

# Biogeography-Based Optimization

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- 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**

# Biogeography

- 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.**

# Biogeography

- 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.**

# Biogeography

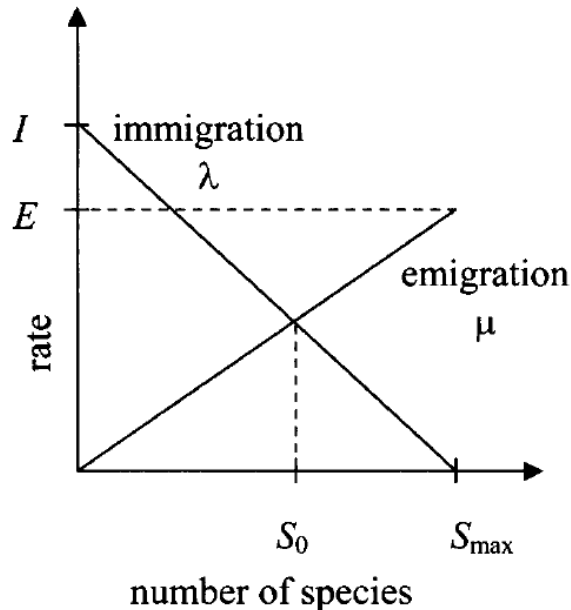
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# Biogeography

- 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**.

# Biogeography

- 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].  $S_0$  is the equilibrium species count.

# BIOGEOGRAPHY-BASED OPTIMIZATION

- 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**.



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# BIOGEOGRAPHY-BASED OPTIMIZATION

- **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**.

# BIOGEOGRAPHY-BASED OPTIMIZATION

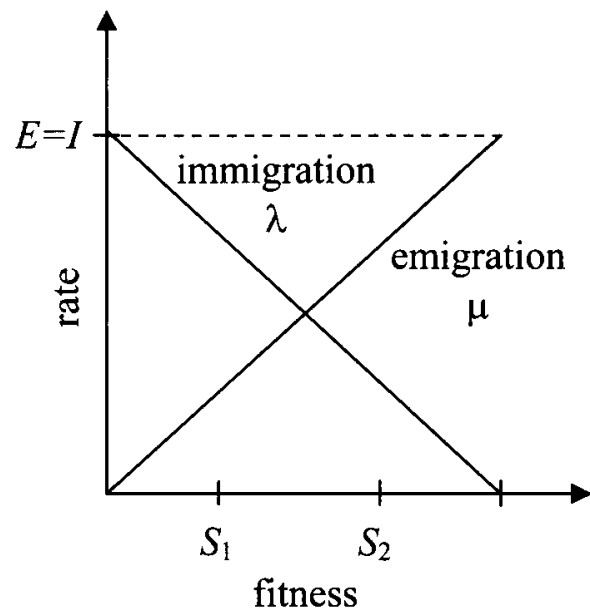
- **Poor individuals** are likely to **accept new features** from good individuals, just like less habitable islands are likely to **receive many immigrants** from highly habitable islands.
- The **addition of new features** to poor individuals may **raise the quality** of those individuals.
- The EA that is based on this approach is called **biogeography-based optimization (BBO)**.

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# BIOGEOGRAPHY-BASED OPTIMIZATION

- 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 *S2* 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.**

# BIOGEOGRAPHY-BASED OPTIMIZATION

- 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**.

# BIOGEOGRAPHY-BASED OPTIMIZATION

- 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

# BIOGEOGRAPHY-BASED OPTIMIZATION

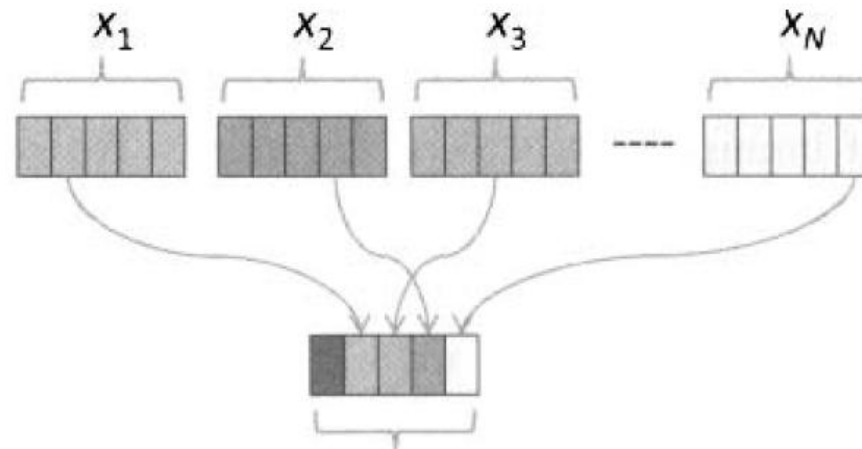
- If a solution feature is selected to be replaced, then we select the emigrating solution with a probability that is proportional to the emigration probabilities  $\{\mu_i\}$

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



# BIOGEOGRAPHY-BASED OPTIMIZATION

- **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**



roulette-wheel selection

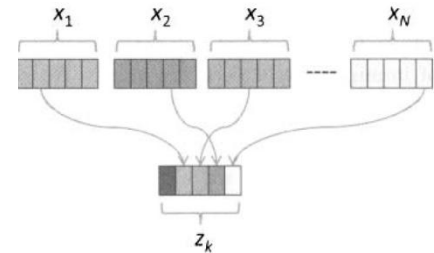
$\lambda_k$  = Probability that  $s$ -th independent variable in  $x_k$  will be replaced  $z_k$

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

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

# BIOGEOGRAPHY-BASED OPTIMIZATION

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

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

# BIOGEOGRAPHY-BASED OPTIMIZATION

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))

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

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

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

# Simple BBO experiment

| String<br>number | $x$ (binary) | $x$ (decimal) | $f(x) = x^2$ | $\mu$ | $\lambda$ |
|------------------|--------------|---------------|--------------|-------|-----------|
| 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

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

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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.

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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.

# Simple BBO experiment

| String<br>number | $x$ (binary) | $x$ (decimal) | $f(x) = x^2$ | $\mu$ | $\lambda$ |
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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.

# Simple BBO experiment

| String<br>number | $x$ (binary) | $x$ (decimal) | $f(x) = x^2$ | $\mu$ | $\lambda$ |
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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).

$$z_1 = 01111$$



# Simple BBO experiment

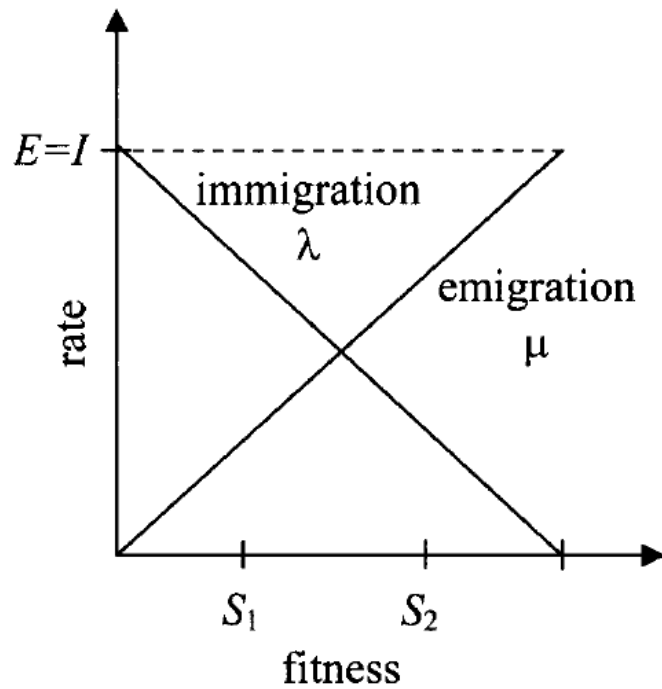
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4. We repeat steps 1–3 for  $z_2$ ,  $z_3$ , and  $z_4$ .
5. We next consider the possibility of mutation for each bit in each temporary individual  $z_1$ ,  $z_2$ ,  $z_3$ , and  $z_4$ .
6. Now that we have a modified population of  $\{z_k\}$  individuals, 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

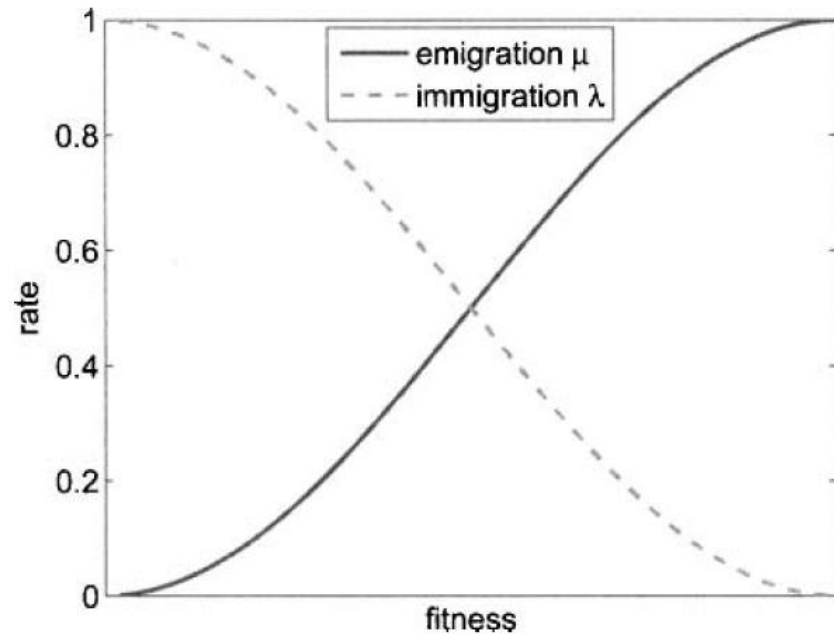
# Migration Curves



$$\mu_k = r_k$$

$$\lambda_k = 1 - r_k$$

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 | Sinusoidal Migration |  |
|---------------|------------------|----------------------|--|
| Ackley        | 1.0373           | 1                    | population size of 50                    |
| Fletcher      | 1.2015           | 1                    |  |
| Griewank      | 1.2367           | 1                    |  |
| Penalty #1    | 1.4249           | 1                    | generation limit of 50                   |
| Penalty #2    | 4.3265           | 1                    |  |
| Quartic       | 1.6876           | 1                    | mutation rate of 1% per solution feature |
| Rastrigin     | 1.0665           | 1                    |  |
| 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                    |  |

set of 20-dimensional benchmark

# 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.

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

standard BBO algorithm

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

blended migration in BBO

# Blended Migration

| Benchmark     | Standard BBO<br>( $\alpha = 0$ ) | Blended BBO<br>( $\alpha = 0.5$ ) |
|---------------|----------------------------------|-----------------------------------|
| 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  $\mu_k \propto$  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  $z_j$

$z_j(s) \leftarrow x_k(s)$

End if

Next solution feature

Next individual

Probabilistically mutate  $\{z_k\}$

$\{x_k\} \leftarrow \{z_k\}$

Next generation

(there is only one solution feature is considered for immigration at a time)

# Total immigration-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  $\mu_k \propto$  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  $z_k$

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  $x_j$

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

Next solution feature

End if

Next individual

$\{x_k\} \leftarrow \{z_k\}$

Next generation



# Total emigration-based BBO

Initialize a population of candidate solutions  $\{x_k\}$  for  $k \in [1, N]$

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For each  $x_k$ , set emigration probability  $\mu_k \propto$  fitness of  $x_k$ , with  $\mu_k \in [0, 1]$

For each individual  $x_k$ , define immigration probability  $\lambda_k = 1 - \mu_k$

$\{z_k\} \leftarrow \{x_k\}$

For each individual  $x_k$

Use  $\mu_k$  to probabilistically decide whether to emigrate  $x_k$

If emigrating then

For each solution feature  $s$

Use  $\{\lambda_i\}$  to probabilistically select the immigrating solution  $z_j$

$z_j(s) \leftarrow x_k(s)$

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 $_k \leftarrow [0 \ 0 \ \dots \ 0] \in R^n$

For each solution feature  $s = 1$  to  $n$

Use fitness values to probabilistically select individual  $x_j$

Child $_k(s) \leftarrow x_j(s)$

Next solution feature

Probabilistically mutate Child $_k$

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**