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Mathematical Modelling of Migration Process to Measure Population Diversity of Distributed Evolutionary Algorithms

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Abstract

Background/Objectives: Evolutionary Algorithms (*EAs*) have a major role in solving optimization problems. Distributed Evolutionary Algorithms (*dEAs*) improve the performance of classical *EAs*. In *dEAs*, the initial population is divided into a number of subpopulations and an independent as well as cooperative coevolution happens among the subpopulations. **Methods/Statistical Analysis:** The success of *dEAs* is mainly attributed to the migration process they follow, during the evolution. The migration process alters the diversity of the subpopulations. The contribution of the migration process over the success of *dEAs* can be better understood and/or improved in the light of changes it brings in the diversity of subpopulations. Three methodologies used in the modelling process are the theoretical approach, statistical approach and the empirical approach. **Findings:** This paper is to analyze and design a mathematical model of the migration process, for its better understanding. A statistical equation to measure the diversity changes in the subpopulation during the migration process is also derived. The derived equation is validated on different types of populations. **Application/Improvement:** The derived equation can be applied to study and improve the performance of distributed evolutionary algorithms.

Keywords: Distributed Evolutionary Algorithms, Migration, Modelling Migration, Population Diversity, Population Variance

1. Introduction

Evolutionary Computation (*EC*), is a field in computer science, which adopts Darwinian principles of biological evolution. It comprises of a pool of algorithms, collectively known as Evolutionary Algorithms (*EA*). This collection includes algorithms such as Evolution Strategy (*ES*), Evolutionary Programming (*EP*), Genetic Algorithm (*GA*), Genetic Programming (*GP*) and Differential Evolution (*DE*). Evolutionary Algorithms are population based, systematic random search algorithms. For a given optimization problem, they search for the global optimal solution from a possible set of random solutions. In EA terminology, each random solution is named as a candidate and the set of candidates is known as a population. The primary step for any *EA* is initialization of the population. With the randomly initialized initial population, the *EAs* undergo the common evolutionary processes like *selection* of parents, *recombination* of parents, *mutation* of the offspring and *selection* of the best candidate for the next generation. The completion of all the above processes for all the candidates in the current population is termed as the end of one *generation*. This whole process (*generations*) will be repeated until a user defined termination condition is reached.

In the process of searching for the global solution in the search space of random solutions, the mutation and recombination processes add new candidates in the population. Thus they are the techniques for increasing the diversity of the population. This phase in evolutionary search is commonly known as *exploration* phase. The selection processes (parent selection and survivor

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selection) involves finding the best candidates among all the (or few) candidates in the population. This phase in evolutionary search is the *exploitation* phase, which results in decrease in the population diversity. The contributions of both the *exploration* and *exploitation* phases are important, for an evolutionary search to end successfully. Even though, the *EAs* are searching for the solution with balanced exploration and exploitation processes (by mixing exploration (through mutation and recombination processes) and exploitation (through selection process) at every generation, their performance can still be improved with proper additional mechanism for balancing the effect of exploration and exploitation processes.

The distributed evolutionary algorithms (*dEA*) is one among the techniques to improve the performance of *EAs*. The subpopulation of *dEAs* cooperate with each other by an exchange mechanism termed as migration. The migration process transfers the candidate among the subpopulation. This exchange has a greater impact on the population diversity of subpopulation, thus becoming an important phase of *dEA*. Hence it is useful and essential for the researchers in the *EC* community to understand the effect of migration process on the population diversity.

This paper focuses on modelling the migration process mathematically to understand its impact on population diversity. The paper follows three different approaches to gain insight about the impact of migration on population diversity. As a part of the study, a mathematical equation is derived to measure the new variance of a population after the migration. The derived equation is validated on different sample data sets.

The insights presented in the paper will definitely form a subset to the researchers to analyze the diversity changes in the subpopulation during their co-evolution with migration. This may even form another line of research to work on tuning the performance of *dEA*, further, by adding suitable improvements to the migration process in the light of its impact on population diversity.

2. Distributed Evolutionary Algorithms (dEA)

There are several methods available in the literature to improve the performance of *EAs*. One among these methods is parallelization of *EAs*. There are several ways of bringing parallelism. The island based distributed model is one among the ways to parallelize *EAs*. In this model, the initial population of the *EA* is divided into *n* subpopulations and they are distributed to *n* nodes of the parallel system. Now the *EA* will run on each node separately, with the subpopulation at that node. The *n* nodes can be *n* separate machines in a cluster or *n* differ process with in the same machine.

The distributed evolutionary algorithms (*dEA*) drastically outperform the classical *EAs*. The reason behind the success of *dEA* involves the cooperative co-evolution of the subpopulations. The subpopulations use a coordination mechanism termed as migration. In migration process, the candidates are exchanged among the subpopulations at a specific interval. Since the migration process injects new candidates to the existing population, the direction of search within the subpopulations is changed. It also alters the diversity of the subpopulations. However, the diversity of the subpopulations should neither decrease nor increase too fast. The quick decrease or increase in population will result in premature convergence or stagnation problems. The diversity should gradually decrease or increase as it reaches the global optimum.

Since (generally) *dEAs* outperforms classical *EAs*, it is evident that the migration process maintains the steadiness in the decrease and increase of the population diversity. Hence, it is of research interest to investigate the novelty that is happening during the migration process in altering the population diversity. This paper is intended to present the insights gained by the authors based on the mathematical analysis done in this research direction.

Beyer in the year 1998[1] and Feoktistov in 2006[2] stated, "*the ability of an EA to find a global optimal solution depends on its ability to find the right relation between exploitation of the elements found so far and exploration of the search space*". The *EAs* which do not balance the exploration and exploitation processes lose their search capability and fall in premature convergence or stagnation problems according to Zaharie in the year 2001[3], Zaharie and Zamfirache, 2006[4], Angela et al., 2008[5], Zaharie, 2001[6].

To improve the performance of *EAs*, by balancing exploration and exploitation, advanced techniques are proposed by the researchers of *EC* community. The technique of parallelization of *EAs* is one among them. An extensive review on parallelization models used in evolutionary algorithms is presented by Alba and Tomassini in 2002[7].

Potter and DeJong in 1994 put forward the idea of co-operative co-evolution for genetic algorithm (CCGA)[8]. The concept of CCGA had been applied to all the *EAs* by Liu et al.[9] Sofge et al.[10] and Bergh and Engelbrecht, 2004[11].

It follows Divide-and-Conquer strategy of problem solving. The co-operative co-evolution architecture was designed with three components viz. Problem decomposition, Subcomponent optimization and Subcomponent co-adaptation. The wide acceptance of the Evolutionary Algorithms and its repository has led to its widespread usage in almost all the fields of science like data clustering[12], congestion management[13], medicine[14], etc

One of the parallelization model with co-operative co-evolutionary concept is island based distributed model. The efficacy of this model is due to many parameters involved in the distribution. In the year 2004 and 2005, Skolicki and Jong[15, 16]and Cantu-Paz in 2001[17] analyzed the influence of that parameters. The distributed models of *EAs* follow the exchange process called migration, to send and receive candidates among the populations. The migration process itself involves many parameters as stated in Cantu-Paz[17] in 2001 and Skolicki and Jong[15], in 2004. The successful application of island based distributed model was extended to almost all of algorithms in *EA* repository. Extensive empirical analysis on performance efficacy of island models for *DE* algorithm are reported in various studies[18-20].

Since the migration process is the root cause for the success of *dEA*, which also brings changes in the diversity of the subpopulations in the island, we are motivated to measure and analyze the population diversity during the migration process. The population diversity is a measure to state how diversified the candidates are in the population. This may give a *NULL* value (if all the candidates are same), a *HIGH* value (if all the candidates are totally different) or a *MEDIUM* value (for other cases). According to Zaharie[21], the mathematical way to measure the population diversity is to measure the population variance. The higher value of population variance indicates HIGH diversity, zero value indicates NULL diversity and other values indicate MEDIUM diversity. Zaharie[22] in the year 2003 stated that this value can be used as an indicator to balance the exploration and exploitation process.

Zaharie made a significant contribution by deriving an equation to measure the expected population variance in 2001[3] and extended the work in 2002[23,24]. However, this equation is to measure the variance for a single population classical Differential Evolution (*DE*) variant named '*DE/rand/1/bin*'. In 2010, Jeyakumar and ShunmugaVelayutham[25], and Thangavelu et al., in 2015[26] derived the expressions to measure the expected population variance of other variants of Differential Evolution algorithm. Extending this idea to *dEAs*, which involve distributed subpopulations coevolving with migration, is a noteworthy research direction. This paper is taking initial steps, by analysing the migration and diversity, in this direction of research.

3. Modelling the Migration Process

The migration process of *dEAs* depends on many parameters: *Number_of_Islands*, *Migration_Policy*, *Migration_Topology*, *Migration_Frequency* and *Migration_Size*. The *Number_of_Islands* is the number of nodes/processes used for scattering the subpopulations of the initial population. *Migration_Policy* uses selection policy to decide the candidate to migrate and uses replacement policy to decide candidate to be replaced. *Migration_Frequency* is the migration interval. *Migration_Size* is the number of candidates being migrated. *Migration_Topology* decides the interconnection among the islands. A migration scheme is depicted in Figure 1. In the depicted scheme *Number_ of_Islands* = 4, *Selection_Policy* selects best candidate, *Replacement_Policy* selects random candidate, *Migration_Topology* = ring, *Migration_frequency* = 10 generations and *migration_size* = 1. An empirical analysis of migration with different parameters, for *DE* algorithm, is presented by Jeyakumar and Shunmuga Velayutham in 2010[27].

The migration process, at the interval of migration frequency, among the subpopulations exchanges the candidates among them. This process alters the diversity of the subpopulations, which suitably redirect the search. The success of *dEA* is largely due to this mechanism. The pattern of changes (increasing or decreasing) in the

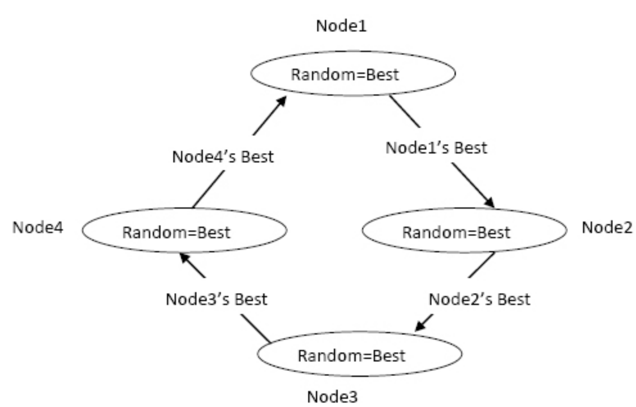


Figure 1. A Simple Migration Scheme.

population diversity, can be measured and analyzed with proper modelling of the migration process. The objective of the modelling presented in this paper is to measure the population variance after migration from the value of the population variance before the migration.

We followed three different methodologies to model the migration process, to get clear insight about calculating the diversity in the population before and after the migration process. There exists many ways to measure the population diversity. We used population variance, which is the most commonly used in the literature. The methodologies used in our study are named as follows.

- Theoretical Approach
- Statistical Approach and
- Empirical Approach

3.1 Theoretical Approach

In *dEA*, the initial population is divided into subpopulations and scattered to all the islands. For easy understanding, in our distributed model the parameters for the migration process are assumed as follows

- *Number_of_Islands*= 2 (named as S_1 and S_2).
- *Migration_Policy* : *Selection_Policy:* best, *Replacement_Policy*: random
- *Migration_Topology:* ring
- *Migration_Interval* = 10
- *Migration_Size:*1

During migration, each subpopulation replaces a local candidate by a foreign candidate sent by its neighbour. In our model, the foreign candidate is the best candidate of the sender subpopulation and the local candidate is a random candidate of the receiver subpopulation. With ring as *migration_topology* and *migration_size* as 1, each node receives only one best candidate from its previous neighbour and sends only one best candidate to its next neighbour. The Figure 2 shows our distributed model.

Since the migration scheme specifies the *migration_interval*, the migration takes place only at that particular interval. Usually, *migration_interval* specifies the number of generations after which the migration should take place. Until reaching the next migration point, each of the subpopulation evolves only with the candidates available at the subpopulation. Hence, the change in the population diversity at each subpopulation, at the end of every generation, is due to the evolutionary processes

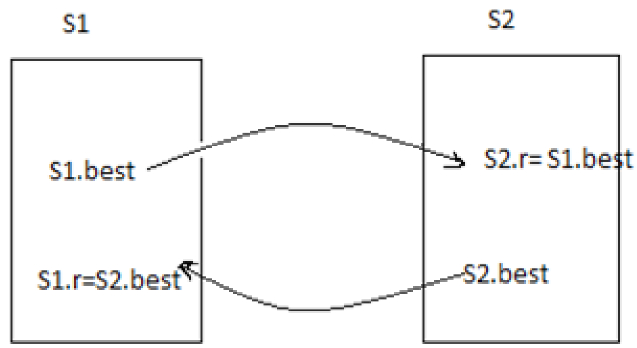


Figure 2. The distributed model used.

(mutation, crossover and selection) done only with the local candidates. In this phase of evolution, the population variance can be mathematically measured. For *DE* algorithm, theoretical equations are given by Zaharie in 2001[3], by Jeyakumar and Shunmuga Velayutham in 2010[25] and by Thangavelu et al, 2015[26] to measure population variance at any arbitrary generation.

At the migration point (assume n^{th} generation), a best candidates of *S1* (*S2*) replaces a random candidate of *S2*(*S1*). Since a local candidate is replaced by a foreign candidate, the diversity of the subpopulation eitherwill increase or decrease or remain unchanged. If the population variance before the migration point (at $n\text{-}1^{th}$ generation) is $V_{old,}$ then new variance (V_{new}) after the migration is expressed as a theoretical equation below

$$V_{new} = V_{old} \pm Change_V \tag{1}$$

Where $Change_V$ is the amount of change (±) in the population variance after migration. Equation (1) states that the population variance after migration is calculated by adding or subtracting either a zero or a non zero value with the population variance before migration. If node *S1's* random candidate (*S1.r*) is replaced by node *S2's* best candidate (*S2.best*). The value for the variable *Change_V*, at node *S1*, can be proportionally calculated by finding any one of the following

(1) Similarity of (or distance between) the candidates *S1.r* and *S2.best*
(2) Similarity of (or distance between) *S2.best* and *S1's* centre of the population.

Based on the population representation the similarity values will vary for different *EAs*. The similarity value is denoted as S_{Val}. This can be calculated using usual distance metrics viz Euclidean distance, Manhattan distance etc. With sufficient sample analysis, a threshold range for S_{val} for three different changes (increase, decrease and no change) in the population variance can be described as follows

$$Change_V = \begin{cases} +cv & if \quad S_{val} \geq ub \\ -cv & if \quad S_{val} \leq lb \\ 0 \; if & lb < S_{val} < ub \end{cases} \tag{2}$$

Where, *cv* is a value to be calculated proportional to S_{val}, from $S_{val.}$

lb and *ub* are the lower and upper bound for S_{val}.

From the equations (1) and (2) the cases of population variance with increasing, decreasing and unchanged are modelled with the equation (3)

$$\sigma_{new} = \begin{cases} \sigma_{old} + cv & if \quad S_{val} \geq ub \\ \sigma_{old} - cv & if \quad S_{val} \leq lb \\ \sigma_{old} & if \; lb < S_{val} < ub \end{cases} \tag{3}$$

This section has presented the theoretical view of measuring the population variance of the subpopulations after migration, from the known population variance at previous generation. This analysis was done to understand the impact of migration process in altering population diversity of the subpopulation. The critical issue found in this analysis is calculating the *cv* value proportional to S_{val}, from $S_{val.}$ The next subsection is intended to provide a different perspective for population variance calculation, without taking into account the similarity between the local candidate and the foreign candidate of the subpopulation.

3.2 Statistical Approach

The objective of this section is to analyze the different cases of changes in population variance (increase, decrease and no change) after migration, with random samples of numbers. This analytical work was done using MS-Excel spreadsheet software. We used two set of numbers from 1 to 10 as our initial subpopulations, named as S_1 and S_2. A basic schematic diagram to show this migration model, used in this study, is presented in Figure 3. Now, the migration process among S_1 and $S_2$is replacing any one of the integer (randomly) in S_1 by any one of the best integer (any integer) from S_2.Themigration process was simulated by replacing all the integers in S_1, one by one, by all the integers in S_2. For example, the result of replacing the number 3 (for example) of $S_1$by all the numbers ofS_2 is shown in Table 1.

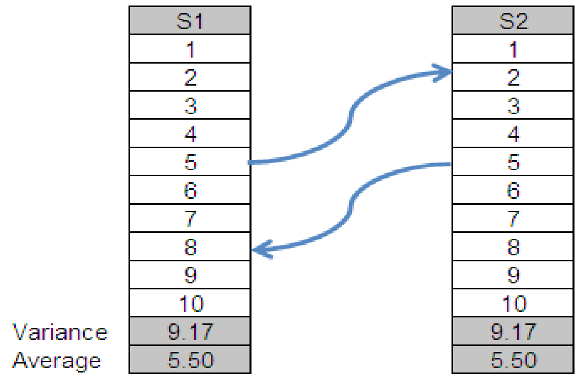


Figure 3. Migration Modelling of two populations with integers.

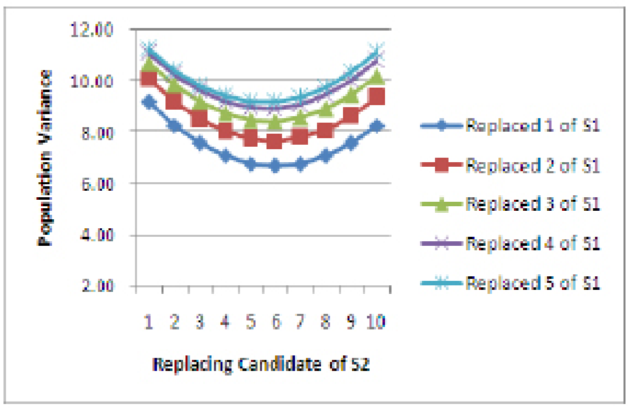
Table 1. A sample migration – with changes in population variance

	S1's	Replaced by S2's									
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
	1	1	1	1	1	1	1	1	1	1	1
	2	2	2	2	2	2	2	2	2	2	2
	3	1	2	3	4	5	6	7	8	9	10
	4	4	4	4	4	4	4	4	4	4	4
	5	5	5	5	5	5	5	5	5	5	5
	6	6	6	6	6	6	6	6	6	6	6
	7	7	7	7	7	7	7	7	7	7	7
	8	8	8	8	8	8	8	8	8	8	8
	9	9	9	9	9	9	9	9	9	9	9
	10	10	10	10	10	10	10	10	10	10	10
Variance=	9.17	10.68	9.82	9.17	8.71	8.46	8.40	8.54	8.89	9.43	10.18
Average=	5.50	5.30	5.40	5.50	5.60	5.70	5.80	5.90	6.00	6.10	6.20

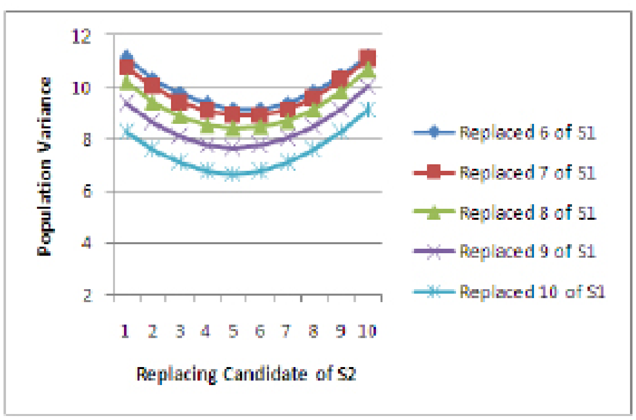
It is observed from Table 1 that, after migration there is a pattern of change in population variance in relation to the centre of the population (ie, average of the population, for S_1 it is 5.50). The population variance after migration either increases or decreases proportionally with respect to the distance of the replacing candidate from the centre of the population. This change is also dependent on the distance of the replaced candidate from the centre of the population. The simulation experiment conducted by replacing all the candidates of S_1, one by one, by all the candidates of S_2, resulted in the combined result shown in Table 2. The graph depicting the population variance changes is shown in Figure 4.a and 4.b.The graphs show bell shaped patterns for the changes in the variance, in all the cases. It was evident from our simulation results

Table 2. The combined result of the simulation

S2's	Population Variance on Replacing S1's Candidate									
	1	2	3	4	5	6	7	8	9	10
1	9.17	10.04	11	11	11	11	11	10	9.34	8.27
2	8.27	9.17	9.8	10	10	10	10	9.4	8.62	7.57
3	7.57	8.49	9.2	9.6	9.8	9.7	9.4	8.9	8.1	7.07
4	7.07	8.01	8.7	9.2	9.4	9.3	9.1	8.5	7.78	6.77
5	6.77	7.73	8.5	8.9	9.2	9.2	8.9	8.4	7.66	6.67
6	6.67	7.66	8.4	8.9	9.2	9.2	8.9	8.5	7.73	6.77
7	6.77	7.78	8.5	9.1	9.3	9.4	9.2	8.7	8.01	7.07
8	7.07	8.10	8.9	9.4	9.7	9.8	9.6	9.2	8.49	7.57
9	7.57	8.62	9.4	10	10	10	10	9.8	9.17	8.27
10	8.27	9.34	10	11	11	11	11	11	10	9.17



(a)



(b)

Figure 4. Change in Population Variance of S1 after migration. **(a)** For replacing number 1 to 5. **(b)** For replacing numbers 6 to 10.

that the variance of a population after migration either decreases or increases based on a close relationship between the replaced, replacing and centre candidates of the population.

3.2.1 Statistical Equation

This section is intended to present the statistical equation derived, by the authors, to measure the variance of a population after migration. For a set of random numbers, the variance and mean are denoted as σ^2_{old} and μ_{old}, respectively. If a number in the set X_{old} (replaced candidate) is replaced by a new number X_{new} (replacing candidate), the new mean (μ_{new}) is

$$\mu_{new} = \mu_{old} + \frac{(X_{new} - X_{old})}{n} \quad (4)$$

The general equation for finding variance of n numbers is

$$\sigma^2_{old} = \frac{1}{n-1}\sum_{i=1}^{n}(X_i - \mu_{old})^2 \quad (5)$$

$$\sigma^2_{new} = \frac{1}{(n-1)}\sum_{i=1}^{n}(X_i - \mu_{new})^2 - \frac{(X_{old} - \mu_{new})^2}{n-1} + \frac{(X_{new} - \mu_{new})^2}{n-1}$$

$$= \frac{1}{n-1}\left[\sum_{i=1}^{n}\left[X_i - \left(\mu_{old} + \frac{X_{new} - X_{old}}{n}\right)\right]^2 - \left[X_{old} - \left(\left[\mu_{old} + \frac{X_{new} - X_{old}}{n}\right)\right]^2 + \left[X_{new} - \left(\left[\mu_{old} + \frac{X_{new} - X_{old}}{n}\right)\right]^2\right]$$

$$= \frac{1}{n-1}\left[\sum_{i=1}^{n}(X_i - m_{old})^2 + \sum_{i=1}^{n}\left(\frac{(X_{new} - X_{old})}{n}\right)^2 - \frac{2}{n}\sum_{i=1}^{n}[(X_i - m_{old})(X_{new} - X_{old})]\right]$$

where $[\frac{2}{n}\sum_{i=1}^{n}(X_i - \mu_{old})(X_{new} - X_{old}) = 0]$

$$= \frac{1}{n-1}(n-1)s^2_{old} + (X_{new} - X_{old})^{\frac{2}{n}} - (X_{old} - m_{old})^2 - \left(\frac{(X_{new} - X_{old})}{n}\right)^2 + 2(X_{old} - m_{old})\left(\frac{(X_{new} - X_{old})}{n}\right) + (X_{new} - m_{old})^2 + \left(\frac{(X_{new} - X_{old})}{n}\right)^2$$

$$= \frac{1}{n-1\left[(n-1)s_{old}^2 + \frac{(X_{new}-X_{old})^2}{n} - (X_{old}-m_{old})^2 + (X_{new}-m_{old})^2 - 2\frac{(X_{new}-X_{old})^2}{n}[X_{new}-X_{old}-m_{old}+m_{old}]\right]}$$

$$= \frac{1}{n-1\left[(n-1)\sigma_{old}^2 + (X_{new}-\mu_{old})^2 - (X_{old}-\mu_{old})^2 - \frac{(X_{new}-X_{old})^2}{n}\right]}$$

$$\sigma_{old}^2 + \frac{(X_{new}-\mu_{old})^2}{n-1} - \frac{(X_{old}-\mu_{old})^2}{n-1} - \frac{(X_{new}-X_{old})^2}{n(n-1)} \quad (6)$$

Thus the equation derived to measure the variance of a population of numbers after replacing any of its number by a new number is

$$\sigma_{new}^2 = \sigma_{old}^2 + \frac{(X_{new}-\mu_{old})^2}{n-1} - \frac{(X_{old}-\mu_{old})^2}{n-1} - \frac{(X_{new}-X_{old})^2}{n(n-1)} \quad (7)$$

The equation (7) was validated with two sample set of numbers *A* ={29, 23, 21,29, 34, 37, 48, 24, 15, 20} and *B*={29, 23, 21, 19, 1, 37, 48, 2, 15, 20}. The mean and variance of the set *A* are $\mu_{old} = 27$ and $\sigma^2_{old} = 101.33$, respectively. For replacing 34 (X_{old}) of *A* by 1 (X_{new}) of *B*, the new variance after replacement (σ^2_{new}) is calculated using the equation (7) as

$$\sigma_{new}^2 = 101.33 + \frac{(1-27)^2}{9} - \frac{(34-27)^2}{9} - \frac{(1-34)^2}{9*10}$$
$$= 101.33 + 75.11 - 5.44 - 12.10$$
$$= 158.90$$

The obtained result was verified with the MS-Excel's VAR function, which returns the sample variance for a sample. A comparison of new variances calculated for various sample replacements by using the equation (7) and VAR function is presented in Table 3. The results in Table 3 proved the validity of the equation derived in this paper.

Even though, the validity of the equation (7) was verified in the above section, it was done for two populations with only set of numbers. But, in EAs the populations are of two-dimensional structure. In *EA's* population structure, each row means a candidate of the population and each column means a particular property of the candidate. Thus the population is the group of candidates with similar properties. Hence, it necessitates verifying the validity of the equation for migration among populations of *EAs*. This study is done in the next section.

Table 3. Validation Results for the Equation (7)

Sno	σ^2_{new}	
	Using MS Excel	**Using Equation (7)**
1	158.9	158.9
2	207.6556	207.6556
3	274.4	274.4001
4	204.5444	204.5444
5	183.2111	183.2111
6	135.73244	135.7322
7	205.8727	205.8727

3.3 *Empirical Approach*

To get sample populations for this study, we used *Differential Evolution* algorithm. *DE*, introduced by R. Storn and K. Price[28], is one of the most powerful addition to *EA* repository. Two random samples of populations were generated by running *DE* algorithm, for the benchmarking function '*Sphere Model*'. *DE* is a powerful stochastic algorithm which is a recent addition to the EA repository. There are different variants for the *DE* algorithm which are compared for multi objective optimization by Aswani et al.[29] and for global optimization by Efrnn et al[30]. For the two dimensional population structures, the population variance is calculated as the average of the population variances of the individual parameters (columns). In our study we considered a population of 15 candidates, with 4 parameters each. The Figure 5 shows the initial subpopulations (S_1 and S_2) generated by *DE* algorithm. The mean and variance calculated using MS-Excel formula are also shown in the Figure. Now, to simulate the migration process, we selected (randomly) the candidate 8 of S_1 as replaced candidate and candidate 13 of S_2 as replacing candidate. The migration from S_2 to S_1 is performed by replacing the candidate 8 of S_1 by the candidate S_2 of 13. The subpopulation S_1 after migration is shown in Table 4. The new population variance of the parameters of S_1 is calculated using the equation (7), and the average of all these measures is calculated as the variance of the population after migration.

This simulation was repeated for many sample replacing and replaced candidates, and the new population variance is calculated using the equation (7) and MS-Excel formula. We found that the results obtained using the equation (7) is exactly matching with the results calculated using MS-Excel (Table 5). This is reiterating the validity of the equation derived for measuring population variance for the population chosen from *EAs* (*DE*) also.

Candidate	Parameters			
	1	2	3	4
1	-14.96	52.04	-88.65	-59.59
2	-36.83	-97.34	91.96	40.70
3	55.88	-4.14	8.82	-45.95
4	96.29	35.64	-51.04	-47.74
5	51.00	87.05	-57.51	-35.90
6	-4.19	45.01	47.71	-57.76
7	-43.41	-12.91	58.45	45.17
8	-82.86	-30.22	16.76	6.02
9	9.88	33.39	-43.55	-51.73
10	76.37	-51.13	33.50	-9.88
11	-41.41	-16.46	54.35	0.03
12	-1.13	-86.67	-15.89	-5.11
13	48.12	-75.46	88.74	-23.47
14	-75.84	-20.75	6.37	-40.13
15	-53.35	3.44	96.48	29.44
σ^2_{old}	3134.49	2894.71	3405.53	1268.64
Population Variance: 2675.84				

(a)

Candidate	Parameters			
	1	2	3	4
1	24.67	3.28	24.19	-4.88
2	24.67	3.28	24.19	-4.88
3	13.76	8.40	2.64	-27.73
4	12.42	-4.09	11.84	-16.65
5	-5.10	14.88	-11.04	31.14
6	31.68	-4.31	33.34	-24.00
7	1.13	-26.36	28.70	-11.61
8	-0.37	-9.39	5.34	-31.76
9	33.02	-20.74	3.91	-43.17
10	-4.52	-17.23	-10.35	-15.21
11	-18.58	-1.83	35.18	36.49
12	-21.92	0.68	0.06	20.67
13	-10.85	19.73	25.71	-7.03
14	33.28	-16.66	-12.53	-40.13
15	9.15	-9.54	41.17	16.19
σ^2_{old}	345.57	170.12	324.71	611.25
Population Variance: 362.91				

(b)

Figure 5. Initial Subpopulations generated by DE algorithm. **(a)** Subpopulation S_1 and **(b)** Subpopulation S_2.

Table 4. The subpopulation S_1, after migration

Candidate	Parameters			
	1	2	3	4
1	−14.96	52.04	−88.65	−59.59
2	−36.83	−97.34	91.96	40.70
3	55.88	−4.14	8.82	−45.95
4	96.29	35.64	−51.04	−47.74
5	51.00	87.05	−57.51	−35.90
6	−4.19	45.01	47.71	−57.76
7	−43.41	−12.91	58.45	45.17
8	−10.85	19.73	25.71	−7.03
9	9.88	33.39	−43.55	−51.73
10	76.37	−51.13	33.50	−9.88
11	−41.41	−16.46	54.35	0.03
12	−1.13	−86.67	−15.89	−5.11
13	48.12	−75.46	88.74	−23.47
14	−75.84	−20.75	6.37	−40.13
15	−53.35	3.44	96.48	29.44
σ^2_{new}	**2639.10**	**2911.29**	**3411.29**	**1236.96**
Population Variance: 2549.66				

Table 5. Validation Results of the equation (7) for population migration

Sno	σ^2_{new}	
	Using MS Excel	Using formula
1	2639.10	2639.10
2	2911.29	2911.29
3	3411.29	3411.29
4	1236.96	1236.96
5	1400.15	1400.15
6	3744.17	3744.17
7	2415.82	2415.82
8	3213.45	3213.45

4. Conclusions

The mathematical modelling of the migration process of the Distributed Evolutionary Algorithms (*dEAs*) presented in this paper followed three approaches: 1) Theoretical

2) Statistical and 3) Empirical. The theoretical approach explained the conceptual view of the migration process among the population, and also a theoretical expression to measure the population diversity. In the statistical approach, the migration process was modelled for population with a set of numbers. This approach expressed a view that the changes in the population diversity after migration depend on the positional difference between the replaced, replacing and centre of the population. An equation to measure the population variance after migration from the current variance is also derived and verified for sample population. In empirical approach, the population structure of *EAs* is explained and the migration process is modelled with two subpopulations derived from *DE* algorithm. The validity of the statistical equation derived above is also verified with each of the subpopulation of *DE*.

As an attempt in the direction of analyzing the migration process of *dEAs*, the insight provided in this paper is in its basic form. We admit that the authors need to investigate more in this direction to come up with more simplified equation to measure the diversity during migration, which may state a strong one-to-one relationship between the migration policy and the diversity enhancement policy.

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