# Biogeography-Based Optimization

## **Biogeography-Based Optimization**

- Biogeography is the study of the speciation, extinction, and geographical distribution of biological species.
- Behavior of biological ants ant colony optimization
- Science of genetics genetic algorithms
- Study of animal swarms particle swarm optimization
- Science of biogeography biogeography-based optimization

• The science of biogeography can be traced to the work of **19th century** naturalists, most notably Alfred Wallace [Wallace, 2006] and Charles Darwin [Keynes, 2001].

Alfred Wallace - Father of biogeography

• Charles Darwin - Theory of evolution.

- Mathematical models of biogeography describe **speciation** (the evolution of new species), the **migration** of species between islands, and the **extinction** of species.
- An **island** is considered any habitat that is geographically isolated from other habitats.

• An island is isolated from other habitats by water, isolated by stretches of desert, rivers, mountain ranges, predators, man-made artifacts, or other obstacles.

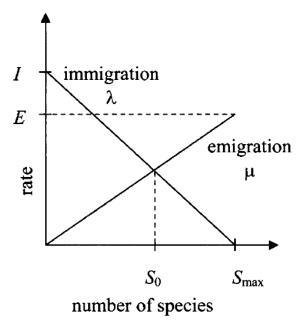
- Mathematical models of biogeography describe **speciation** (the evolution of new species), the **migration** of species between islands, and the **extinction** of species.
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- Geographical areas that are **friendly to life** are said to have a **high habitat suitability index** (HSI).
  - Features that correlate with HSI include such factors as rainfall, vegetative diversity, topographic diversity, land area, and temperature.
- The variables which characterize habitability are called suitability index variables (SIVs)

• SIVs are the independent variables of the habitat and HSI is the dependent variable.

• Islands with a **high HSI** tend to support many species, and islands with a **low HSI** can support only a few species.



Species migration model of an island, based on [MacArthur and Wilson, 1967]. So is the equilibrium species count.

- Biogeography is nature's way of distributing species and optimizing environments for life, and is analogous to mathematical optimization.
- Suppose that we have an optimization problem and some candidate solutions, which we call individuals.
- Good individuals perform well on the problem, and poor individuals perform poorly.
- A **good individual** is analogous to an island with a high HSI, and a **poor individual** is analogous to an island with a low HSI.

- Biogeography is nature's way of distributing species and optimizing environments for life, and is analogous to mathematical optimization.
- Suppose that we have an optimization problem and some candidate solutions, which we call individuals.
- Good individuals perform well on the problem, and poor individuals perform poorly.
- A **good individual** is analogous to an island with a high HSI, and a **poor individual** is analogous to an island with a low HSI.

- Good individuals resist change more than poor individuals, just like highly habitable islands have lower immigration rates than less habitable islands.
- Good individuals tend to share their features (that is, their independent variables) with poor individuals, just like highly habitable islands have high emigration rates.

• Poor individuals are likely to accept new features from good individuals, just like less habitable islands are likely to receive many immigrants from highly habitable islands.

• The addition of new features to poor individuals may raise the quality of those individuals.

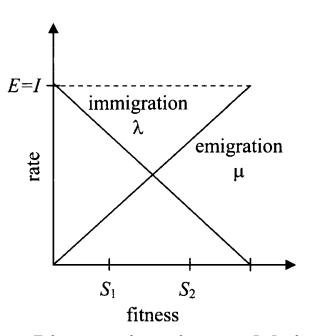
• The EA that is based on this approach is called biogeography-based optimization (BBO).

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• The EA that is based on this approach is called biogeography-based optimization (BBO).

• Assume that each BBO individual is represented by an identical species count curve with E = I for simplicity.



S1 represents a poor individual, while S2 represents a good individual.

The **immigration** rate for S1 will be relatively high, which means that it will be likely to receive new features from other candidate solutions.

The **emigration** rate for \$2 will be relatively high, which means that it will be likely to share its features with other individuals.

Linear migration model since the I and E values are linear functions of fitness.

- We use the migration rates of each individual to probabilistically share information between individuals.
- There are several different ways to implement the details of BBO here we are concentrating method by **D** Simon, 2008.

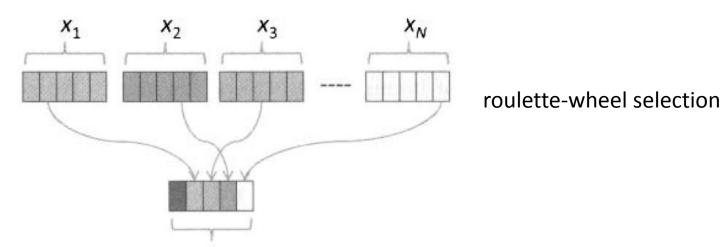
- Population size of N
- $X_k$  is the k-th individual in the population
- $X_k(s)$  is the s-th independent variable in  $X_k$ ,
  - where  $k \in [1, N]$  and  $s \in [1, n]$ .
- At each generation and for each solution feature in the k-th individual, there is a probability of  $\lambda_k$  (immigration probability) that it will be replaced.

 $\lambda_k$  = Probability that s-th independent variable in  $x_k$  will be replaced

• If a solution feature is selected to be replaced, then we select the emigrating solution with a probability that is proportional to the emigration probabilities  $\{\mu_i\}$ 

$$\Pr(x_j)$$
 is selected for emigration  $=\frac{\mu_j}{\sum_{i=1}^N \mu_j}$ .

• Migration and mutation of each individual in the current generation occurs before any of the individuals are replaced in the population, which requires the use of the temporary population z



 $\lambda_k$  = Probability that s-th independent variable in  $x_k$  will be replaced  $Z_k$ 

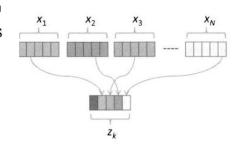
$$\Pr(x_j)$$
 is selected for emigration  $=\frac{\mu_j}{\sum_{i=1}^N \mu_j}$ . (14.14)

Depicts a generational BBO algorithm as opposed to a steady-state algorithm.

- 1. Immigration is *not* selected for the first feature; that is why the first feature in  $z_k$  remains unchanged.
- 2. Immigration is selected for the second feature, and Equation (14.14) chooses  $x_1$  as the emigrating individual; that is why the second feature in  $z_k$  is replaced by the second feature from  $x_1$ .
- 3. Immigration is selected for the third feature, and Equation (14.14) chooses  $x_3$  as the emigrating individual; that is why the third feature in  $z_k$  is replaced by the third feature from  $x_3$ .
- 4. Immigration is selected for the fourth feature, and Equation (14.14) chooses  $x_2$  as the emigrating individual; that is why the fourth feature in  $z_k$  is replaced by the fourth feature from  $x_2$ .
- 5. Finally, immigration is selected for the fifth feature, and Equation (14.14) chooses  $x_N$  as the emigrating individual; that is why the fifth feature in  $z_k$  is replaced by the fifth feature from  $x_N$ .

 $\lambda_k$  = Probability that s-th independent variable in  $x_k$  will be replaced

$$\Pr(x_j)$$
 is selected for emigration  $=\frac{\mu_j}{\sum_{i=1}^N \mu_j}$ . (14.14)



```
Initialize a population of candidate solutions \{x_k\} for k \in [1, N]
While not(termination criterion)
      For each x_k, set emigration probability \mu_k \propto fitness of x_k, with \mu_k \in [0,1]
      For each individual x_k, set immigration probability \lambda_k = 1 - \mu_k
      \{z_k\} \leftarrow \{x_k\}
      For each individual z_k
            For each solution feature s
                   Use \lambda_k to probabilistically decide whether to immigrate to z_k
                         (see Equation (14.13))
                   If immigrating then
                         Use \{\mu_i\}_{i=1}^N to probabilistically select emigrating individual x_j
                                (see Equation (14.14))
                         z_k(s) \leftarrow x_i(s)
                   End if
            Next solution feature
            Probabilistically mutate \{z_k\}
      Next individual
      \{x_k\} \leftarrow \{z_k\}
                                      \lambda_k = Probability that s-th independent variable in x_k will be replaced
```

Next generation

 $\Pr(x_j)$  is selected for emigration  $=\frac{\mu_j}{\sum_{i=1}^N \mu_j}$ .

(14.14)

String number	x (binary)	x (decimal)	$f(x) = x^2$	$\mu$	λ
1	01101	13	169	2/5	3/5
2	11000	24	576	4/5	1/5
3	01000	8	64	1/5	4/5
4	10011	19	361	3/5	2/5

$$N = 4$$

use 1/N as the minimum values for  $\lambda$  and  $\mu$ , and (N-1)/N as the maximum values

$$z_1(1) = 0$$
,  $z_1(2) = 1$ ,  $z_1(3) = 1$ ,  $z_1(4) = 0$ ,  $z_1(5) = 1$ .

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Since  $z_1$  is the third most fit individual, immigration rate  $\lambda_1 = 3/5$ , so there is a 60% chance of immigrating to each bit in  $z_1$ . We generate a random number  $r \sim U[0,1]$  for each bit in  $z_1$  to determine whether or not we should immigrate to that bit.

$$z_1(1) = 0$$
,  $z_1(2) = 1$ ,  $z_1(3) = 1$ ,  $z_1(4) = 0$ ,  $z_1(5) = 1$ .

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1. Suppose r = 0.7. Since  $r > \lambda_1$ , we will not immigrate to  $z_1(1)$ , so  $z_1(1)$  remains equal to 0.

String number	x (binary)	x (decimal)	$f(x) = x^2$	$\mu$	λ
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2. Suppose the next random number that we generate is r = 0.3. Since  $r < \lambda_1$ , we will immigrate to  $z_1(2)$ . We use roulette-wheel selection to choose the immigrating bit.  $x_3(2)$  has the greatest probability of immigrating to  $z_1(2)$ ,  $x_1(2)$  has the second greatest probability,  $x_4(2)$  has the third greatest probability, and  $x_2(2)$  has the least probability. We could exclude  $x_1(2)$  from consideration since  $z_1$  is a copy of  $x_1$ , but this is an implementation detail that depends on the preference of the engineer. Suppose that this roulette-wheel selection process results in the choice of  $x_3(2)$  for immigration. Then  $z_1(2) \leftarrow x_3(2) = 1$ . Even though we immigrated to  $z_1(2)$ , it did not change from its original value.

String number	x (binary)	x (decimal)	$f(x) = x^2$	$\mu$	λ
1	01101	13	169	2/5	3/5
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3	01000	8	64	1/5	4/5
4	10011	19	361	3/5	2/5

- 3. We continue this process for  $z_1(3)$ ,  $z_1(4)$ , and  $z_1(5)$ . Suppose that the random numbers generated result in the following:
  - $z_1(3) = 1$  (no immigration);
  - $z_1(4) \leftarrow x_4(4) = 1$  (immigration); and
  - $z_1(5) = 1$  (no immigration).

$$z_1 = 01111$$

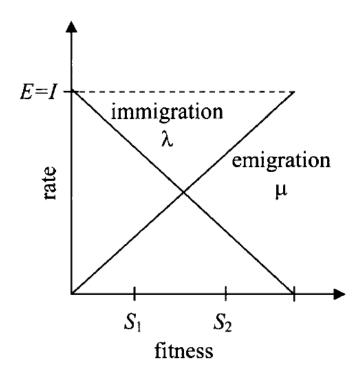
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- 4. We repeat steps 1-3 for  $z_2$ ,  $z_3$ , and  $z_4$ .
- 5. We next consider the possibility of mutation for each bit in each temporary individual  $z_1$ ,  $z_2$ ,  $z_3$ , and  $z_4$ .
- 6. Now that we have a modified population of  $\{z_k\}$  individuals, we copy  $z_k$  to  $x_k$  for  $k \in [1, 4]$ , and the first BBO generation is complete.

#### **BBO EXTENSIONS**

- Migration curve shapes,
- Blended migration
- Alternative approaches

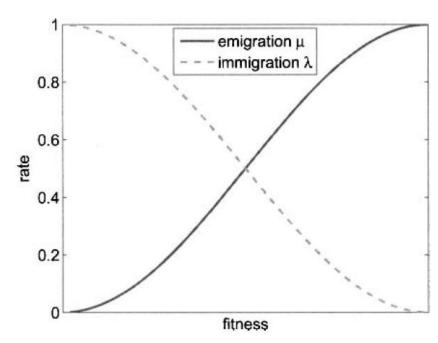
## **Migration Curves**



$$\mu_k = r_k$$

$$\lambda_k = 1 - r_k$$

linear



$$\mu_k = \frac{1}{2} (1 - \cos(\pi r_k/N))$$

$$\lambda_k = 1 - \mu_k.$$

Sinusoidal BBO migration model

The table shows the normalized minimum found by the two BBO versions, averaged over 50 Monte Carlo simulations.

## **Migration Curves**

Benchmark	Linear Migration	Sinusoid Migratio	
Ackley	1.0373	1	_
Fletcher	1.2015	1	population size of 50
Griewank	1.2367	1	P - P
Penalty #1	1.4249	1	generation limit of 50
Penalty #2	4.3265	1	generation inint of 50
Quartic	1.6876	1	mutation rate of 1% per
Rastrigin	1.0665	1	solution feature
Rosenbrock	1.0759	1	
Schwefel 1.2	1.0980	1	
Schwefel 2.21	1.0468	1	
Schwefel 2.22	1.0721	1	
Schwefel 2.26	1.2471	1	
Sphere	1.2582	1	
Step	1.2683	1	
Average	1.4319	1	_

#### **Blended Migration**

• In blended GA crossover, instead of copying a single parent's gene to a child gene, the child gene is obtained as a convex combination of two parent genes.

$$z_k(s) \leftarrow x_j(s)$$
.

$$z_k(s) \leftarrow \alpha z_k(s) + (1 - \alpha)x_j(s)$$

standard BBO algorithm

blended migration in BBO

## **Blended Migration**

Benchmark	Standard BBO $(\alpha = 0)$	Blended BBO $(\alpha = 0.5)$
Ackley	1.6559	1.0
Fletcher	1.0	2.388
Griewank	3.4536	1.0
Penalty #1	701.47	1.0
Penalty #2	8817.7	1.0
Quartic	49.663	1.0
Rastrigin	1.0	1.6892
Rosenbrock	3.9009	1.0
Schwefel 1.2	12.63	1.0
Schwefel 2.21	4.0846	1.0
Schwefel 2.21	1.3280	1.0
Schwefel 2.26	1.0	4.8213
Sphere	5.4359	1.0
Step	4.5007	1.0
Average	686.34	1.4213

#### Other Approaches to BBO

Partial emigration-based BBO

```
Initialize a population of candidate solutions \{x_k\} for k \in [1, N]
While not(termination criterion)
      For each x_k, set emigration probability \mu_k \propto \text{fitness of } x_k, with \mu_k \in [0,1]
      For each individual x_k, define immigration probability \lambda_k = 1 - \mu_k
      \{z_k\} \leftarrow \{x_k\}
      For each individual x_k
            For each solution feature s
                  Use \mu_k to probabilistically decide whether to emigrate x_k(s)
                  If emigrating then
                         Use \{\lambda_i\} to probabilistically select the immigrating solution z_i
                        z_i(s) \leftarrow x_k(s)
                  End if
            Next solution feature
      Next individual
                                                 (there is only one solution feature is considered
      Probabilistically mutate \{z_k\}
                                                     for immigration at a time)
      \{x_k\} \leftarrow \{z_k\}
Next generation
```

## **Total immigration-based BBO**

```
Initialize a population of candidate solutions \{x_k\} for k \in [1, N]
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      \{z_k\} \leftarrow \{x_k\}
      For each individual z_k
            Use \lambda_k to probabilistically decide whether to immigrate to z_k
            If immigrating then
                  For each solution feature s
                         Use \{\mu_i\} to probabilistically select the emigrating solution x_i
                         z_k(s) \leftarrow x_j(s)
                  Next solution feature
            End if
      Next individual
      \{x_k\} \leftarrow \{z_k\}
Next generation
```

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Initialize a population of candidate solutions \{x_k\} for k \in [1, N]
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                         z_i(s) \leftarrow x_k(s)
                  Next solution feature
            End if
      Next individual
      \{x_k\} \leftarrow \{z_k\}
Next generation
```

#### **BBO** and Genetic Algorithms

#### GA/GUR (BBO is a specific type of GA/GUR)

Initialize a population of candidate solutions  $\{x_k\}$  for  $k \in [1, N]$ While not(termination criterion)

For 
$$k = 1$$
 to  $N$   
 $Child_k \leftarrow \begin{bmatrix} 0 & 0 & \cdots & 0 \end{bmatrix} \in R^n$ 

For each solution feature s = 1 to n

Use fitness values to probabilistically select individual  $x_j$  Child<sub>k</sub> $(s) \leftarrow x_j(s)$ 

Next solution feature

Probabilistically mutate Child<sub>k</sub>

Next child

$$\{x_k\} \leftarrow \{\text{Child}_k\}$$

Next generation

If we use **global uniform recombination**, and if we also use **fitness-based selection** for each solution feature in each offspring.

Immigration probability is one

## Thank you