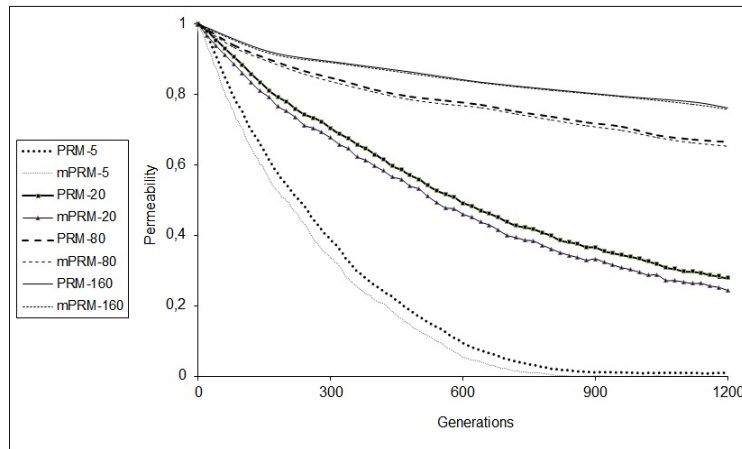


Figure 5. The permeability values for migration interval 5, 20, 80, 160 obtained from the population individuals and the individuals that will migrate

5. Migration individuals and diversity

Migration in PGAs is an important process for increasing the diversity and the performance since it adds new individuals to the subpopulation. Therefore, the analysis of the individuals that will migrate becomes important. In this study, diversity values of migration individuals for different migration methods and migration intervals have been given. In the diversity analysis, the differences of the individuals of all subpopulations that will migrate, have been calculated and by averaging it a final diversity value has been produced. In Figure 6, the diversity values obtained from the individuals that E_PGA, R_PGA and FC_PGA used in the migration respectively for the migration interval 20 and 160 are presented. In Figure 6(a) it is seen that for migration interval 20, the migration individuals that E_PGA has used, have higher diversity values. Especially, in the first half of the iteration steps the diversity formed by E_PGA is much more successful than the other methods. For this reason, it provides a faster convergence to good results. In Figure 6(b), in the trials done for the migration interval 160 while the migration individuals belonging to R_PGA produce more successful diversity values, in the following steps they take close values.

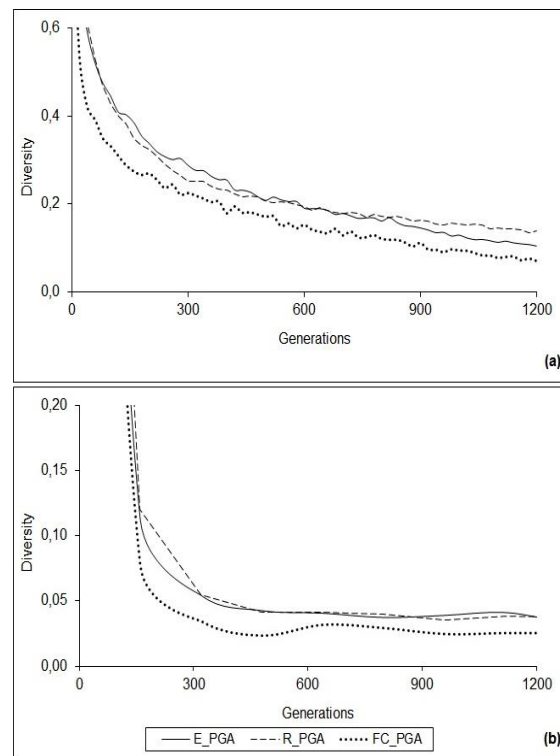


Figure 6. Diversity values of individuals belonging to different migration methods for migration interval (a) 20 and (b) 160

In both graphics it is seen that FC_PGA has produced low diversity results. The reason of this is that while the diversity analysis is being done, 7.2% of the individuals in E_PGA ordered according to the fitness value in the

subpopulations is exposed to evaluation and 10% of it in R_PGA, but this analysis is done for 1.25% in FC_PGA. Although E_PGA is exposed to evaluation with lower rate than R_PGA, it produces close diversity values in migration individuals. This result is one of the reasons of E_PGA's production of successful results [16].

6. Results

In order PGAs to produce more successful results, it is important in which phase the migration process will be done. It has been shown with the trials done for linear and parabolic changing migration intervals that more frequently done migration in exploration phase has been effective to obtain good results in early steps. With this study, the contribution of the migration process to the permeability has been exhibited. In order to increase the contribution of the migration to the performance the analysis of the migration individual is also important as well as the phase in which the migration has been done. For the purpose of doing this evaluation, the permeability belonging to the migration individuals and the whole of the subpopulations for different migration intervals has been examined. According to the obtained results, the permeability obtained from the whole of the subpopulations takes bigger values than the permeability obtained only for the individuals that will migrate. It has been shown that as the migration interval increases, the permeability values of migration individuals and the whole populations get close to each other. Besides this, it has been put forward that as the migration interval decreases, both permeability values decrease, namely better permeability has been provided. In addition to this, diversity results belonging to the migration individuals for different migration methods and migration intervals have been given. The differences of the migration individuals have been examined for E_PGA, R_PGA and FC_PGA. Although E_PGA is evaluated for lower migration rate than R_PGA, it has produced close diversity values to R_PGA both at 20 and 160 migration intervals.

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