

Biogeography in optimization algorithms: a closer look

Padarabinda Palai¹, Debani Prashad Mishra², Surender Reddy Salkuti³

¹Department of Computer Science Engineering, IIIT Bhubaneswar, Odisha, India

²Department of Electrical and Electronics Engineering, IIIT Bhubaneswar, Odisha, India

³Department of Railroad and Electrical Engineering, Woosong University, Daejeon, Republic of Korea

Article Info

Article history:

Received Jan 23, 2021

Revised Sep 14, 2021

Accepted Sep 25, 2021

Keywords:

Biogeography

Immigration rate

Migration

Nature inspired algorithms

Optimization

ABSTRACT

Biogeography can be broken down into bio and geography, which would imply the geography, i.e., the dispersion of biological organisms. The entire field of biology inspired algorithm is inclined towards providing the most optimal solution for a given problem set. Computer science experts want to always learn from the surroundings. Nature is sporadic and spontaneous and the erratic nature of a habitat is the very differentiating factor between a real world and an ideal world problem. Things change and that nothing remains constant. The diversification of a certain habitat is bound to change through external influences, some for the better, and some for the worse. This paper tries to mimic the natural influences in a habitat in a python environment and try to come up with a minimal objective value after iterating through the given metaheuristic algorithm.

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Corresponding Author:

Surender Reddy Salkuti

Department of Railroad and Electrical Engineering

Woosong University

17-2, Jayang-dong, Dong-gu, Daejeon-34606, Republic of Korea

Email: surender@wsu.ac.kr

NOMENCLATURE

μ	Emigration rate
λ	Immigration rate
I	Maximum immigration rate
E	Maximum emigration rate
S_{\max}	Largest number of species in habitat
m	User-characterized boundary

1. INTRODUCTION

Biogeography is a field that has been worked upon by naturalists in Charles Darwin and Wallace [1]. However not until recently the mathematical modelling of such a domain had not been worked on. In the 60 s scientists really looked into how the distribution of a certain island changed when there was an influx of individuals or outflow of masses due to disasters. The very aspect of extinction as well as migrating to nearby habitats also created a lot of interest for developing a mathematical model that would be efficient and less error prone [2]. However, science hadn't evolved a lot back then. Right now, things are different and we have access to practically any piece of science. Several challenges have been faced while trying to model the behaviour of the organisms in a specific habitat [3]. However with exponential advancements in technology and increasing computational advantages it has now become possible to optimize the problems people once thought were not feasible [4]. Biogeography when used in computer science has similar effects that other

algorithms that are population based have had in the past [5]. It is a field that is still in a very nascent phase and obviously has a very large scope for research and development [6]. This paper tries to provide a very pragmatic and basic solution and tries to come up with a visual output of the function that has been minimized after repeated iterations in ideal conditions where the values are properly assumed [7].

To introduce the paper, two terminologies are very crucial, i.e., habitat suitability index (HSI) and suitability index variable (SIV) [8]. The former is dependent on the latter while the opposite doesn't hold true. SIV denotes the set of factors that affect a certain habitat like weather, temperature, humidity, precipitation rates, contrast in seasons, availability of food and water. These determine how good a certain habitat is [8]. Naturally it makes sense that habitats with a high habitat suitability index prosper more in comparison with habitats with very minimal habitat suitability index [9]. Where there is a very high value of HSI, there obviously more species and individuals would exist. The dispersion of species does not change and tends to reach a state of saturation [10]. The species in such habitats have high emigration rates and those with low HSI, tend to have high immigration rates [10]. The chances are really low with the species of such habitats. There are also chances if the species remain static in their dispersion rates and that they are likely to go extinct. But the high immigration rate ensures diversity in comparison with islands with high habitat suitability index. Again, the SIV values are crucial in determining the HSI values [11].

The objectives of this paper are twofold. To begin with, we need to give an overall introduction of the new metaheuristic algorithm in "biogeography-based optimization (BBO)" [12]. The plain biogeography is considered, computed and at that point summing it up to get a universally useful optimization calculation. Second, we need to thoroughly study the plots of the benchmarks of the BBO optimization. This paper has demonstrated how BBO, a research into the topographical dispersion of biological habitats, can be used to determine optimization algorithms. Such a set of algos give rise to biogeography based optimization. We have coded the entire algorithm in a python 3.8 virtual environment and have received values for user determined inputs for a habitat that has been coded assuming ideal conditions. The algorithm has been run 500 times and that the elitism parameter has been kept as 2. The way this paper mimics the actual behaviour of a habitat and comes up with optimal solutions efficiently is something that is really commendable. This paper is fundamental and, consequently, provides massive scope of opportunities for additional exploration.

2. RESEARCH METHOD

This paper attempts to initiate the research into the topic of biogeography by first understanding the basics of a species model [13]. A species model provides a graphical overview as to how the species count of a certain habitat changes with inflow or the outflow due to external factors [14]. The graph as shown in Figure 1 shows the behaviour of immigration and emigration under ideal conditions [15]. However, things aren't ideal and the curves will change depending on circumstances [16]. However with the sole objective of understanding the concept, we assume that conditions are ideal. Figure 1 shows the species abundance in a single habitat.

The entire aspect of emigration is governed by the very aspect that more the number of individuals in a certain island, more is the dispersion in species and that higher is the opportunity of the population to emigrate off to a new island [17]. Now, let's discuss equilibrium. It is an ideal state where the lambda and mu values are the same and that the species distribution lying near this point has the possibility of dominating the data set [18]-[20]. It is denoted by S_0 . This value will change positively and negatively with spurts of immigrating species and disastrous events like disease outbreak, ravenous predators respectively. After a major perturbation, nature will take a massive amount of decades to reach a point of stability (i.e., S_0) [21]. Code for calculating emigration rate (μ) and immigration rate (λ) is given below:

```
for i in range(PopSize):
    mu[i]=(PopSize+1 - (i)) / (PopSize+1)
    lambda[i]=1 - mu[i]
end
```

The probability in P_s that a habitat contains S species in time t while the time changes with Δt is given by (1),

$$P_S(t + \Delta t) = P_S(t)(1 - \lambda_S \Delta t - \mu_S \Delta t) + P_{S-1} \lambda_{S-1} \Delta t + P_{S+1} \mu_{S+1} \Delta t \quad (1)$$

The (1) is true for time change (Δt) and one of the following condition must be satisfied:

- At initial time t , the number of species, i.e., S did not change
- When one species immigrated, the number of species was $S-1$
- When one species emigrated, the number of species was $S+1$

The assumption in this work is Δt is so minimal so as to nullify emigration and immigration [22]. Taking the limit of aforementioned equation at $\Delta t \rightarrow 0$ is given by (2),

$$P_S = \begin{cases} -(\lambda_S + \mu_S)P_S + \mu_{S+1}P_{S+1} & \text{for } S = 0 \\ -(\lambda_S + \mu_S)P_S + \lambda_{S-1}P_{S-1} + \mu_{S+1}P_{S+1} & \text{for } 1 \leq S \leq (S_{max} - 1) \\ -(\lambda_S + \mu_S)P_S + \lambda_{S-1}P_{S-1} & \text{for } S = S_{max} \end{cases} \quad (2)$$

Figure 2 depicts the species model, and from this figure, it is clear that S_1 is a poorer solution in comparison to S_0 . This is because the fitness of S_1 is significantly higher than that of S_0 and hence it would resist change to any of its SIV values.

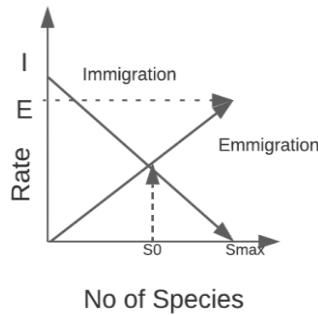


Figure 1. Behaviour of immigration and emigration under ideal conditions

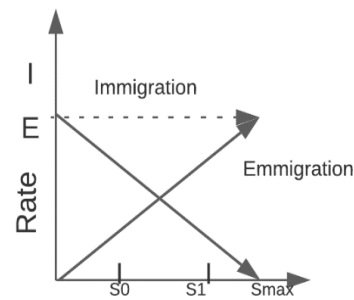


Figure 2. Species model

From the species model, one can determine,

$$\mu_k = \frac{Ek}{n} \quad (3)$$

$$\lambda_k = I \left(1 - \frac{k}{n} \right) \quad (4)$$

now for the $E=I$ (a special case), satisfies the following condition,

$$\mu_k + \lambda_k = 1 \quad (5)$$

2.1. Migration

Migration is a core concept of this paper. This paper has initialized the population of a habitat in terms of an array of integers in python programming with finite dimensions. Each solution index of the array can be considered an SIV. The array in the program is analogous to vectors of integers in the paper [23]. Now as mentioned previously the HSI value, often referred to as fitness, is a very important concept. The more the HSI value, the more is the emigration and less HSI means more immigration. The objective of this paper is to share the λ and μ data between different solutions to optimize the algorithm [24], [25]. With probability P_{Mod} , we change each solution on the basis of others [26]. Say a certain iteration step is picked then we use the lambda to probabilistically decide if the suitability index variable is to be modified [27]. If a specific dimension of a solution is specified then we decide if the mu rate is to be applied to another solution whose SIV will be random.

Step 1: Initializing the population

```
#Initializing Population with SIV values
pos=numpy.random.uniform(0,1,(PopSize,dim)) * (ub-lb)+lb
#Calculate objective function for each particle
for i in range(PopSize):
    # Performing the bound checking
    pos[i,:]=numpy.clip(pos[i,:], lb, ub)
    fitness=objf(pos[i,:])
    fit[i]=fitness
```

Step 2: Migration

```

#Performing Migration operator
for k in range(PopSize):
    for j in range(dim):
        if random.random() < lambda1[k]:
            # Performing Roulette Wheel
            RandomNum = random.random() * sum(mu);
            Select = mu[1];
            SelectIndex = 0;
            while (RandomNum > Select) and (SelectIndex < (PopSize-1)):
                SelectIndex = SelectIndex + 1;
                Select = Select + mu[SelectIndex];
            Island[k,j] = pos[SelectIndex,j]
        else:
            Island[k,j] = pos[k,j]

```

2.2. Mutation

Disastrous functions can radically change the habitat suitability index of a function domain i.e a habitat. What happens is that the population count diversifies and the fact that the entire act is inevitable makes mutation a very important aspect of biogeography. We use this algorithm to train a model on suitability index variable mutation and that population count is used to make sure of the mutation [28], [29].

$$m(s) = m_{max} \left(\frac{1 - P_s}{P_{max}} \right) \quad (6)$$

This step will mainly disperse the dataset causing greater variance. With this it is also ensured that all solutions have an equal chance of being dominant in the search space. The (2) will govern the aforementioned step in mutating species [30], [31]. What happens is that high HSI and low HSI solutions are not probable because they do not lie in the middle of the curve shown in the species model. The solutions that lie in the middle i.e equilibrium are very much probable to exist. So the extremities have to mutate to exist and that is the law of nature.

Mutation is coded

```

#Performing Mutation:
for k in range(PopSize):
    #PopSize: Population Size
    for parnum in range(dim):
        if pmutate > random.random(): #pmutate: mutation probability
            Island[k,parnum]=lb+(ub-lb) * random.random()

```

The steady state value for existence of each species is governed by (7),

$$P(\infty) = \frac{v}{\sum_{i=1}^{n+1} v_i} \quad (7)$$

where the value of v is equal to an eigen vector which has been defined as sets of arrays in the python models that this paper presents [32], [33]. The set of vectors are initialized in an uniform random distribution and only then the computation starts to ensure that the model is flexible in its approach in mimicking a natural habitat and the corresponding behaviour of the species existing in it.

2.3. Algorithm

The Biogeography based optimization algorithm by combining the migration and mutation phases has been presented next:

```

Create an island, H1,H2,...,Hn
Find out the HSI Values
while ( halting criteria isn't satisfied ) do
    Compute immigration rate
    for (each habitat(solution)) do
        for (each SIV(solution feature)) do
            Select Habitat Hi with probability αλ
            if ( Hi is selected) then
                Select Hj with probability αμ
                if (Hj is selected) then
                    Hi (SIV) ← αHi (SIV) + (1-α) Hj (SIV)
                Select Hi (SIV) based on mutation probability
                if (Hi is selected) then

```

Replace H_i (SIV) with random SIV

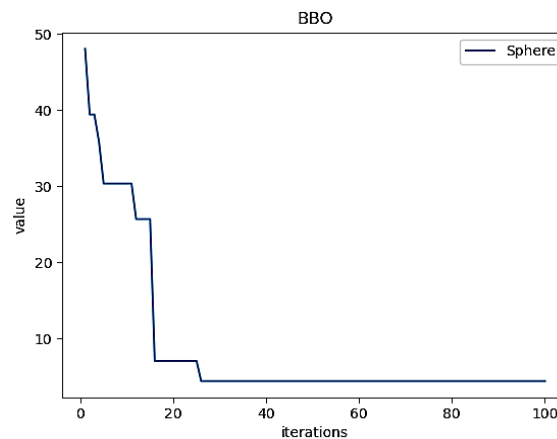
Recompute HSI value

3. RESULTS AND DISCUSSION

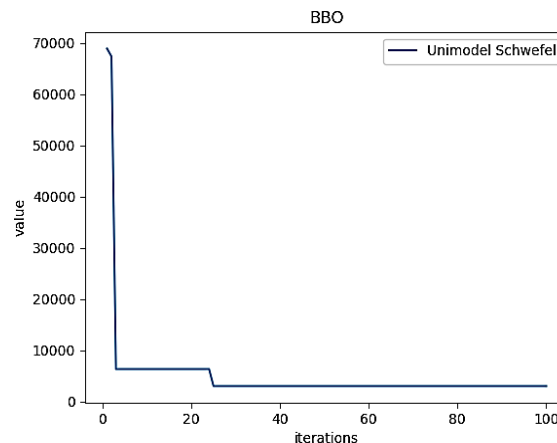
This section compares BBO techniques against different algorithms that are based on population behavior [34]. This paper has displayed a set of tables that consists of norms of benchmarks that serve as a source of comparison with the biogeography based algorithms. and Then we display the entire project that was coded in Python 3.8 to implement the paper.

3.1. Benchmark results

To gauge the efficiency of this algorithm we execute it 100 times over 2 generations and observe the plot over various benchmark functions. The granularity of every single domain was 0.1 but the quartic function had 0.01 [35]. The functions provided in the table are commonly used in research works in PB algorithms as a standard comparison measure. Some have a single, unique minima, while some have multiple i.e., they are multimodal. Some can be differentiated at every point in the search space and some cannot be separated. Figure 3 shows that around the 17th iteration there is a steep decline in the fitness values or a considerable increase in the convergence rate. BBO performs faster than GAs on this benchmark. Figure 3(a) shows that around the 17th iteration there is a steep decline in the fitness values or a considerable increase in the convergence rate. BBO performs faster than GAs on this benchmark. Figure 3(b) shows that the BBO minimizes the values rapidly only after a few iterations. The convergence rate is very high for this benchmark and it gradually closes in on 0 after the 24th iteration.



(a)



(b)

Figure 3. Plot of n-dimensional: (a) unimodal convex spherical benchmark, (b) unimodal continuous schwefel benchmark

Figure 4(a) shows that on a multimodal function the steep convergence occurs on a couple of occasions. After a few iterations the fitness minimizes significantly and then around the 10th iteration it converges to 0. For rastrigin function as shown in Figure 4(b), the fitness value converges to 0 after gradual declinations on the 3rd, 15th, 38th iteration. It's faster than the PSO on this benchmark.

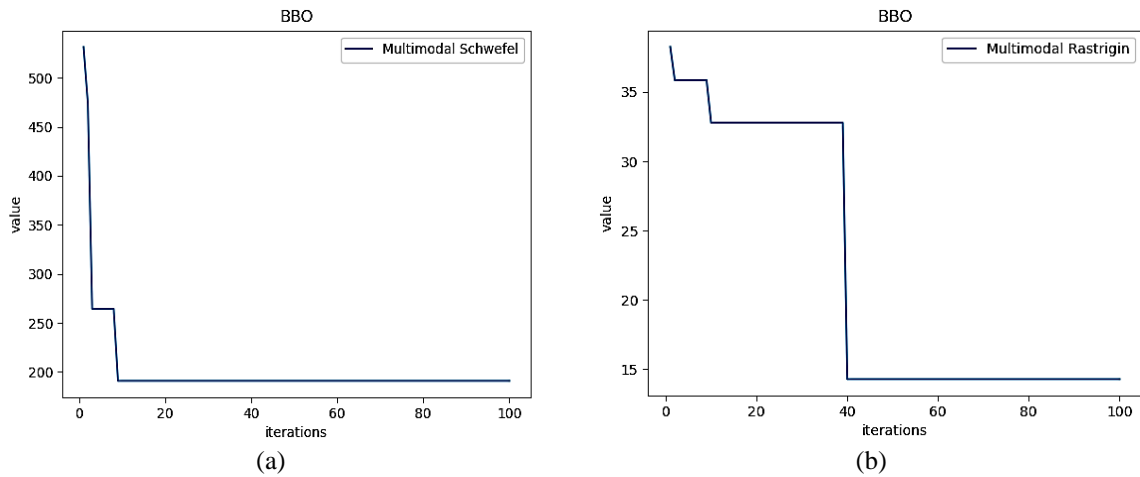


Figure 4. Plot of: (a) continuous non-convex multimodal schwefel benchmark, (b) multimodal n-dimensional convex multimodal rastrigin benchmark

In the Ackley benchmark the BBO has the fastest convergence rate and obtains the local minima fastest of all the population based algorithms and it is shown in Figure 5(a). Figure 5(b) is a combined plot of all the benchmarks. The Y-axis denotes the fitness value and X-axis denotes the number of iterations.

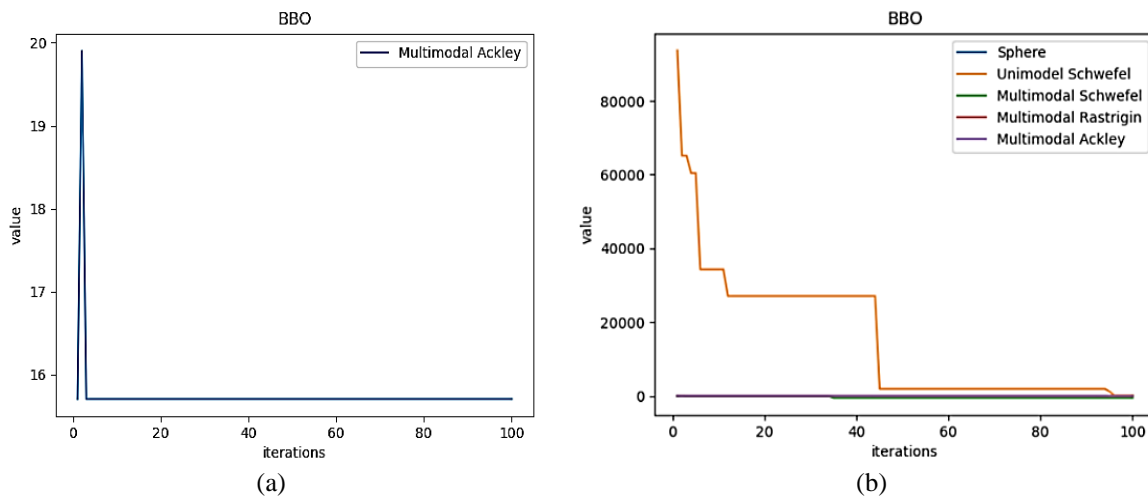


Figure 5. Plot of: (a) n-dimensional convex continuous multimodal Ackley benchmark, (b) combined benchmarks

From the figures 4 and 5, it can be observed that the BBO minimizes the benchmark functions over a certain number of iterations. Normally around the 30th iteration mark the minima of the objective function is reached and the fitness of the solution continues to be marginally decremented until the 100th iteration. As is the case with optimization algorithms-the main objective is to reach the local and global optima of a function as fast as possible and with as few iterations as possible. When we compare the efficacy of the BBO with other population based algorithms like the particle swarm optimization or the genetic algorithm, it has been proven that BBO is much faster and hence is the state of the art optimization algorithm.

4. CONCLUSION

The presented BBO algorithm is generally in a way that is better than different strategies, or the other way around, considering the no free lunch hypothesis. Nonetheless, it might be studied and researched further to evaluate the exhibition of biogeography based optimization techniques comparative with different techniques for issues with explicit highlights. There is also a prospect of probabilistic sharing of data between species in a habitat likewise in the solutions between which a comparison paradigm can be drawn. It is inevitable that species will migrate to neighbouring places that are near to their homeland. It is in their nature. In genetic algorithms, niching also works in the same manner. BBO is an amalgamation of a handful of PB algorithms. The subtleties of the species model can always be referred to improve a given solution in terms of speed of optimization. We utilized direct, straight mu and lambda curves. However the curves will change under changing circumstances given rise to much better results. It is always assumed that habitats with basic non zero habitat suitability index provide impetus to any species that would give animal types a minimal bound that is more noteworthy than zero.

ACKNOWLEDGEMENTS

This research work was funded by “Woosong University’s Academic Research Funding-2021”.

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