

Equilibrium Species Counts and Migration Model Tradeoffs for Biogeography-Based Optimization

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Abstract—Motivated by the migration mechanisms of ecosystems, various extensions to biogeography-based optimization (BBO) are proposed. BBO is an original optimization method based on the mathematical model of organism distribution in biological systems. BBO is an evolutionary process that achieves information sharing by species migration. This paper generalizes the equilibrium species count in biogeography theory, discusses various migration models in BBO, and investigates performance through benchmark functions. The performance study shows the most effect migration scheme for BBO and shows that it is a promising candidate for optimization.

Keywords—optimization algorithm; biogeography; species migration; computer intelligence

I. INTRODUCTION

Evolutionary algorithms (EAs) [1] have been introduced to solve complex optimization problems. Some well-established and commonly used EAs are genetic algorithms (GAs) [2], ant colony optimization (ACO) [3], and particle swarm optimization (PSO) [4]. Each of these methods has its own characteristics, strengths, and weaknesses. Biogeography-based optimization (BBO) is a new EA developed for global optimization. This stochastic EA was introduced by Simon [5] in 2008 and demonstrated good convergence properties on various benchmark functions. It is expected to become a popular EA once its true potential has been explored and once it has successfully been applied to more practical cases.

BBO is an application of biogeography to EAs. It is modeled after the immigration and emigration of species between islands [6]. One characteristic of BBO is that the original population is not discarded after each generation. It is rather modified by migration. Also, for each generation, BBO uses the fitness of each solution to determine its emigration and immigration rate.

The remainder of this paper is organized as follows: Section 2 describes the theoretical foundations of biogeography and migration models, and proves a new theorem about species count probabilities. Section 3 describes the BBO algorithm. Analysis of BBO performance is presented in Section 4, and conclusions and directions for future research are given in Section 5.

II. BIOGEOGRAPHY THEORY

Consider a model of species abundance in a single habitat, whose state at any time is represented by the number of species in the habitat at that time. Suppose that whenever there are k species in the habitat, new arrivals enter the habitat at an immigration rate λ_k , and species leave the habitat at an emigration rate μ_k . Suppose the largest possible number of species that the habitat can support is n . Now consider the probability P_k that the habitat contains exactly k species. P_k changes from time t to time $(t + \Delta t)$ as follows [5].

$$P_k(t + \Delta t) = P_k(t)(1 - \lambda_k \Delta t - \mu_k \Delta t) + P_{k-1} \lambda_{k-1} \Delta t + P_{k+1} \mu_{k+1} \Delta t \quad (1)$$

This equation holds because in order to have k species at time $(t + \Delta t)$, one of the following conditions must hold:

(1) There were k species at time t , and no immigration or emigration occurred between t and $(t + \Delta t)$; or, (2) There were $(k - 1)$ species at time t , and one species immigrated; or, (3) There were $(k + 1)$ species at time t , and one species emigrated.

Assume that Δt is small enough so that the probability of more than one immigration or emigration can be ignored. Taking the limit of (1) as $\Delta t \rightarrow 0$, gives

$$\dot{P}_k = \begin{cases} -\lambda_0 P_0 + \mu_1 P_1, & k = 0 \\ -(\lambda_k + \mu_k) P_k + \lambda_{k-1} P_{k-1} + \mu_{k+1} P_{k+1}, & 1 \leq k \leq n-1 \\ -\mu_n P_n + \lambda_{n-1} P_{n-1}, & k = n \end{cases} \quad (2)$$

Define $P = [P_0 \ \cdots \ P_n]^T$ for notational simplicity. We obtain

$$\dot{P} = AP \quad (3)$$

where the matrix A is given as

$$A = \begin{bmatrix} -\lambda_0 & \mu_1 & 0 & \cdots & 0 \\ \lambda_0 & -(\lambda_1 + \mu_1) & \mu_2 & \ddots & \vdots \\ \vdots & \ddots & \ddots & \ddots & \vdots \\ \vdots & \ddots & \lambda_{n-2} & -(\lambda_{n-1} + \mu_{n-1}) & \mu_n \\ 0 & \cdots & 0 & \lambda_{n-1} & -\mu_n \end{bmatrix} \quad (4)$$

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

$$P_k = \begin{cases} P_0 = \frac{1}{1 + \sum_{k=1}^n \frac{\lambda_0 \lambda_1 \cdots \lambda_{k-1}}{\mu_1 \mu_2 \cdots \mu_k}}, & k = 0 \\ P_k = \frac{\lambda_0 \lambda_1 \cdots \lambda_{k-1}}{\mu_1 \mu_2 \cdots \mu_k \left(1 + \sum_{k=1}^n \frac{\lambda_0 \lambda_1 \cdots \lambda_{k-1}}{\mu_1 \mu_2 \cdots \mu_k} \right)}, & 1 \leq k \leq n \end{cases} \quad (5)$$

The foregoing equations also show us what condition is necessary for these limiting probabilities to exist. Namely, it is necessary that $\mu_k \neq 0$ for all k . This condition also may be shown to be sufficient.

Proof: See the appendix.

According to different mathematical models of biogeography, we obtain four migration models.

Model 1 (constant immigration rate and emigration rate):

$$\begin{aligned} \lambda_k &= \lambda = \frac{I}{n}, (\text{constant}) \\ \mu_k &= \mu = \frac{E}{n}, (\text{constant}) \end{aligned} \quad (6)$$

Where I, E respectively denote constant immigration rate to the habitat which can support the number of species count n and constant emigration rate. As the number of species increases, the immigration rate λ_k and the emigration rate μ_k are invariable in this model.

Model 2 (constant immigration rate and linear emigration rate):

$$\begin{aligned} \lambda_k &= \lambda = \frac{I}{n}, (\text{constant}) \\ \mu_k &= \frac{E - \theta}{n} k + \theta \end{aligned} \quad (7)$$

Where I is a constant, the emigration rate μ_k is linear with respect to the solution ranking, and θ is the minimal emigration rate. If there are no species in the habitat, then the emigration rate is equal to the lower bound θ . As the number of species increases, the emigration rate increases. The maximum emigration rate is E , which occurs when the habitat contains the largest number of species that it can support.

Model 3 (linear immigration rate and constant emigration rate):

$$\begin{aligned} \lambda_k &= I \left(1 - \frac{k}{n} \right) \\ \mu_k &= \mu = \frac{E}{n}, (\text{constant}) \end{aligned} \quad (8)$$

Where E is a constant, the immigration rate λ_k is linear with respect to the solution ranking. As the number of species increases, the immigration rate decreases. The maximum possible immigration rate to the habitat is I , which occurs when there are zero species in the habitat. The largest possible number of species that the habitat can support is n , at which point the immigration rate becomes zero.

Model 4 (linear immigration rate and linear emigration rate):

$$\lambda_k = I \left(1 - \frac{k}{n} \right) \quad (9)$$

$$\mu_k = \frac{E - \theta}{n} k + \theta$$

In this model, the immigration rate λ_k and the emigration rate μ_k are linear functions of the number of species in the habitat. When the number of species increases, the habitat becomes more crowded, fewer species are able to successfully survive immigration to the habitat, and the immigration rate decreases, while more species are able to leave the habitat to explore other possible residences and the emigration rate increases.

III. BIOGEOGRAPHY-BASED OPTIMIZATION

In this section we discuss how the biogeography theory of the previous section can be applied to optimization problems.

Migration is a probabilistic operator that adjusts a habitat H . The probability that H_i is modified is proportional to its immigration rate λ_i , and the probability that the source of the modification comes from H_j is proportional to the emigration rate μ_j . Migration is defined by

$$H_i(\text{SIV}) \leftarrow H_j(\text{SIV}) \quad (10)$$

In biogeography, an SIV is a suitability index variable which characterizes the habitability of an island. In BBO, an SIV is a solution feature, equivalent to a “gene” in other population-based optimization algorithm (GAs, for example).

Migration process can loosely be described as follows:

Select H_i with probability based on λ_i ;
 If H_i is selected
 Select H_j with probability based on μ_j ;
 If H_j is selected
 Randomly select an SIV s from H_j ;
 Replace a random SIV in H_i with s ;
 End
 End

Mutation is a probabilistic operator that randomly modifies a habitat’s SIV based on the habitat’s a priori probability of existence. For classic BBO, the mutation

rate m is inversely proportional to the solution probability, which is defined by

$$m = m_{max} \left(1 - \frac{P}{P_{max}} \right) \quad (11)$$

Where m_{max} is a user-defined parameter. This mutation scheme tends to increase diversity among the population. Mutation can be described as follows:

Use λ_i and μ_i to update the probability P_i ;
 Compute mutation probability m_i ;
 Select an SIV s in H_i with probability based on m_i ;
 If $H_i(\text{SIV})$ is selected
 Replace $H_i(\text{SIV})$ with a randomly generated SIV s ;
 End

The BBO algorithm can be informally described with the following algorithm:

Step 1 Initialize the BBO parameters, including the maximum species count n , the maximum migration rates E and I , the maximum mutation rate m_{max} , and the minimal emigration rate θ .

Step 2 Initialize a random set of habitats, each habitat corresponding to a potential solution to the given problem.

Step 3 For each habitat, map the fitness to the number of species k , the immigration rate λ_k , and the emigration rate μ_k based on migration models as discussed in section 2.

Step 4 Probabilistically use immigration and emigration to modify each habitat based on (10) as discussed in section 3, then compute each habitat’s fitness.

Step 5 For each habitat, update the probability of its species count using (5). Then mutate each habitat based on (11), and recompute each habitat’s fitness.

Step 6 Go to step (3) for the next iteration. This loop can be terminated after a predefined number of generations, or after an acceptable problem solution has been found.

IV. BBO PERFORMANCE ANALYSIS

In this section we look at the performance of BBO based on different migration models. A representative set of benchmark functions has been used for performance verification of the proposed approach [7, 8]. The definitions

of the benchmark functions are listed in Table 1. The notation “ $\lfloor \cdot \rfloor$ ” in function f_6 means the greatest lower bound integer.

TABLE I. BENCHMARK FUNCTIONS

Name	Function	Variable
Ackley	$f_1(x) = -20 \exp \left(-0.2 \sqrt{\frac{\sum_{i=1}^D x_i^2}{D}} \right) - \exp \left(\frac{\sum_{i=1}^D \cos(2\pi x_i)}{D} \right) + 20 + e$	$-32 \leq x_i \leq 32$
Griewank	$f_2(x) = \sum_{i=1}^D \frac{x_i^2}{4000} - \prod_{i=1}^D \left(\cos \left(\frac{x_i}{\sqrt{i}} \right) \right) + 1$	$-600 \leq x_i \leq 600$
Rastrigin	$f_3(x) = 10D + \sum_{i=1}^D (x_i^2 - 10 \cos(2\pi x_i))$	$-10 \leq x_i \leq 10$
Rosenbrock	$f_4(x) = \sum_{i=1}^{D-1} [100(x_{i+1} - x_i^2)^2 + (1 - x_i)^2]$	$-2 \leq x_i \leq 2$
Sphere	$f_5(x) = \sum_{i=1}^D x_i^2$	$-5.12 \leq x_i \leq 5.12$
Step	$f_6(x) = \sum_{i=1}^D (\lfloor x_i + 0.5 \rfloor)^2$	$-100 \leq x_i \leq 100$

Comparison between BBO and other EAs has already been done [5], so this paper compares only various migration approaches in BBO. To get reasonable performance, we use the following parameters: maximum species count $n = 50$, maximum migration rates $E = 1$ and $I = 1$, minimal emigration rate $\theta = 0.05$, and maximum mutation rate $m_{max} = 1$, dimension of each function $D = 20$.

In fact, by repetitious experiments, we find that θ with small value is fitter to improve the result, and θ of 0.05 almost always better than others. In addition, mutation m_{max} is not helping to solution for the population size of 50. Note that mutation is helpful to increase diversity and increase the changes for a good solution only if population size is smaller, like 10 or 20. Similarly, it doesn't seem to benefit for results when parameters I and E change. We tested four BBO models as discussed in section 2 and ran for 50 generations. We ran 100 Monte Carlo simulations on each benchmark to get representative performances. Table 2 and table 3 respectively show the average and best performance of the simulations for different migration models.

TABLE II. AVERAGE PERFORMANCE OF DIFFERENT MIGRATION MODELS

Function	BBO			
	Model 1	Model 2	Model 3	Model 4
f_1	20.550	17.752	16.046	9.129
f_2	60.904	44.312	40.562	19.227
f_3	140.563	94.129	85.578	54.484
f_4	452.892	258.746	122.021	92.341
f_5	13.905	7.926	5.164	3.747
f_6	1025.21	492.17	327.66	256.89

From Table 2 and Table 3 we see that model 4 performs the best and is the most effective at finding function minima on these benchmarks, while model 3 is the second most effective. The results confirm that migration rates which dynamically change with the number of species outperform constant migration rates, and the immigration rate is more important for performance than the emigration rate.

TABLE III. BEST PERFORMANCE OF DIFFERENT MIGRATION MODELS

Function	BBO			
	Model 1	Model 2	Model 3	Model 4
f_1	18.382	14.275	12.823	6.129
f_2	52.427	34.214	30.183	9.258
f_3	115.912	78.821	55.875	21.967
f_4	403.328	134.890	81.754	67.713
f_5	11.596	6.929	4.217	2.676
f_6	792.126	332.034	219.591	186.959

V. CONCLUSION

Biogeography theory has been generalized and different migration models are proposed. New results for the equilibrium BBO species count and probabilities P have been obtained. Experimental results clearly show that different migration models in BBO result in significant changes in performance, and dynamic migration rates outperform constant migration rates. BBO presents promising potential but still requires additional theoretical and empirical investigations. How the equilibrium P changes with various migration models and what implications has is a direction for future study. Adaptive migration rates and control parameter selection are additional directions for future study.

APPENDIX

This appendix provides a proof of Theorem 1. If the species count probabilities are in steady state, then from (3) we have $AP = 0$, namely

$$\begin{bmatrix} -\lambda_0 & \mu_1 & 0 & \cdots & 0 \\ \lambda_0 & -(\lambda_1 + \mu_1) & \mu_2 & \ddots & \vdots \\ \vdots & \ddots & \ddots & \ddots & \vdots \\ \vdots & \ddots & \lambda_{n-2} & -(\lambda_{n-1} + \mu_{n-1}) & \mu_n \\ 0 & \cdots & 0 & \lambda_{n-1} & -\mu_n \end{bmatrix} \begin{bmatrix} P_0 \\ P_1 \\ \vdots \\ P_{n-1} \\ P_n \end{bmatrix} = 0 \quad (12)$$

From (12) we obtain

$$\begin{aligned} \lambda_0 P_0 &= \mu_1 P_1 \\ (\lambda_1 + \mu_1) P_1 &= \lambda_0 P_0 + \mu_2 P_2 \\ &\dots \\ (\lambda_{n-1} + \mu_{n-1}) P_{n-1} &= \lambda_{n-2} P_{n-2} + \mu_n P_n \\ \mu_n P_n &= \lambda_{n-1} P_{n-1} \end{aligned} \quad (13)$$

By adding each equation to the equation preceding it, we get

$$\begin{aligned} \lambda_0 P_0 &= \mu_1 P_1 \\ \lambda_1 P_1 &= \mu_2 P_2 \\ &\dots \\ \lambda_{n-1} P_{n-1} &= \mu_n P_n \end{aligned} \quad (14)$$

Solving in terms of P_0 yields

$$\begin{aligned} P_1 &= \frac{\lambda_0}{\mu_1} P_0 \\ P_2 &= \frac{\lambda_1}{\mu_2} P_1 = \frac{\lambda_1 \lambda_0}{\mu_2 \mu_1} P_0 \\ &\dots \\ P_n &= \frac{\lambda_{n-1}}{\mu_n} P_{n-1} = \frac{\lambda_{n-1} \lambda_{n-2} \cdots \lambda_1 \lambda_0}{\mu_n \mu_{n-1} \cdots \mu_2 \mu_1} P_0 \end{aligned} \quad (15)$$

By using the fact that $\sum_{k=0}^n P_k = 1$, we obtain

$$P_0 + P_0 \sum_{k=1}^n \frac{\lambda_{k-1} \cdots \lambda_1 \lambda_0}{\mu_k \cdots \mu_2 \mu_1} = 1 \quad (16)$$

QED

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