A Comprehensive Comparison of the Original Forms of Biogeography-Based Optimization Algorithms

Ali R. Alroomi[1], Fadhel A. Albasri[2] and Jawad H. Talaq[3]

[1,2,3]Department of Electrical Engineering, University of Bahrain, Sakhir, Bahrain

ABSTRACT

Biogeography-based optimization (BBO) is a new population-based evolutionary algorithm and one of meta-heuristic algorithms. This technique is based on an old mathematical study that explains the geographical distribution of biological organisms. The first original form of BBO was introduced in 2008 and known as a partial migration based BBO. After three months, BBO was re-introduced again with additional three other forms and known as single, simplified partial, and simplified single migration based BBOs. Then a lot of modifications and hybridizations were employed to boost-up the performance of BBO and solve its weak exploration. However, the literature lacks the explanations and the reasons on which the modifications of the BBO forms are based on. This paper tries to clarify this issue by making a comparison between the four original BBO algorithms through 23 benchmark functions with different dimensions and complexities. The final judgment is confirmed by evaluating the performance based on the effect of the problem's dimensions, the side constraints and the population size. The results show that both single and simplified single migration based BBOs are faster, but have less performance as compared to the others. The comparison between the partial and the simplified partial migration based BBOs shows that the preference depends on the population size, problem's complexity and dimensions, and the values of the upper and lower side constraints. The partial migration model wins when these factors, except the population size, are increased, and vice versa for the simplified partial migration model. The results can be used as a foundation and a first step of modification for enhancing any proposed modification on BBO including the existing modifications that are described in literature.

KEYWORDS

Biogeography-Based Optimization, BBO, Simplified BBO, Meta-Heuristic Algorithms, Evolutionary Algorithms, Partial Migration, Single Migration

1. INTRODUCTION

The science of biology becomes one of the main resources of inspiration to develop the modern optimization techniques, such as ant colony optimization (ACO), bee colony optimization (BCO), wasp swarm optimization (WSO), bacterial foraging optimization (BFO), genetic algorithm (GA), evolutionary strategy (ES), differential evolution (DE), particle swarm optimization (PSO), etc. Biogeography-based optimization (BBO) is a new population-based evolutionary algorithm (EA) that was introduced by Dan. Simon in 2008 [1], and its performance was evaluated based on 14 benchmark functions, and then was tested to solve a real sensor selection problem for aircraft engine health estimation. BBO did well and proved that it is a very competitive method as compared to the other EAs. Since then, a lot of researches have been conducted, some of them to solve practical problems such as *economic emission load dispatch* [20], *land cover feature extraction* [21], and *unit commitment* [22]; while the others were focused to enhance its performance, by modifying its

algorithm or/and hybridizing it by adding sub-algorithms form other optimization techniques [23,24,25,26,27,29,33].

The objective of this paper is to outline a clear path for selecting the best algorithm among the four original forms, and thus, any present modification with wrong selected form can be reviewed again with this guidance to enhance its performance. In addition, it can be used as a foundation for any future modification.

This paper is organized as follows: Section II gives a quick introduction about the theory of island biogeography to be as a strong basis to understand the principles of the original BBOs which are described in Section III; after that, Section IV gives a comparison between the original forms of BBO. Section V is set for the conclusions and suggestions.

2. THE THEORY OF ISLAND BIOGEOGRAPHY

Biogeography is a branch of biology, and it is a synthetic discipline, relying heavily on theory and data from ecology, population biology, system matics, evolutionary biology, and the earth sciences [4]. Biogeography seeks to describe, analyze and explain the geographic patterns and changing distributions of ecosystems and fossil species of plants (flora) and animals (fauna) through geological space and time [5, 6].

Island, in biogeography, is any area of suitable habitat (local environment occupied by an organism [7]) surrounded by an expense of unsuitable habitat and is endowed with exceptionally rich reservoirs of endemic, exclusive, strange and relict species [8]. Islands as ecological systems have such salient features as simple biotic, varying combinations of biotic and a biotic factors, and variability in isolation, shape, and size. Thus, island could be aquatic island, desert oasis, individual plants, caves, lakes or ponds, mountain-tops (sky-islands), microcosms or even patches of terrestrial ecosystems. [9,14]. With these characteristics, islands represent themselves as natural experiments, and got highly attentions by the nineteenth century naturalists of the first rank, such as Alfred R. Wallace in East Indies [10], Charles Darwin in Galapagos Islands [11] and Joseph D. Hooker in Southern Ocean [12].

Island biogeography is a special field within biogeography science. This field was initially started by the ecologists Robert H. MacArthur and Edward O. Wilson in 1960 to 1963 with their published paper [2], and continued their studies till 1967 when the final achievement were presented in [3]; and recently, this theory has been revisited and expanded more in [13].

Island biogeography theory fully integrates much of ecology, population biology, evolution, and paleontology, with important implications for conservation of species [13]. It was developed with mathematical models for attempting to translate the ecology and biogeography from the traditional view to analytical view, and answering why some islands are rich of species while the others are poor, by establishing and explaining the biotic (like predation, competition and interactions between species) and a biotic (like wind, water, sunlight, temperature, pressure and soil) factors that affect the species richness of natural communities in an island [15]. Thus, it gives the ability to predict the species counts that migrate between islands and then can find the optimum conservation areas [4,5,6,8].

The equilibrium theory of island biogeography proposes that the number of inhabited species on an island is based on the dynamic equilibrium between new immigrated species onto an island and the extinct species out from that island [2,3,13].

Fig. 1 graphically represents the equilibrium model with exponential immigration (or speciation) rate λ and emigration (or extinction) rate μ, where they can also be plotted as a logistic, linear or any proper function [4,16,17], while the equilibrium location will be shifted to the right or left side based on the type of rate functions, the island's area and/or the distance (isolation) between the source and recipient islands [4,3,13].
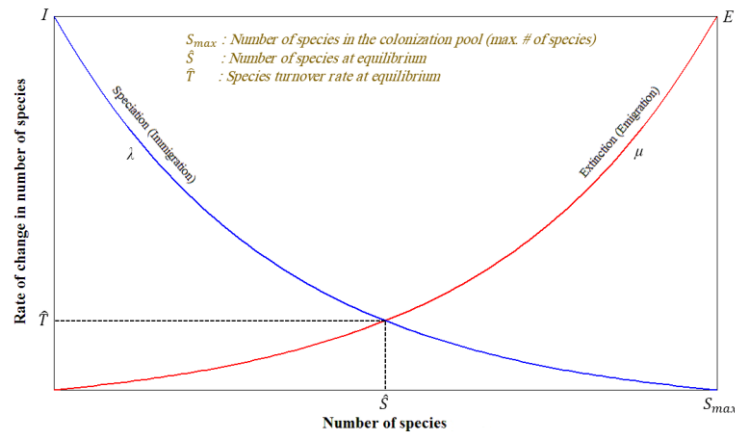

Figure 1. Equilibrium model of a biota of a single island

I and E are the maximum possible immigration and emigration rates, respectively. $\hat{S}$ is the number of species at equilibrium, $\hat{T}$ is the species turnover rate at equilibrium, and S_{max} is the maximum number of species on that island.

I occurs when there is no colonization process, or in other word, the island is empty and offers maximum opportunity to the species on the other islands for immigrating to settle on it; and as the number of arrived species on that island increases, the opportunity for settlement will decrease and thus the immigration rate λ will decrease too. Based on that, the species density increases, so the predation, competition and parasitism factors will increase; and as a result, the emigration rate μ will increase, and reaches its maximum value E at the minimum value of λ [18].

MacArthur and Wilson [2,3] simplified the exponential model to be as a linear function, where $I=E$ as shown in Fig. 2 with mathematical expressions in order to theoretically explain how the migration process on a single island happens.
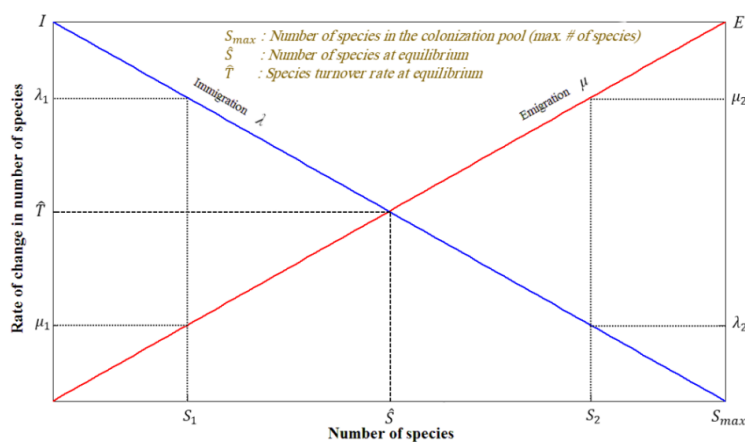

Figure 2. Simplified equilibrium model of a biota of a single island

Now, let at time t, the recipient island has S species with probability $P_s(t)$, and λ_s and μ_s are respectively the immigration and emigration rates at the present of S species on that island. Then the variation from $P_s(t)$ to $P_s(t + \Delta t)$ can be described as:

$$P_s(t + \Delta t) = P_s(t)(1 - \lambda_s \Delta t - \mu_s \Delta t) + P_{s-1}(t)\lambda_{s-1}\Delta t + P_{s+1}(t)\mu_{s+1}\Delta t \tag{1}$$

Also, $\hat{S}$ can be found by using different methods. From the basic of trigonometry:

$$\frac{\hat{T}}{\hat{S}} = \frac{E}{S_{max}} \quad \Rightarrow \quad \hat{T} = \frac{E}{S_{max}}\hat{S} \tag{2}$$

$$\frac{\hat{T}}{(S_{max} - \hat{S})} = \frac{I}{S_{max}} \tag{3}$$

Substituting Eq. 2 in Eq. 3 for $\hat{T}$:

$$\hat{S} = \left(\frac{I}{I + E}\right) S_{max} \tag{4}$$

Eq. 4 can also be obtained by equalizing λ_s and μ_s rates at $\hat{S}$ as follows:

$$\mu_s = \frac{E}{S_{max}}S \tag{5}$$

$$\lambda_s = 1 - \mu_s = I\left(1 - \frac{S}{S_{max}}\right) \tag{6}$$

$$at\ S = \hat{S}: \quad \lambda_s = \mu_s \quad \Rightarrow \quad I\left(1 - \frac{\hat{S}}{S_{max}}\right) = \frac{E}{S_{max}}\hat{S} \tag{7}$$

Solving Eq. 7 for $\hat{S}$ gives Eq. 4; where at the intersection point, the island's biota will be at a state of dynamic equilibrium, and thus $P_s(t + \Delta t) = P_{max}$ [1,3,17].

From Eq. 1, to have S at time $(t + \Delta t)$, one of the following three conditions should hold:
1. S species at time t, and no immigration or emigration took place during the interval Δt;
2. $(S - 1)$ species at time t, and one species immigrated;
3. $(S + 1)$ species at time t, and one species emigrated.

To neglect the probability of more than one immigration or emigration, then Δt has to be set with small value. As Δt approaches 0, the ratio $\left(\frac{\Delta P_s}{\Delta t}\right)$ approaches $\dot{P}_s(t)$:

$$\frac{dP_s(t)}{dt} \cong \lim_{\Delta t \to 0} \frac{P_s(t+\Delta t) - P_s(t)}{\Delta t} \cong -(\lambda_s + \mu_s)P_s(t) + \lambda_{s-1}P_{s-1}(t) + \mu_{s+1}P_{s+1}(t) \tag{8}$$

By considering the previous three conditions, Eq. 8 becomes:

$$\dot{P}_s(t) = \begin{cases} -(\lambda_s + \mu_s)P_s + \mu_{s+1}P_{s+1}, & S = 0 \\ -(\lambda_s + \mu_s)P_s + \lambda_{s-1}P_{s-1} + \mu_{s+1}P_{s+1}, & 1 \leq S \leq S_{max} - 1 \\ -(\lambda_s + \mu_s)P_s + \lambda_{s-1}P_{s-1}, & S = S_{max} \end{cases} \tag{9}$$

The value of $\dot{P}_s(t)$ can also be determined by using a matrix technique [1].

14

Thus, using the known values of $P_s(t)$ and $\dot{P}_s(t)$, the value of $P_s(t + \Delta t)$ given in Eq. 1 can be approximated as:

$$P_s(t + \Delta t) \cong P_s(t) + \dot{P}_s(t)\Delta t \tag{10}$$

Eq. 10 is the final form that has to be used in the program of BBO for calculating $P_s(t + \Delta t)$.

For finding $P_s(t)$, Dan Simon in [1] used two methods; either by solving Eq. 9 numerically, or by applying the following theorem:

Theorem 1: The steady-state value for the probability of the number of each species is given by:

$$P(\infty) = \frac{v}{\sum_{i=1}^{S_{max}+1} v_i} \tag{11}$$

where v and v_i are computed as:

$$v = [v_1, v_2, \dots, v_{S_{max}+1}]^T \tag{12}$$

$$v_i = \frac{S_{max}!}{(S_{max} + 1 - i)!\,(i - 1)!} \qquad (i = 1, \dots, S_{max} + 1) \tag{13}$$

3. BIOGEOGRAPHY-BASED OPTIMIZATION (BBO)

The involvement of the science of biogeography into BBO is that the general problem solution means the natural distribution of species [1]. Each island represents one solution, where the good solution in biogeography means that the island has many species, and the density of these species depends on the availability of good features offered by that island (the good things of biotic "*living: trees, shrubs, meadow, diversity of prey, etc*" and a biotic "*non-living: wind, temperature, humidity, water, area, etc*" factors [19] - *as described in section II*), and vice versa for the poor solution islands [18]. Each feature is called suitability index variable (*SIV*), and represents the independent variable of such a problem in BBO [30].

Island suitability index (*ISI*) depends on the availability of those features on that island; and, in BBO, *ISI* is the dependent variable [30]. Thus, for problem with *n*-independent variables and *k*-islands or individuals, then it can be expressed as:

$$ISI_i = f(SIV_1, SIV_2, \dots, SIV_n) \quad i = 1,2, \dots, k \tag{14}$$

The algorithm of BBO consists of two main sub-algorithms, migration and mutation.

The original forms of BBO depend on the type of the migration process, which are partial migration based (PMB-BBO), single migration based (SMB-BBO), simplified partial migration based (SPMB-BBO), and simplified single migration based (SSMB-BBO) [1,28].

3.1. Migration

Considering Eq. 14, the high *ISI* for island *i* represents a good solution, and also high *ISI* means large number of available species on that island, which forces immigration rate λ_s to be low and

emigration rate μ_s to be high; while low *ISI* for island *i* represents a poor solution, which means a shortage indication in the availability of species on that island, where at this condition λ_s is high and μ_s is low.

Referring to Fig. 2, S_1 is located before $\hat{S}$, where λ_s is high, μ_s is low and the solution ISI_1 is poor; while S_2 is located after $\hat{S}$, where λ_s is low, μ_s is high and the solution ISI_2 is good. Thus, λ_s and μ_s are indications of poor and good solutions, respectively.

In migration process, the high *ISI* islands share their features to modify the low *ISI* islands, where the islands of both sides are probabilistically selected. The high *ISI* islands become the source of modification, while the low *ISI* islands become the recipients to those emigrated species.

Although the species will emigrate from the rich islands to the poor islands, this phenomena does not mean that the species will completely disappear from its home islands. However, only a few representatives emigrate [1]. Thus, the recipient islands are enhanced, and at the same time the source islands are kept away from any shortage on its richness of species.

The migration process of the four original forms of BBO can be described as:-

3.1.1. PMB-BBO Model:

Let ISI_i denote the *i*th population member and contains *n* features
For each island ISI_i (where $i=1,2,3,...,k$)
  For each *SIV s* (where $s=1,2,3,...,n$)
    Use λ_i to probabilistically select the immigrating island ISI_i
      If rand $< \lambda_i$
        For $j=1$ to k
          Use μ_j to probabilistically decide whether to emigrate to ISI_i
            If ISI_j is selected
              Randomly select an *SIV σ* from ISI_j
              Replace a random *SIV s* in ISI_i with *SIV σ*
            end if
        end for
      end if
    next *SIV*
next island

3.1.2. SMB-BBO Model:

Let ISI_i denote the *i*th population member and contains *n* features
For each island ISI_i (where $i=1,2,3,...,k$)
  Use λ_i to probabilistically select the immigrating island ISI_i
    If rand $< \lambda_i$
      Pick a random *SIV s* (where $s=1,2,3,...,n$)
      For $j=1$ to k
        Use μ_j to probabilistically decide whether to emigrate to ISI_i
        If ISI_j is selected
          Randomly select an *SIV σ* from ISI_j
           Replace a random *SIV s* in ISI_i with *SIV σ*
        end if
      end for
    end if
next island

The simplified models (SPMB and SSMB) are similar to the previous normal models (PMB and SMB), except that the simplified models will always use the best obtained solution as the emigrating island instead of doing an internal loop checking. It is apparent that the simplified models have two conflicting issues. They are faster (less CPU time) because the internal looping is eliminated. However, they could trap in a local minima because they always depend on the best solution, and consequently the probability of finding other better solutions reduces.

3.1.3. SPMB-BBO Model:

Let *ISI$_i$* denote the *i*th population member and contains *n* features
For each island *ISI$_i$* (where *i=1,2,3,…,k*)
    For each *SIV s* (where *s=1,2,3,…,n*)
        Use λ_i to probabilistically select the immigrating island *ISI$_i$*
        If rand $< \lambda_i$
            Select the best obtained solution as the emigrating island *ISI$_{best}$*
            If *ISI$_{best}$* is selected
                Randomly select an *SIV σ* from *ISI$_{best}$*
                Replace a random *SIV s* in *ISI$_i$* with *SIV σ*
            end if
        end if
    next *SIV*
next island

3.1.4. SSMB-BBO Model:

Let *ISI$_i$* denote the *i*th population member and contains *n* features
For each island *ISI$_i$* (where *i=1,2,3,…,k*)
    Use λ_i to probabilistically select the immigrating island *ISI$_i$*
    If rand $< \lambda_i$
        Pick a random *SIV s* (where *s=1,2,3,…,n*)
        Select the best obtained solution as the emigrating island *ISI$_{best}$*
        If *ISI$_{best}$* is selected
            Randomly select an *SIV σ* from *ISI$_{best}$*
            Replace a random *SIV s* in *ISI$_i$* with *SIV σ*
        end if
    end if
next island

3.2. Mutation

The features available on an island (i.e., *n-SIV*) can be changed dramatically due to random events called mutations [31], which forces $\hat{S}$ to deviate from its equilibrium value [1].

In nature, the mutation process could happen on one feature or multiple of features. Most observed mutations are harmful, like predators from other islands, tsunamis, volcanos, diseases or earthquakes, which are not directed to be useful [17]. On the other hand, there are some useful events that can enhance those *n-SIV* to give better solutions, such as wind-carrying seeds (wind pollination) or flotsams (shipwreck) [18].

In BBO, this mutation process is modeled as *SIV* mutation, where the mutation rate *m* can be determined by involving species count probabilities *P$_s$* into the following equation:

17

$$m = m_{max} \left(1 - \frac{P_s}{P_{max}} \right) \tag{15}$$

where $P_{max} = max(P_s)$ and m_{max} is a user-defined maximum mutation rate that m can reach. From Eq. 15, m reaches to its minimum "*zero*" at the maximum value of P_s, and vice versa. Thus, m is inversely proportional to P_s.

The objective of using mutation rate is to set the low and high *ISI* solutions likely to mutate, which gives them an ability to enhance their results more than what they already have, where the solutions at the equilibrium point are not mutated [1].

The mutation process can be described as:

For $i = 1$ to k (where k is the number of islands, see Eq. 14)
    Calculate probability P_s based on λ_s and μ_s (by numerical or direct method)
    Calculate mutation rate m (using Eq. 15)
    Select *ISI_i* with probability proportional to P_s
    If *ISI_i* is selected
        Replace *SIV* of *ISI_i* with a randomly generated *SIV*
    end if
end for

3.3. BBO Algorithm

The steps of the general BBO algorithm can be listed as:

1. Initialize the BBO parameters *(S_{max}, I, E, m_{max}, etc)*.
2. Find species count probabilities P_s and mutation rate m based on the calculated immigration rate λ_s and emigration rate μ_s by Eqs. 5 and 6.
3. Generate k random islands, where each island represents one solution to a given problem with *n-SIV*.
4. Sort the solutions *k-ISI* for all islands, so the first best solution should be mapped with the highest number of species and the highest emigration rate μ_s (or the lowest immigration rate λ_s), and continue the descending order till reaching to the worst solution.
5. Do elitism process for saving the required best solutions for the next generation; it is an optional step [30].
6. Probabilistically select the source islands based on μ_s, and the islands which need to be modified "the recipient islands" based on λ_s, and do the migration process. Then, update all *k-ISI* before ending this step.
7. Do mutation process for the islands based on their probabilities that are listed in the probability vector after calculated in step (2). Then, update all *k-ISI* once the mutation process is completed.
8. Return to step (4) for the next iteration. This loop can be terminated either if reaching to an acceptable tolerance or after completing the desired number of generations.

4. PERFORMANCE COMPARISON

The main problem associated with all the modified BBOs is that the modifications were done on an arbitrary selected form of the four original forms. There is no clarification on which form the proposed modification stands on and why.

The four original forms of BBO have been tested through 23 benchmark functions with different dimensions and complexities.

These functions can be classified into three groups: unimodal, multimodal with few local minima and multimodal with many local minima. Functions f01-f13 are high-dimensional problems. Functions f01-05 and f07 are high-dimensional and unimodal, f06 is a high-dimensional step function with one discontinuous minimum. Functions f08-13 are high-dimensional and multimodal with many local minima, and the remaining functions are low-dimensional and multimodal with few local minima [33]. The details of these benchmark functions can be found in the Appendix.

The parameters that have been used here are similar to those used in [25,29]: population size of 50, $I=E=1$, $m_{max}=0.01$, generation limit of 20,000 for f01-13 and 1000 for f14-23, elitism parameter of 1, and Monte-Carlo simulation with 30 trails.

Table 1 summarizes the performance of PMB, SMB, SPMB and SSMB models for 23 benchmark functions. The highlighted cells in the tables represents the best result among the four BBO algorithms. It can be clearly seen that the performance of PMB and SPMB are superior as compared to SMB and SSMB. For high-dimensional problems, PMB wins with 7 best solutions, 10 mean and 8 standard deviation out of 13; while SPMB wins with 6 best solutions, 3 mean and 5 standard deviation. On the other hand, for low-dimensional problems, SSMB enters this competition, and gives better Best, Mean and Standard deviation than that of the PMB for the functions f16,f17,f18, but it does not win as compared to SPMB. Single and simplified single migration based models are not valid for f21-23, because these problems are 1-dimensional problems, and the migration process is done within only one independent variable.

Table 1. Comparison of the results for 30 trails of the original four BBO models, where Best, Mean, and StdDev stands for the smallest error, the mean of all errors, and the standard deviation, respectively.

f #	n	Biogeography Based Optimization (BBO)											
		Partial Migration Based			Single Migration Based			Simplified Partial Migration Based			Simplified Single Migration Based		
		Best	Mean	StdDev	Best	Mean	StdDev	Best	Mean	StdDev	Best	Mean	StdDev
f01	30	1.8518E+00	3.8843E+00	1.3964E+00	1.6999E+02	3.1652E+02	9.9742E+01	2.2588E+00	4.3027E+00	1.3073E+00	8.1588E+01	3.5592E+02	1.5209E+02
f02	30	4.0024E-01	7.0184E-01	1.3458E-01	3.8978E+00	6.1515E+00	1.3348E+00	5.1678E-01	7.6268E-01	1.0545E-01	5.4535E+00	7.3952E+00	1.1782E+00
f03	30	4.2433E+02	1.9527E+04	1.1268E+04	3.3679E+03	3.0638E+04	1.3227E+04	1.9048E+03	3.2307E+04	8.3231E+03	4.4645E+02	2.7268E+04	1.4724E+04
f04	30	3.2007E+00	6.2387E+00	1.1469E+00	2.3978E+01	3.4745E+01	6.0946E+00	2.8725E+00	5.6856E+00	1.2431E+00	2.8262E+01	3.8791E+01	4.1634E+00
f05	30	1.0517E+02	2.6058E+02	7.9555E+01	5.0807E+03	2.3564E+04	1.6310E+04	1.3597E+02	2.7246E+02	1.1116E+02	7.4418E+03	3.9130E+04	3.2640E+04
f06	30	2.0000E+00	4.7333E+00	1.8245E+00	1.7400E+02	3.9163E+02	2.0465E+02	1.0000E+00	4.7667E+00	2.4315E+00	1.3900E+02	4.5263E+02	2.8296E+02
f07	30	2.8562E-07	1.2406E-06	1.2872E-06	7.6867E-04	1.2135E-02	1.4628E-02	1.9837E-07	1.3833E-06	1.1343E-06	1.0547E-03	1.3451E-02	1.4276E-02
f08	30	4.4291E-06	1.3876E-05	5.7466E-06	3.5004E-04	1.6463E-03	2.1669E-03	5.0828E-06	1.3322E-05	7.4610E-06	5.9656E-04	1.8382E-03	1.0377E-03
f09	30	9.4594E-01	1.9351E+00	6.4580E-01	2.3807E+01	3.3102E+01	5.6152E+00	1.0236E+00	1.9211E+00	5.7860E-01	2.6082E+01	3.4796E+01	6.4496E+00
f10	30	6.3026E-01	9.9236E-01	2.3065E-01	4.3719E+00	5.7651E+00	6.6010E-01	4.9817E-01	1.0345E+00	2.5990E-01	4.6872E+00	5.9257E+00	6.9267E-01
f11	30	8.6708E-01	1.0263E+00	3.4402E-02	2.1095E+00	4.4318E+00	1.3255E+00	9.4245E-01	1.0357E+00	2.7730E-02	2.1708E+00	5.0205E+00	1.9755E+00
f12	30	5.0934E-03	2.9591E-02	3.2559E-02	1.0493E+00	3.5616E+00	3.8957E+00	3.8794E-03	3.1228E-02	3.5340E-02	1.4325E+00	6.3746E+01	3.2648E+02
f13	30	9.3001E-02	1.6875E-01	6.0757E-02	5.3779E+00	3.1883E+03	1.3051E+04	8.1548E-02	2.0015E-01	8.0590E-02	6.9544E+00	2.3081E+03	8.1029E+03
f14	2	2.1720E-11	8.0558E-08	2.1865E-07	6.4942E-10	1.4595E-04	5.4076E-04	6.1392E-12	3.8090E-10	3.2748E-10	8.4939E-11	1.0718E-07	5.3020E-07
f15	4	3.9927E-04	8.0573E-04	3.2529E-04	5.6999E-04	1.3729E-03	4.5011E-04	1.8923E-04	7.0160E-04	3.1929E-04	4.5865E-04	1.3658E-03	5.8181E-04
f16	2	2.3455E-07	9.1217E-05	1.2481E-04	1.6640E-05	4.1018E-04	4.3907E-04	3.5869E-10	4.8485E-06	4.7243E-06	5.7770E-08	2.7089E-05	3.9141E-05
f17	2	5.6480E-07	9.6466E-05	1.6743E-04	3.6639E-06	3.4432E-04	3.9477E-04	1.2486E-07	1.9438E-05	2.7087E-05	4.4129E-07	7.3364E-05	9.1485E-05
f18	2	2.7778E-05	1.5749E-03	1.6278E-03	6.0816E-05	5.8628E-03	6.6169E-03	1.2784E-07	8.1736E-05	8.7004E-05	9.2851E-06	2.9315E-04	3.7882E-04
f19	3	7.6177E-06	5.0374E-04	3.8211E-04	2.5507E-04	1.6343E-03	1.2888E-03	5.9005E-07	5.0688E-05	5.9545E-05	1.6327E-06	5.2029E-04	4.9816E-04
f20	6	1.8781E-03	6.9158E-02	6.0706E-02	3.6659E-02	1.6534E-01	7.1746E-02	3.3727E-03	7.9192E-02	5.6884E-02	2.1696E-02	1.5974E-01	6.5199E-02
f21	1	9.8030E-08	2.8723E-05	4.2939E-05	For 1-dimensional problems, SMB-BBO is not applicable; (SMB=PMB)			3.8113E-09	3.3121E-06	6.0656E-06	For 1-dimensional problems, SSMB-BBO is not applicable; (SSMB=SPMB)		
f22	1	8.1958E-10	2.1546E-05	5.2185E-05				2.2393E-08	3.4060E-05	4.6055E-05			
f23	1	1.7454E-08	7.4624E-05	1.8726E-04				1.0113E-07	3.7714E-05	5.3672E-05			

Although, in overall, SSMB has respectively the first and second worst performance for high and low-dimensional problems, it achieved the fastest algorithm as shown in Table 2. This is logical, because of two reasons. First, it does a migration on one randomly selected *SIV* for each island rather than all *n-SIV* as in PMB and SPMB. Second, it will always select the best found solution as a source island for migration instead of doing a loop checking as in SMB. This is why the simplified versions of PMB and SMB trip in local minima particularly as the complexity, side constraints and/or dimensions increases and as the number of islands or population size decreases. In this situation, PMB has the best exploration and exploitation, especially when the mutation stage that compensate the weakness of the migration algorithm is absent, in which the performance of SPMB is significantly decreased, as shown in Table 3.

Table 2. Normalized CPU time for the high-dimensional problems f01-f13

f #	BBO Models			
	PMB-BBO	SMB-BBO	SPMB-BBO	SSMB-BBO
f01	1.4804E+00	1.0084E+00	1.3181E+00	**1.0000E+00**
f02	1.4687E+00	1.0086E+00	1.3103E+00	**1.0000E+00**
f03	1.1672E+00	1.0082E+00	1.1104E+00	**1.0000E+00**
f04	1.5018E+00	1.0086E+00	1.3355E+00	**1.0000E+00**
f05	1.4717E+00	1.0074E+00	1.3133E+00	**1.0000E+00**
f06	1.4721E+00	1.0079E+00	1.3113E+00	**1.0000E+00**
f07	1.4089E+00	1.0070E+00	1.2769E+00	**1.0000E+00**
f08	1.4521E+00	1.0074E+00	1.2969E+00	**1.0000E+00**
f09	1.4621E+00	1.0068E+00	1.3041E+00	**1.0000E+00**
f10	1.4299E+00	1.0052E+00	1.2815E+00	**1.0000E+00**
f11	1.4256E+00	1.0070E+00	1.2876E+00	**1.0000E+00**
f12	1.3703E+00	1.0056E+00	1.2437E+00	**1.0000E+00**
f13	1.3878E+00	1.0021E+00	1.2505E+00	**1.0000E+00**
Avg CPU Time	1.4230E+00	1.0070E+00	1.2800E+00	**1.0000E+00**

Table 3. The overall performance of PMB and SPMB with/without mutation stage

f #	Function Name	n	Mutation Stage	Biogeography Based Optimization (BBO)					
				Partial Migration Based			Simplified Partial Migration Based		
				Best	Mean	StdDev	Best	Mean	StdDev
f05	Generalized Rosenbrock	30	Activated	**1.0517E+02**	**2.6058E+02**	**7.9555E+01**	1.3597E+02	2.7246E+02	1.1116E+02
			Not-Activated	**1.7036E+02**	**6.0492E+02**	**6.4746E+02**	2.2803E+02	7.5845E+02	8.8977E+02
f08	Generalized Schwefel F2.26	30	Activated	**4.4291E-06**	1.3876E-05	**5.7466E-06**	5.0828E-06	**1.3322E-05**	7.4610E-06
			Not-Activated	**8.1593E-06**	**2.9257E-05**	**1.1255E-05**	1.2890E-05	3.7150E-05	1.3349E-05
f14	Shekel's Foxholes	2	Activated	2.1720E-11	8.0558E-08	2.1865E-07	**6.1392E-12**	**3.8090E-10**	**3.2748E-10**
			Not-Activated	**5.4152E-08**	**2.2467E-03**	**8.6667E-03**	1.6396E-07	7.6697E-03	1.3175E-02
f18	Goldstein-Price	2	Activated	2.7778E-05	1.5749E-03	1.6278E-03	**1.2784E-07**	**8.1736E-05**	**8.7004E-05**
			Not-Activated	**1.4627E-04**	**2.5692E-02**	**2.2876E-02**	2.0330E-03	4.0344E-02	5.0549E-02

To verify this conclusion, three performance tests have been conducted as shown in Tables 4, 5 and 6. Each one of these three tests is focused on one criteria.

Test I is shown in Table 4, and it is used to study the performance of PMB and SPMB algorithms as the problem's dimension decreases. The parameters used for this test are similar to that used in Table 1, except that the generation limit are set as: 1000 for *n*=2,4,6 ; 5000 for *n*=10 ; 10,000 for *n*=20 and 20,000 for *n*=30.

Whereas, Test II shown in Table 5 is used to study the performance of PMB and SPMB algorithms as the number of islands or population size increases for two of low-dimensional problems.

Finally, Test III shown in Table 6 is used to study the performance of PMB and SPMB algorithms under different upper and lower limits of the variable bounds (also known as domain, search space, side constraints, etc).

As can be seen from Table 4, the SPMB performs better as the problem's dimension decreases. But when the population size is small, the PMB will perform better even for the low-dimensional problems, as shown in Table 5. From Table 6, if the search space is large, the PMB wins too.

Fig. 3 shows the curves of fitness functions of PMB, SMB, SPMB, and SSMB for the Schwefel's problem 1.2 "f03", Generalized Rosenbrock's function "f05", Generalized Rastrigin's function "f09" and Generalized Griewank's function "f11". For functions f05,f09 and f11, it can be clearly seen that the PMB and SPMB algorithms outperform the SMB and SSMB algorithms, and the gap between the convergences is large. For the function f03, SSMB enters this competition and shows better fitness as compared to SPMB. However, the PMB algorithm is again has the best convergence.

Table 4. Performance Test I – f05 with different dimensions

| f # | Name | Dimensions | Biogeography Based Optimization (BBO) | | | | | |
| | | | Partial Migration Based | | | Simplified Partial Migration Based | | |
			Best	Mean	StdDev	Best	Mean	StdDev
f05a	Generalized Rosenbrock's Function	2	5.0569E-06	3.0404E-04	2.9421E-04	1.1454E-06	4.3368E-04	7.0482E-04
f05b		4	2.6016E+00	1.3546E+02	1.0058E+02	3.8176E-01	3.0585E+01	3.2854E+01
f05c		6	4.5589E+01	8.1933E+02	7.3780E+02	4.0158E+01	8.3004E+02	7.5869E+02
f05d		10	2.8495E+01	2.1690E+02	1.8675E+02	7.1550E+01	2.4654E+02	1.7535E+02
f05e		20	8.7400E+01	3.3766E+02	2.4278E+02	1.3913E+02	3.5894E+02	4.0126E+02
f05f		30	1.0517E+02	2.6058E+02	7.9555E+01	1.3597E+02	2.7246E+02	1.1116E+02

Table 5. Performance Test II – f15 and f16 with different populations

| f # | Name | Population Size | Biogeography Based Optimization (BBO) | | | | | |
| | | | Partial Migration Based | | | Simplified Partial Migration Based | | |
			Best	Mean	StdDev	Best	Mean	StdDev
f15a	Kowalik's Function	5	3.0566E-04	1.1017E-03	5.6436E-04	4.2186E-04	1.4561E-03	7.5693E-04
f15b		10	5.1379E-04	1.2970E-03	7.7744E-04	2.1192E-04	1.0605E-03	7.2553E-04
f15c		50	3.9927E-04	8.0573E-04	3.2529E-04	1.8923E-04	7.0160E-04	3.1929E-04
f15d		200	1.9935E-04	6.2320E-04	2.2726E-04	1.4958E-04	4.4200E-04	1.7749E-04
f16a	Six-Hump Camel-Back Function	5	1.0557E-05	6.5798E-04	7.0515E-04	1.1389E-05	8.7138E-04	8.0479E-04
f16b		10	1.1365E-07	2.9963E-04	4.1067E-04	2.4790E-06	1.8534E-04	2.8880E-04
f16c		50	2.3455E-07	9.1217E-05	1.2481E-04	5.7770E-08	2.7089E-05	3.9141E-05
f16d		200	1.7238E-07	2.2757E-05	2.7229E-05	5.7634E-09	5.9924E-07	7.5759E-07

Table 6. Performance Test III – f11 with different side constraints

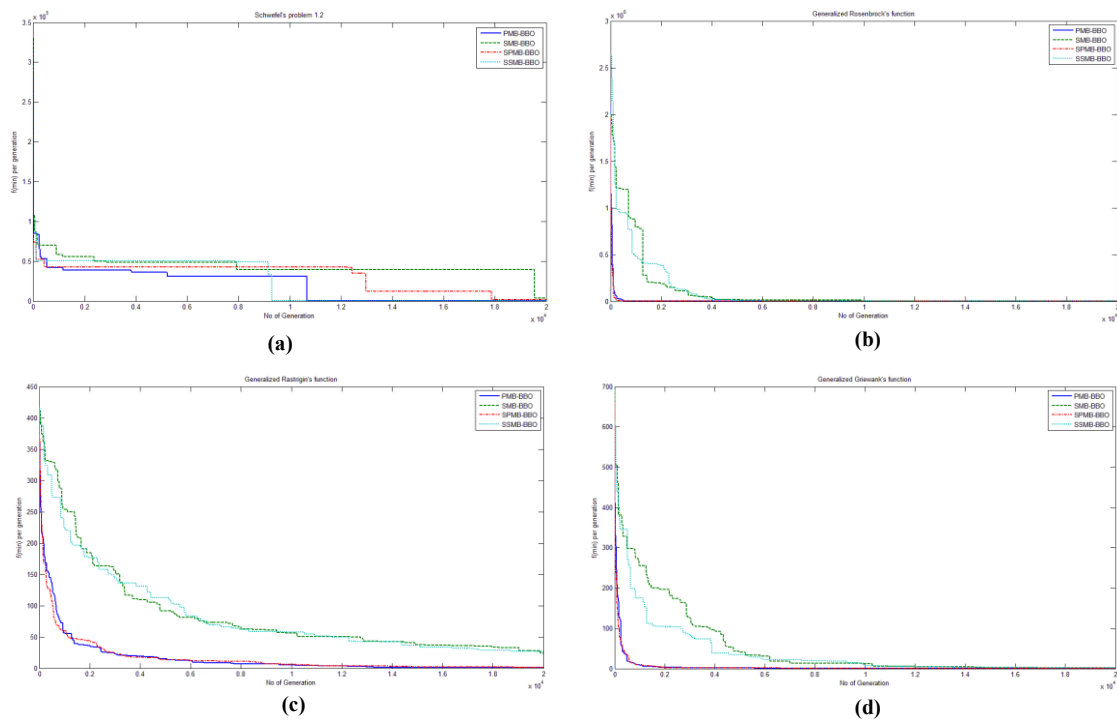| f # | Name | Side Constraints | Biogeography Based Optimization (BBO) | | | | | |
| | | | Partial Migration Based | | | Simplified Partial Migration Based | | |
			Best	Mean	StdDev	Best	Mean	StdDev
f11a	Generalized Griewank's Function	Xi ∈ [-60,60]	8.6106E-02	2.3591E-01	8.7067E-02	5.3899E-02	2.1482E-01	7.9380E-02
f11b		Xi ∈ [-600,600]	8.7314E-01	1.2508E+00	2.3871E-01	9.6562E-01	1.3044E+00	2.2903E-01
f11c		Xi ∈ [-6000,6000]	4.9293E+00	3.2079E+01	2.4023E+01	6.0255E+00	3.7802E+01	2.7235E+01

Figure 3. Curves of fitness functions of PMB, SMB, SPMB, and SSMB for some selected functions. **(a)** f03, **(b)** f05, **(c)** f09, **(d)** f11

5. CONCLUSIONS AND SUGGESTIONS

The performance of the four original forms of BBO algorithms (PMB, SMB, SPMB and SSMB) have been extensively tested and compared using 23 benchmark functions of different dimensions and complexities, as well as different scenarios have been done for some selected functions. The results show that the PMB, which is the first presented model in 2008, gives the best performance as the complexity, side constraints and/or dimensions of a given problem increases and as the number of islands or population size decreases. However, the PMB is found to be the slowest algorithm which requires around 42.30% more CPU time than that of the SSMB as shown in Table 2. To compromise between the cost and convergence speed under the above scenarios, SPMB is found to be the best choice as it requires around 28.00% more CPU time, but its exploration and exploitation will decrease significantly. The performance of the SMB algorithm found to be the worst as compared to the others.

The results obtained in this paper can be used as a foundation and a first step for enhancing any prospective modification on the BBO algorithm including the existing modifications that are described in literature.

APPENDIX

This appendix includes a complete list that have been used in this paper. The details of these benchmark functions can be found in [32]. The global minimums of the functions (f08, f14, f15, f16, f17, f19, f20, and f21-f23) are rounded in [32]. In this paper, the correct values are taken instead from [34,35,36,37,38], respectively.

f01: **Sphere Model**

$$f(x) = \sum_{i=1}^{n} x_i^2$$

- $-100 \leq x_i \leq 100, \quad i = 1,2,\dots,n$
- $f_{min}(X^*) = 0, \quad x_i^* = 0$

f02: **Schwefel's Problem 2.22**

$$f(x) = \sum_{i=1}^{n} |x_i| + \prod_{i=1}^{n} |x_i|$$

- $-10 \leq x_i \leq 10, \quad i = 1,2,\dots,n$
- $f_{min}(X^*) = 0, \quad x_i^* = 0$

f03: **Schwefel's Problem 1.2**

$$f(x) = \sum_{i=1}^{n} \left(\sum_{j=1}^{i} x_j \right)^2$$

- $-100 \leq x_i \leq 100, \quad i = 1,2,\dots,n$
- $f_{min}(X^*) = 0, \quad x_i^* = 0$

f04: **Schwefel's Problem 2.21**

$$f(x) = max_i\{|x_i|, 1 \leq i \leq n\}$$

- $-100 \leq x_i \leq 100, \quad i = 1,2,\dots,n$
- $f_{min}(X^*) = 0, \quad x_i^* = 0$

f05: **Generalized Rosenbrock's Function**

$$f(x) = \sum_{i=1}^{n-1} \left[100\left(x_{i+1} - x_i^2\right)^2 + (x_i - 1)^2 \right]$$

- $-30 \leq x_i \leq 30, \quad i = 1,2,\dots,n$
- $f_{min}(X^*) = 0, \quad x_i^* = 1$

f06: **Step Function**

$$f(x) = \sum_{i=1}^{n} (\lfloor x_i + 0.5 \rfloor)^2$$

- $-100 \leq x_i \leq 100, \quad i = 1,2,\dots,n$
- $f_{min}(X^*) = 0, \quad x_i^* = 0$

f07: **Quartic Function**

$$f(x) = \sum_{i=1}^{n} i x_i^4$$

- $-1.28 \leq x_i \leq 1.28, \quad i = 1,2,\dots,n$
- $f_{min}(X^*) = 0, \quad x_i^* = 0$

f08: **Generalized Schwefel's Problem 2.26**

$$f(x) = -\sum_{i=1}^{n} \left[x_i sin\left(\sqrt{|x_i|}\right) \right]$$

- $-500 \leq x_i \leq 500, \quad i = 1,2,\dots,n,$
- $f_{min}(X^*) = -418.9828872724337998079913601398n, \quad x_i^* = 420.968748$

f09: **Generalized Rastrigin's Function**

$$f(x) = \sum_{i=1}^{n} \left[x_i^2 - 10cos(2\pi x_i) + 10 \right]$$

- $-5.12 \leq x_i \leq 5.12, \quad i = 1,2,\dots,n$
- $f_{min}(X^*) = 0, \quad x_i^* = 0$

f10: **Ackley's Function**

$$f(x) = -20e^{\left(-0.2\sqrt{\frac{1}{n}\sum_{i=1}^{n} x_i^2}\right)} - e^{\left(\frac{1}{n}\sum_{i=1}^{n} cos(2\pi x_i)\right)} + 20 + e^{(1)}$$

- $-32 \leq x_i \leq 32, \quad i = 1,2,\dots,n$
- $f_{min}(X^*) = 0, \quad x_i^* = 0$

f11: **Generalized Griewank's Function**

$$f(x) = \frac{1}{4000}\sum_{i=1}^{n} x_i^2 - \prod_{i=1}^{n} cos\left(\frac{x_i}{\sqrt{i}}\right) + 1$$

- $-600 \leq x_i \leq 600, \quad i = 1,2,\dots,n$
- $f_{min}(X^*) = 0, \quad x_i^* = 0$

f12: **Generalized Penalized No.1 Function**

$$f(x) = \frac{\pi}{n}\left\{ 10sin^2(\pi y_1) + \sum_{i=1}^{n-1}(y_i - 1)^2[1 + 10sin^2(\pi y_{i+1})] + (y_n - 1)^2 \right\} + \sum_{i=1}^{n} u(x_i, a, k, m)$$

where

$$y_i = 1 + \frac{1}{4}(x_i + 1), \quad u(x_i, a, k, m) = \begin{cases} k(x_i - a)^m & x_i > a \\ 0 & -a \leq x_i \leq a \\ k(-x_i - a)^m & x_i < -a \end{cases}$$

- $a = 10, \quad k = 100 \quad \& \quad m = 4$
- $-50 \leq x_i \leq 50, \quad i = 1,2,\dots,n$
- $f_{min}(X^*) = 0, \quad x_i^* = 1$

f13: **Generalized Penalized No.2 Function**

$$f(x) = 0.1\left\{ sin^2(3\pi x_1) + \sum_{i=1}^{n-1}(x_i - 1)^2[1 + sin^2(3\pi x_{i+1})] + (x_n - 1)^2[1 + sin^2(2\pi x_n)] \right\}$$
$$+ \sum_{i=1}^{n} u(x_i, a, k, m)$$

where

$$u(x_i, a, k, m) = \begin{cases} k(x_i - a)^m & x_i > a \\ 0 & -a \le x_i \le a \\ k(-x_i - a)^m & x_i < -a \end{cases}$$

- $a = 5, \quad k = 100 \quad \& \quad m = 4$
- $-50 \le x_i \le 50, \quad i = 1,2, \dots, n$
- $f_{min}(X^*) = 0, \quad x_i^* = 1$

f14: Shekel's Foxholes Function

$$f(x) = \left[\frac{1}{500} + \sum_{j=1}^{25} \frac{1}{j + \sum_{i=1}^{2}(x_i - a_{i,j})^6} \right]^{-1}$$

where

$$a_{i,j} = \begin{bmatrix} -32 & -16 & 0 & 16 & 32 & -32 & \dots & 0 & 16 & 32 \\ -32 & -32 & -32 & -32 & -32 & -16 & \dots & 32 & 32 & 32 \end{bmatrix}$$

- $-65.536 \le x_i \le 65.536, \quad i = 1,2$
- $f_{min}(X^*) \approx 0.998003837794449325873406851315, \quad x_i^* \approx -31.97833$

f15: Kowalik's Function

$$f(x) = \sum_{j=1}^{11} \left[a_j - \frac{x_1(b_j^2 + b_j x_2)}{b_j^2 + b_j x_3 + x_4} \right]^2$$

- $-5 \le x_i \le 5, \quad i = 1,2,3,4$
- $f_{min}(X^*) \approx 0.00030748598780560421684043449710{\,}09,$
- $x_i^* \approx \begin{Bmatrix} 0.19283345274433530131494258512{\,}3 \\ 0.1908362422032358009153036664{\,}43 \\ 0.12311729602924741073868937292{\,}0 \\ 0.135765991801668826273045769995 \end{Bmatrix}$

Table 6. Data for Kowalik's Function

j	a_j	b_j^{-1}
1	0.1957	0.25
2	0.1947	0.5
3	0.1735	1
4	0.1600	2
5	0.0844	4
6	0.0627	6
7	0.0456	8
8	0.0342	10
9	0.0323	12
10	0.0235	14
11	0.0246	16

f16: Six-Hump Camel-Back Function

$$f(x) = 4x_1^2 - 2.1x_1^4 + \frac{1}{3}x_1^6 + x_1 x_2 - 4x_2^2 + 4x_2^4$$

- $-5 \le x_i \le 5, \quad i = 1,2$

- $f_{min}(X^*) = -1.031628453489877$ "It has four global minimum",
- $x_i^* = (\pm 0.08984201368301331, \pm 0.7126564032704135)$

f17: Branin RCOS Function

$$f(x) = \left(x_2 - \frac{5.1}{4\pi^2}\right)x_1^2 + \left(\frac{5}{\pi}x_1 - 6\right)^2 + 10\left(1 - \frac{1}{8\pi}\right)\cos(x_1) + 10$$

- $-5 \leq x_1 \leq 10, \quad 0 \leq x_2 \leq 15$
- $f_{min}(X^*) = 0.39788735772973816$ "It has three global minimum",
- $x_i^* = (-\pi, 12.275), (\pi, 2.275), (9.42478, 2.475)$

f18: Goldstein-Price Function

$$f(x) = f_1(x)f_2(x)$$

where

$$f_1(x) = 1 + (x_1 + x_2 + 1)^2(19 - 14x_1 + 3x_1^2 - 14x_2 + 6x_1x_2 + 3x_2^2)$$
$$f_2(x) = 30 + (2x_1 - 3x_2)^2(18 - 32x_1 + 12x_1^2 + 48x_2 - 36x_1x_2 + 27x_2^2)$$

- $-2 \leq x_i \leq 2, \quad i = 1,2$
- $f_{min}(X^*) = 3, \quad x_i^* = (0, -1)$

f19,20: Hartman's Family

$$f(x) = -\sum_{i=1}^{m} c_i \, exp\left[-\sum_{j=1}^{n} a_{i,j}(x_j - p_{i,j})^2\right]$$

- $m = 4, \quad n = 3,6 \ for \ f19 \ and \ f20, respectively$
- $0 \leq x_j \leq 1, \quad j = 1,2,\ldots,n$

- $f19: f_{min}(X^*) = -3.86278214782076, \quad x_i^* = \begin{Bmatrix} 0.1, \\ 0.55592003, \\ 0.85218259 \end{Bmatrix}$

- $f20: f_{min}(X^*) = -3.32236801141551, \quad x_i^* = \begin{Bmatrix} 0.20168952, \\ 0.15001069, \\ 0.47687398, \\ 0.27533243, \\ 0.31165162, \\ 0.65730054 \end{Bmatrix}$

Table 7. Data for Hartman's Function 1

i	$a_{i,j}, \ j = 1,2,3$			c_i	$p_{i,j}, \ j = 1,2,3$		
1	3	10	30	1	0.3689	0.1170	0.2673
2	0.1	10	35	1.2	0.4699	0.4387	0.7470
3	3	10	30	3	0.1091	0.8732	0.5547
4	0.1	10	35	3.2	0.038150	0.5743	0.8828

Table 8. Data for Hartman's Function 2

i	c_i	$a_{i,j}, \ j = 1,2,\ldots,6$						$p_{i,j}, \ j = 1,2,\ldots,6$					
1	1	10	3	17	3.5	1.7	8	0.1312	0.1696	0.5569	0.0124	0.8283	0.5886
2	1.2	0.05	10	17	0.1	8	14	0.2329	0.4135	0.8307	0.3736	0.1004	0.9991
3	3	3	3.5	1.7	10	17	8	0.2348	0.1415	0.3522	0.2883	0.3047	0.6650
4	3.2	17	8	0.05	10	0.1	14	0.4047	0.8828	0.8732	0.5743	0.1091	0.0381

f21,22,23: **Shekel's Family**

$$f(x) = -\sum_{i=1}^{n} [(x - a_i)(x - a_i)^T + c_i]$$

- $n = 5, 7$ and 10 for *f21*, *f22* and *f23*, respectively
- $0 \leq x \leq 10, \quad i = 1, 2, ..., n$
- *f21:* $f_{min}(x^*) = -10.1531987550848817763568394000251$,
  $x^* = 4.0000852120276195399252334022760$
- *f22:* $f_{min}(x^*) = -10.4028220447077753290705182200751$,
  $x^* = 4.0000895321527399680288865055640$
- *f23:* $f_{min}(x^*) = -10.5362902992947171054273576010022$,
  $x^* = 4.000128161010045329070518200751$

Table 9: Data for Shekel Functions *f21*, *f22*, *f23*

i	$a_{ij}, j = 1,2,3,4$				c_i
1	4	4	4	4	0.1
2	1	1	1	1	0.2
3	8	8	8	8	0.2
4	6	6	6	6	0.4
5	3	7	3	7	0.4
6	2	9	2	9	0.6
7	5	5	3	3	0.3
8	8	1	8	1	0.7
9	6	2	6	2	0.5
10	7	3.6	7	3.6	0.5

REFERENCES

[1] Dan. Simon, "Biogeography-based optimization," *IEEE Trans. On Evolutionary Computation*, vol. 12, no. 6, pp. 702-713, Dec. 2008.

[2] Robert H. MacArthur and Edward O. Wilson, "An Equilibrium Theory of Insular Zoogeography," *Journal of Evolution*, vol. 17, no. 4, pp. 373-387, Dec. 1963.

[3] Robert H. MacArthur and Edward O. Wilson, *The Theory of Island Biogeography*. Princeton, New Jersey: Princeton University Press, 1967.

[4] Mark V. Lomolino, Brett R. Riddle and James H. Brown, *Biogeography*, 3rd ed. Sunderland, Massachusetts: Sinauer Associates Inc., 2009.

[5] R. L. Jones, *Biogeography: Structure, Process, Pattern and Change within the Biosphere*. Amersham, Bucks, England: Hulton Educational Publications, 1980.

[6] C. Barry Cox and Peter D. Moore, *Biogeography: An Ecological and Evolutionary Approach*, 5th ed. Oxford, UK: Blackwell Scientific Publications, 1993.

[7] R. J. Lincoln, G. A. Boxshall and P. F. Clark, *A dictionary of Ecology, Evolution and Systematics*. Cambridge, UK: Cambride University Press, 1982.

[8] Paulami Maiti and Prabodh K. Maiti, *Biodiversity: Perception, Peril and Preservation*. Prentice-Hall of India, 2011.

[9] William A. Nierenberg, *Encyclopedia of Environmental Biology*, vol. 2. San Diego, California: Academic Press Inc., 1995.

[10]   Michael Shermer, *In Darwin's Shadow: The Life and Science of Alfred Russel Wallace*. New York: Oxford University Press, 2002.

[11]   Frank J. Sulloway, "Darwin and His Finches: The evolution of a Legend," *Journal of the History of Biology*, vol. 15, no. 1, pp. 1-53, March 1982.

[12]   Ray Desmond, *Sir Joseph Dalton Hooker: Traveller and Plant Collector*. Woodbridge, Suffolk: UK: Antique Collectors Club, 2007.

[13]   Jonathan B. Losos and Robert E. Ricklefs, *The Theory of Island Biogeography Revisited*. Princeton, New Jersey: Princeton University Press, 2010.

[14]   Alan A. Myers and Paul S. Giller, *Analytical Biogeography: An Integrated Approach to the Study of Animal and Plant Distributions*. London, UK: Chapman and Hall, 1990.

[15]   Glen M. MacDonald, *Biogeography: Space, Time and Life*. New York: John Wiley & Sons Inc., 2003.

[16]   Martin L. Cody, *Plants on Islands: Diversity and Dynamics on a Continental Archipelago*. Berkeley and Los Angeles, California: University of California Press, 2006.

[17]   Robert H. MacArthur and Joseph H. Connell, *The Biology of Populations*. New York: John Wiley & Sons Inc., 1966.

[18]   Robert H. MacArthur, *Geographical Ecology: Patterns in the Distribution of Species*. New York: Harper & Row Publishers Inc., 1972.

[19]   Yu. M. Svirezhev and D. O. Logofet, *Stability of Biological Communities*. Moscow, Soviet Union: Mir Publishers, 1983.

[20]   A. Bhattacharya and P. K. Chattopadhyay, "Biogeography-Based Optimization and its application to nonconvex Economic Emission Load Dispatch problems," *8th International Conference on Advances in Power System Control, Operation and Management (APSCOM 2009)*, pp. 1-6, Nov. 2009.

[21]   V. K. Panchal, S. Goel and M. Bhatnagar, "Biogeography based land cover feature extraction,". *World Congress on Nature & Biologically Inspired Computing. NaBIC 2009*, pp. 1588-1591, Dec. 2009.

[22]   Z. Mohammed and J. Talaq, "Unit commitment by biogeography based optimization method," *16th IEEE Mediterranean Electrotechnical Conference (MELECON)*, pp. 551-554, March 2012.

[23]   M. Ergezer, Dan. Simon and Dawei Du, "Oppositional biogeography-based optimization," *IEEE International Conference on Systems, Man and Cybernetics*. pp. 1009-1014, Oct. 2009.

[24]   Haiping Ma, Suhong Ni and Man Sun, "Equilibrium species counts and migration model tradeoffs for biogeography-based optimization," *Proceedings of the 48th IEEE Conference on Decision and Control, held jointly with the 28th Chinese Control Conference. CDC/CCC 2009*. pp. 3306-3310, Dec. 2009.

[25]   H. Ma, "An analysis of the equilibrium of migration models for biogeography-based optimization," *Information Sciences*, vol. 180, no. 18, pp. 3444-3464, 15 Sept. 2010.

[26]   S. S. Pattnaik, M. R. Lohokare and S. Devi, "Enhanced Biogeography-Based Optimization using modified clear duplicate operator," *Second World Congress on Nature and Biologically Inspired Computing (NaBIC),* pp. 715-720, Dec. 2010.

[27]   Haiping Ma and Dan. Simon, "Blended biogeography-based optimization for constrained optimization," *Engineering Applications of Artificial Intelligence*, vol. 24, no. 3, pp. 517-525, Apr. 2011.

[28]   Dan. Simon. (2009, Feb.). A Probabilistic Analysis of a Simplified Biogeography-Based Optimization Algorithm. Cleveland State University. Cleveland, Ohio. Available: http://academic.csuohio.edu/simond/bbo/simplified/bbosimplified.pdf

[29]   Haiping Ma and Dan. Simon, "Analysis of migration models of biogeography-based optimization using Markov theory," *Engineering Applications of Artificial Intelligence*, vol. 24, no. 6, pp. 1052-1060, Sept. 2011.

[30]   Dan. Simon, M. Ergezer and Dawei Du, "Population distributions in biogeography-based optimization algorithms with elitism," *IEEE International Conference on Systems, Man and Cybernetics,* pp. 991-996, Oct. 2009.

[31]   Dario Floreano and Claudio Mattiussi, *Bio-Inspired Artificial Intelligence: Theories, Methods*, *and Technologies*. Cambridge, Massachusetts: The MIT Press, 2008.

[32]   Xin Yao, Yong Liu and Guangming Lin, "Evolutionary Programming Made faster," *IEEE Trans. on Evolutionary Computation*, vol. 3, no. 2, pp. 82-102, Jul. 1999.

[33]   Wenying Gong, Zhihua Cai and Charles X. Ling, "DE/BBO: A hybrid differential evolution with biogeography-based optimization for global numerical optimization," *Soft Computing*, vol. 15, no. 4, pp. 645-665, Apr. 2011.

[34]   Lappeenranta University of Technology, "The function testbed," [online] May. 2007, http://www.it.lut.fi/ip/evo/functions/functions.html (Accessed: 10 April 2013).

[35]   Chien-Wen Chao, Shu-Cherng Fand and Ching-Jong Liao, "A Tropical cyclone-based method for global optimization," *Journal of Industrial and Management Optimization*, Vol. 8, no. 1, Feb. 2012.

[36]   M. Montaz Ali, Charoenchai Khompatraporn and Zelda B. Zabinsky, "A Numerical Evaluation of Several Stochastic Algorithms on Selected Continuous Global Optimization Test Problems" *Journal of Global Optimization*, vol. 31, no. 4, pp. 635-672, Apr. 2005.

[37]   Andrea Gavana, "Test Functions Index," [online] Feb. 2013, http://infinity77.net/ global_optimization/test_functions.html (Accessed: 01 April 2013).

[38]   Muhammad Aria, "Educational Simulator for Teaching of Particle Swarm Optimization in LabVIEW," *TELEKONTRAN*, vol. 1, no. 1, Jan. 2013.

Authors

Ali Ridha Al-Roomi received the B.Sc. degree in Process Instrumentation and Control Engineering from University of Bahrain, Bahrain, in 2006. In the period between 2009-2013, he covered the electrical courses of the B.Sc. program in Electrical Engineering, and followed by M.Sc. degree from the same university. After B.Sc. graduation, he was selected to be as a project engineer in Moore Control & Engineering till the mid of 2007, when he joined Yokogawa Middle East as a DCS subsystem and graphics engineer. From 2008 to 2012, he worked in Aluminum Bahrain as an instrumentation and control engineer in its power plants, generation and auxiliary C&I maintenance. He is currently working as a researcher in the field of electrical power systems and evolutionary computation.

Fadhel Abbas Al-Basri received the B.Sc. and M.Sc. degrees in Electrical Engineering from University of Bahrain, Bahrain, and Ph.D. degree in the same field from University of Western Ontario, Canada, in 1992, 1997 and 2007, respectively. He worked in Ministry of Electricity and Water, Bahrain, as an electrical engineer from 1993 to 1994. In 1994, he joined the University of Bahrain as teaching and research assistant and currently an assistant professor in the department of electrical engineering. His research interest is power systems protection, power systems analysis and FACTS-devices.

Jawad Hasan Talaq received B.Sc. degree from University of Technology, Baghdad, Iraq (1981), M.Sc. degree from University of Strathclyde, Glasgow, UK (1987), and Ph.D. degree from Technical University of Nova Scotia, Halifax, Canada (1993); all in electrical engineering. He worked in Ministry of Electricity and Water, Bahrain, as a graduate engineer in Riffa power plant from 1981 to 1985, and as a shift charge engineer from 1985 to 1989, till moving from the industrial field to the academic field. He is now an associate professor in the department of electrical engineering, University of Bahrain. His teaching covers power systems operation and control, power systems dynamics, and advanced power systems analysis; where his research topics include power systems operation, control and dynamics, and applied soft computing.