

# Package ‘BioGA’

July 23, 2025

**Type** Package

**Title** Bioinformatics Genetic Algorithm (BioGA)

**Version** 1.2.0

**Description** Genetic algorithm are a class of optimization algorithms inspired by the process of natural selection and genetics. This package allows users to analyze and optimize high throughput genomic data using genetic algorithms. The functions provided are implemented in C++ for improved speed and efficiency, with an easy-to-use interface for use within R.

**License** MIT + file LICENSE

**URL** <https://danymuksha.github.io/BioGA/>

**BugReports** <https://github.com/danymuksha/BioGA/issues>

**Imports** ggplot2, graphics, Rcpp, SummarizedExperiment, animation, rlang, biocViews, sessioninfo, BiocStyle

**Depends** R (>= 4.4)

**Suggests** knitr, rmarkdown, testthat (>= 3.0.0)

**LinkingTo** Rcpp

**VignetteBuilder** knitr

**biocViews** ExperimentalDesign, Technology

**Encoding** UTF-8

**LazyData** false

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.1

**Config/testthat/edition** 3

**git\_url** <https://git.bioconductor.org/packages/BioGA>

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|               |                                                        |
|---------------|--------------------------------------------------------|
| BioGA-package | <i>BioGA: Bioinformatics Genetic Algorithm (BioGA)</i> |
|---------------|--------------------------------------------------------|

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**Description**

Genetic algorithm are a class of optimization algorithms inspired by the process of natural selection and genetics. This package allows users to analyze and optimize high throughput genomic data using genetic algorithms. The functions provided are implemented in C++ for improved speed and efficiency, with an easy-to-use interface for use within R.

**Author(s)**

**Maintainer:** Dany Mukesha <danymukesha@gmail.com> ([ORCID](#))

**See Also**

- Useful links:
- <https://danymukesha.github.io/BioGA/>
  - Report bugs at <https://github.com/danymukesha/BioGA/issues>

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|               |                                                                   |
|---------------|-------------------------------------------------------------------|
| crossover_cpp | <i>Function to perform crossover between selected individuals</i> |
|---------------|-------------------------------------------------------------------|

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**Description**

Function to perform crossover between selected individuals

**Usage**

```
crossover_cpp(selected_parents, offspring_size)
```

**Arguments**

`selected_parents`      Numeric matrix representing the selected individuals.  
`offspring_size`      Number of offspring to generate.

**Value**

Numeric matrix representing the offspring.

**Examples**

```
# example of usage
genomic_data <- matrix(rnorm(100), nrow = 10, ncol = 10)
population <- BioGA::initialize_population_cpp(genomic_data,
  population_size = 5)
fitness <- BioGA::evaluate_fitness_cpp(genomic_data, population)
selected_parents <- BioGA::selection_cpp(population, fitness,
  num_parents = 2)
BioGA::crossover_cpp(selected_parents, offspring_size = 2)
```

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|                      |                                                        |
|----------------------|--------------------------------------------------------|
| evaluate_fitness_cpp | <i>Function to evaluate fitness using genomic data</i> |
|----------------------|--------------------------------------------------------|

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**Description**

Function to evaluate fitness using genomic data

**Usage**

```
evaluate_fitness_cpp(genomic_data, population)
```

**Arguments**

`genomic_data`      Numeric matrix of genomic data where rows represent genes/features and columns represent samples.  
`population`      Numeric matrix representing the population of individuals.

**Value**

Numeric vector of fitness scores for each individual.

**Examples**

```
# example of usage
genomic_data <- matrix(rnorm(100), nrow = 10, ncol = 10)
population <- BioGA::initialize_population_cpp(genomic_data,
                                              population_size = 5)
BioGA::evaluate_fitness_cpp(genomic_data, population)
```

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`initialize_population_cpp`

*Function to initialize the population from genomic data*

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**Description**

Function to initialize the population from genomic data

**Usage**

```
initialize_population_cpp(genomic_data, population_size)
```

**Arguments**

|                              |                                                                                                   |
|------------------------------|---------------------------------------------------------------------------------------------------|
| <code>genomic_data</code>    | Numeric matrix of genomic data where rows represent genes/features and columns represent samples. |
| <code>population_size</code> | Number of individuals in the population.                                                          |

**Value**

Numeric matrix representing the initialized population.

**Examples**

```
# example of usage
genomic_data <- matrix(rnorm(100), nrow = 10, ncol = 10)
BioGA::initialize_population_cpp(genomic_data, population_size = 5)
```

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|              |                                         |
|--------------|-----------------------------------------|
| mutation_cpp | <i>Function to mutate the offspring</i> |
|--------------|-----------------------------------------|

---

**Description**

Function to mutate the offspring

**Usage**

```
mutation_cpp(offspring, mutation_rate)
```

**Arguments**

offspring      Numeric matrix representing the offspring.  
mutation\_rate   Probability of mutation for each individual.

**Value**

Numeric matrix representing the mutated offspring.

**Examples**

```
# example of usage
genomic_data <- matrix(rnorm(100), nrow = 10, ncol = 10)
population <- BioGA::initialize_population_cpp(genomic_data,
  population_size = 5)
fitness <- BioGA::evaluate_fitness_cpp(genomic_data, population)
selected_parents <- BioGA::selection_cpp(population,
  fitness, num_parents = 2)
offspring <- BioGA::crossover_cpp(selected_parents, offspring_size = 2)
BioGA::mutation_cpp(offspring, mutation_rate = 0)
```

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|              |                            |
|--------------|----------------------------|
| plot_fitness | <i>Plot Fitness Values</i> |
|--------------|----------------------------|

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**Description**

Plot the fitness values of the population over generations.

**Usage**

```
plot_fitness(fitness_values)
```

**Arguments**

fitness\_values   A numeric vector containing fitness values.

**Value**

Plot of fitness

**Examples**

```
# example of usage
fitness_values <- c(10, 8, 6, 4, 2)
plot_fitness(fitness_values)
```

---

plot\_fitness\_history    *Plot Fitness Change Over Generations*

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**Description**

Plot the change in fitness values over generations.

**Usage**

```
plot_fitness_history(fitness_history)
```

**Arguments**

fitness\_history  
A list containing fitness values for each generation.

**Value**

Plot of fitness history

**Examples**

```
# example of usage
fitness_history <- list(c(10, 8, 6, 4, 2), c(9, 7, 5, 3, 1))
plot_fitness_history(fitness_history)
```

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|                 |                                     |
|-----------------|-------------------------------------|
| plot_population | <i>Plot Population Distribution</i> |
|-----------------|-------------------------------------|

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**Description**

Plot the distribution of individuals in the population.

**Usage**

```
plot_population(population)
```

**Arguments**

population      A numeric matrix containing the population data.

**Value**

Plot of population

**Examples**

```
# example of usage
population <- matrix(runif(100), nrow = 10, ncol = 10)
plot_population(population)
```

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|                 |                                                                       |
|-----------------|-----------------------------------------------------------------------|
| replacement_cpp | <i>Function to replace non-selected individuals in the population</i> |
|-----------------|-----------------------------------------------------------------------|

---

**Description**

Replace non-selected individuals in the population

**Usage**

```
replacement_cpp(population, offspring, num_to_replace)
```

**Arguments**

population      Numeric matrix representing the population of individuals.  
offspring        Numeric matrix representing the offspring.  
num\_to\_replace   Number of individuals to replace.

**Value**

Numeric matrix representing the updated population.

## Examples

```
# example of usage
genomic_data <- matrix(rnorm(100), nrow = 10, ncol = 10)
population <- BioGA::initialize_population_cpp(genomic_data,
  population_size = 5)
fitness <- BioGA::evaluate_fitness_cpp(genomic_data, population)
selected_parents <- BioGA::selection_cpp(population, fitness,
  num_parents = 2)
offspring <- BioGA::crossover_cpp(selected_parents, offspring_size = 2)
mutated_offspring <- BioGA::mutation_cpp(offspring, mutation_rate = 0)
BioGA::replacement_cpp(population, mutated_offspring, num_to_replace = 1)
```

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selection\_cpp

*Function to select individuals based on fitness scores*

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## Description

Function to select individuals based on fitness scores

## Usage

```
selection_cpp(population, fitness, num_parents)
```

## Arguments

|             |                                                            |
|-------------|------------------------------------------------------------|
| population  | Numeric matrix representing the population of individuals. |
| fitness     | Numeric vector of fitness scores for each individual.      |
| num_parents | Number of individuals to select.                           |

## Value

Numeric matrix representing the selected individuals.

## Examples

```
# example of usage
genomic_data <- matrix(rnorm(100), nrow = 10, ncol = 10)
population <- BioGA::initialize_population_cpp(genomic_data,
  population_size = 5)
fitness <- BioGA::evaluate_fitness_cpp(genomic_data, population)
BioGA::selection_cpp(population, fitness, num_parents = 2)
```

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