

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

Haiping Ma, Suhong Ni, and Man Sun

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.

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 [3], and particle swarm optimization [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 performance on various benchmark functions and a real-world sensor selection problem. It is expected to become a desirable method for solving complex problems once its true potential and merits 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 habitats to achieve information sharing [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 II describes the theoretical foundations of biogeography and migration models, and proves a new

theorem about species count probabilities. Section III describes the BBO algorithm. Analysis of BBO performance is presented in Section IV, and conclusions and directions for future research are given in Section V.

II. BIOGEOGRAPHY THEORY

A. Biogeography

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

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

It is noted that equation (2) is valid for $k = 0, \dots, n$ when $\mu_0 = 0$ and $\lambda_n = 0$.

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

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

where the matrix A is given as

Haiping Ma is with the Department of Physics and Electrical Engineering, Shaoxing University, Shaoxing 312000, Zhejiang, P.R.China (corresponding author to provide phone: 0575-88345673; fax: 0575-88345673; e-mail: Mahp@zscas.edu.cn).

Suhong Ni is with the College of Information Science and Engineering, Hebei University of Science and Technology, Shijiazhuang 050018, Hebei, P.R. China (fudong1979@126.com)

Man Sun is with the Department of Automation and Engineering, Northeastern University at Qinhuangdao, Qinhuangdao 066004, Hebei, P.R.China (sun7661@126.com)

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

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.

B. Migration model

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

Model 1 (constant immigration rate and emigration rate):

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

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):

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

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 immigration rate):

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

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):

$$\begin{aligned} \lambda_k &= I \left(1 - \frac{k}{n}\right) \\ \mu_k &= \frac{E - \theta}{n} k + \theta \end{aligned} \quad (9)$$

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 give a general description of biogeography-based optimization algorithm.

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 be described as follows:

```

Select  $H_i$  with probability based on  $\lambda_i$ ;
If  $H_i$  is selected
    Select  $H_j$  with probability based on  $\mu_j$ ;
    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 basic structure of BBO algorithm is as follows:

Step 1 Initialize the BBO parameters, including the maximum migration rates E and I , the maximum mutation rate m_{max} , and the minimal emigration rate θ . Migration rate is similar to crossover rate in GAs. Mutation rate is the same as in GAs.

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 II.

Step 4 Probabilistically use immigration and emigration to modify each habitat based on (10) as discussed in section III, 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]. Since we do not make any modification of these functions, they are only briefly described in Table I. A more detailed description of these functions can be found in [8]. In addition, the optimal values of all these functions are zero.

Comparison between BBO and other EAs has already been done [5], and the algorithms that are tested include: ant colony optimization (ACO), differential evolution (DE), evolutionary strategy (ES), genetic algorithm (GA), population-based incremental learning (PBIL), particle swarm optimization (PSO). The results have showed in [5] that BBO has good performance compared to the other algorithms.

TABLE I
BENCHMARK FUNCTIONS

Function	Name	Domain
f01	Sphere Model	$-100 \leq x_i \leq 100$
f02	Schwefel's Problem 2.22	$-10 \leq x_i \leq 10$
f03	Schwefel's Problem 1.2	$-100 \leq x_i \leq 100$
f04	Schwefel's Problem 2.21	$-100 \leq x_i \leq 100$
f05	Rosenbrock's function	$-30 \leq x_i \leq 30$
f06	Step's function	$-100 \leq x_i \leq 100$
f07	Quartic's function	$-1.28 \leq x_i \leq 1.28$
f08	Rastrigin's function	$-5.12 \leq x_i \leq 5.12$
f09	Ackley's function	$-32 \leq x_i \leq 32$
f10	Griewank's function	$-600 \leq x_i \leq 600$
f11	Penalized function 1	$-50 \leq x_i \leq 50$
f12	Penalized function 2	$-50 \leq x_i \leq 50$

This paper compares only various migration approaches in BBO. To get reasonable performance, we use the following parameters: population (habitat) size of 50, maximum migration rates $E = 1$ and $I = 1$, minimal emigration rate $\theta = 0.05$, maximum mutation rate $m_{max} = 0.1$, and dimension of each function $D = 20$.

TABLE II
OPTIMIZATION PERFORMANCE OF DIFFERENT MIGRATION MODELS. "BEST" DENOTES THE BEST VALUES, "MEAN" INDICATES THE MEAN VALUES, AND "STDEV" STANDS FOR THE STANDARD DEVIATION OF MEAN VALUES. MEANWHILE, A RESULT WITH BOLDFACE MEANS BETTER VALUE FOUND.

Function		BBO			
		Model 1	Model 2	Model 3	Model 4
f01	Best	7.9218	7.3775	0.4434	0.1814
	Mean	18.862	18.667	1.5112	0.6964
	Stdev	9.8723	9.7583	0.7588	0.4808
f02	Best	1956.2	2163.6	343.19	135.11
	Mean	3059.7	3123.3	710.34	396.44
	Stdev	917.07	859.19	379.21	191.86
f03	Best	5611.3	7583.3	1573.8	1735.5
	Mean	13234	13643	3945.2	3527.3
	Stdev	6069.5	5408.2	2160.1	1850.3
f04	Best	17.569	17.623	2.7145	1.7138
	Mean	27.992	27.996	5.8125	3.7425
	Stdev	8.9639	9.4219	2.7144	1.9151
f05	Best	201.24	142.01	46.143	25.213
	Mean	590.86	468.27	92.457	74.202
	Stdev	339.32	302.93	39.496	43.198
f06	Best	2514.2	2933.1	130.78	108.76
	Mean	6402.1	6634.9	595.04	289.93
	Stdev	3651.3	2516.7	343.93	170.79
f07	Best	0.2645	0.3233	0.0024	0.0007
	Mean	2.2085	2.5274	0.0379	0.0102
	Stdev	1.5978	2.2507	0.0327	0.0068
f08	Best	70.791	73.984	17.673	7.6523
	Mean	112.01	110.71	28.086	19.626
	Stdev	40.441	28.845	8.1895	11.242
f09	Best	12.589	12.431	5.3741	3.9432
	Mean	15.309	15.062	7.2527	5.5126
	Stdev	2.3183	2.4199	1.4946	1.3175
f10	Best	19.705	25.757	3.0197	1.6895
	Mean	67.377	64.901	6.2587	3.4459
	Stdev	42.359	35.296	2.6737	1.4099
f11	Best	220.56	134.32	3.3189	1.6056
	Mean	51275	875.07	251.84	4.5007
	Stdev	31890	563.79	157.82	2.6868
f12	Best	2907.8	163.75	18.389	4.9544
	Mean	98034	63458	35483	4677.7
	Stdev	67322	41125	33061	2330.2

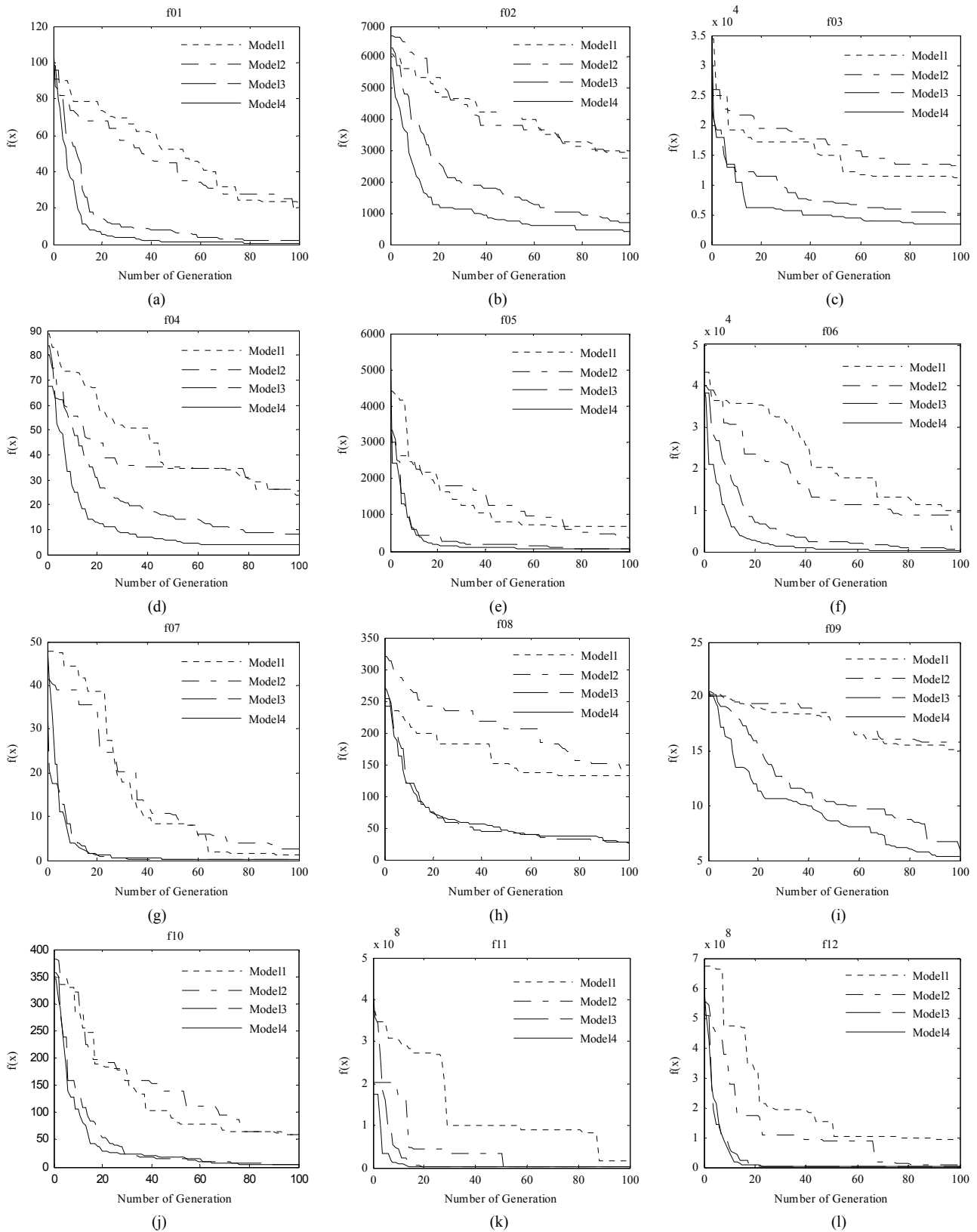


Fig. 1. Curves of fitness functions for four migration models. (a) f01. (b) f02. (c) f03. (d) f04. (e) f05. (f) f06. (g) f07. (h) f08. (i) f09. (j) f10. (k) f11. (l) f12.

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 by the same percentage.

That is because if I and E change, then the migration rates μ and λ will change by the same relative amount for each solution. We tested four BBO models as discussed in section II and ran for 100 generations. We ran 50 Monte Carlo simulations on each benchmark to get the performances. Table II shows the average results of the simulations for different migration models, and Fig. 1 shows the curves of mean value of fitness functions in the evolution process.

From Table II 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. In addition, we find that the immigration rate is more important for performance than the emigration rate.

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. For future work, first of all, we will tune the minimal emigration rate θ , making sure that it can work in the most efficient way. Second, how the equilibrium P changes with various migration models and what implications has is a direction that should be considered. Finally, adaptive migration rates and other 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

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

ACKNOWLEDGMENT

This work was supported by BBO inventor, Dan Simon in the Department of Electrical and Computer Engineering at Cleveland State University.

REFERENCES

- [1] Y. Ho and D. Pepyne, "Simple explanation of the no-free-lunch theorem and its implications," *Journal of Optimization Theory and Applications*, vol. 115, no. 3, pp. 1573-2878, Dec. 2002.
- [2] Z. Michalewicz, *Genetic Algorithms + Data Structures = Evolution Programs*. London, UK: Springer-Verlag, 1996.
- [3] M. Dorigo, L. Gambadella, and M. Middendorf, "Guest editorial: special section on ant colony optimization," *IEEE Trans. on Evolutionary Computation*, vol. 6, no. 4, pp. 317-319, Jul. 2002.
- [4] R. Eberhart, and Y. Shi, "Guest editorial Special issue on particle swarm optimization," *IEEE Trans. on Evolutionary Computation*, vol. 8, no. 3, pp. 201-203, May 2004.
- [5] D. Simon, "Biogeography-based optimization," *IEEE Trans. on Evolutionary Computation*, vol. 12, no. 6, pp. 702-713, Dec. 2008.
- [6] M. Ergezer, D. Simon and D. Du, "Oppositional biogeography-based optimization," unpublished. <http://academic.csuohio.edu/BBO>.
- [7] A. R. Hedar, and M. Fukushima, "Minimizing multimodal functions by simplex coding genetic algorithm," *Optimization Methods and Software*, vol. 18, no. 4, pp. 265-282, Jun. 2003.
- [8] X. Yao, Y. Liu, and G. Lin, "Evolutionary programming made faster," *IEEE Trans. on Evolutionary Computation*, vol. 3, no. 2, pp. 82-102, Jul. 1999.