

# Package ‘MOGAMUN’

May 9, 2026

**Type** Package

**Title** MOGAMUN: A Multi-Objective Genetic Algorithm to Find Active Modules in Multiplex Biological Networks

**Version** 1.23.0

**Description** MOGAMUN is a multi-objective genetic algorithm that identifies active modules in a multiplex biological network. This allows analyzing different biological networks at the same time. MOGAMUN is based on NSGA-II (Non-Dominated Sorting Genetic Algorithm, version II), which we adapted to work on networks.

**License** GPL-3 + file LICENSE

**Encoding** UTF-8

**LazyData** TRUE

**Imports** stats, utils, RCy3, stringr, graphics, grDevices, RUnit, BiocParallel, igraph

**Suggests** knitr, markdown

**biocViews** SystemsBiology, GraphAndNetwork, DifferentialExpression, BiomedicalInformatics, Transcriptomics, Clustering, Network

**URL** <https://github.com/elvanov/MOGAMUN>

**RoxygenNote** 7.1.1

**VignetteBuilder** knitr

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

**git\_branch** devel

**git\_last\_commit** 4e05af7

**git\_last\_commit\_date** 2026-04-28

**Repository** Bioconductor 3.24

**Date/Publication** 2026-05-08

**Author** Elva-María Novoa-del-Toro [aut, cre] (ORCID: <https://orcid.org/0000-0002-6135-5839>)

**Maintainer** Elva-María Novoa-del-Toro <elvanov@hotmail.com>

## Contents

mogamun_init . . . . .	2
mogamun_load_data . . . . .	3
mogamun_postprocess . . . . .	4
mogamun_run . . . . .	5

<b>Index</b>	<b>7</b>
--------------	----------

---

mogamun_init	<i>mogamun_init</i>
--------------	---------------------

---

## Description

initialize evolution parameters

## Usage

```
mogamun_init(
  Generations = 500,
  PopSize = 100,
  MinSize = 15,
  MaxSize = 50,
  CrossoverRate = 0.8,
  MutationRate = 0.1,
  JaccardSimilarityThreshold = 30,
  TournamentSize = 2,
  Measure = "FDR",
  ThresholdDEG = 0.05,
  MaxNumberOfAttempts = 3
)
```

## Arguments

Generations	number of generations to run (default = 500)
PopSize	number of subnetworks in the population (default = 100)
MinSize	minimum size (no. of nodes) of the subnetworks (default = 15)
MaxSize	maximum size (no. of nodes) of the subnetworks (default = 50)
CrossoverRate	rate for the crossover (default = 0.8)
MutationRate	rate for the mutation (default = 0.1)
JaccardSimilarityThreshold	subnetworks over this Jaccard similarity threshold are considered as duplicated (default = 30)
TournamentSize	size of the tournament (default = 2)
Measure	measure to calculate the nodes scores and to determine which genes are differentially expressed (possible values PValue and FDR, default = FDR)
ThresholdDEG	threshold to consider a gene as significantly differentially expressed. Note: if there is a logFC available, it is also considered $ \logFC  > 1$ (default = 0.05)
MaxNumberOfAttempts	maximum number of attempts to find compatible parents (default = 3)

**Value**

EvolutionParameters

**Examples**

```
EvolutionParameters <-  
  mogamun_init(  
    Generations = 1,  
    PopSize = 10,  
    MinSize = 15,  
    MaxSize = 50,  
    CrossoverRate = 0.8,  
    MutationRate = 0.1,  
    JaccardSimilarityThreshold = 30,  
    TournamentSize = 2,  
    Measure = "FDR",  
    ThresholdDEG = 0.05,  
    MaxNumberOfAttempts = 3  
  )
```

---

mogamun\_load\_data      *mogamun\_load\_data*

---

**Description**

Load the data to process

**Usage**

```
mogamun_load_data(  
  EvolutionParameters,  
  DifferentialExpressionPath,  
  NodesScoresPath,  
  NetworkLayersDir,  
  Layers  
)
```

**Arguments**

EvolutionParameters

evolution parameters returned by mogamun\_init()

DifferentialExpressionPath

full path to the differential expression results file (in CSV format). This file must contain at least the columns "gene" with the gene names, and ("PValue" or "FDR"). It can also contain "logFC"

NodesScoresPath

full path to an existing CSV file containing the nodes scores (columns "gene" and "nodescore"). NOTE. If the file does not exist, MOGAMUN will generate it in the provided path with the specified name

NetworkLayersDir	path of the folder that contains the networks that will be the layers of the multiplex. NOTE. Each file must start with a different digit
Layers	string of numbers, where the numbers correspond to the first character of the name of the network files (e.g. "123" builds a multiplex with layers 1, 2, and 3)

**Value**

List with the data to process

**Examples**

```
DEGPath <- system.file("extdata/DE/Sample_DE.csv", package = "MOGAMUN")
NodesScoresPath <-
  system.file("extdata/DE/Sample_NodesScore.csv", package = "MOGAMUN")
LayersPath <-
  paste0(system.file("extdata/LayersMultiplex", package = "MOGAMUN"), "/")
EvolutionParameters <- mogamun_init(Generations = 1, PopSize = 10)
LoadedData <-
  mogamun_load_data(
    EvolutionParameters = EvolutionParameters,
    DifferentialExpressionPath = DEGPath,
    NodesScoresPath = NodesScoresPath,
    NetworkLayersDir = LayersPath,
    Layers = "23"
  )
```

---

mogamun\_postprocess      *mogamun\_postprocess*

---

**Description**

Postprocess the results: i) calculates the accumulated Pareto front, i.e. the individuals on the first Pareto front after re-ranking the results from multiple runs (NOTE. If there is a single run, the result is the set of individuals in the first Pareto front), ii) filters the networks to leave only the interactions between the genes that are included in the results, iii) generates some plots of interest, such as scatter plots and boxplots, and iv) (optional) creates a Cytoscape file to visualize the results, merging the subnetworks with a Jaccard similarity coefficient superior to JaccardSimilarityThreshold (NOTE. Make sure to open Cytoscape if VisualizeInCytoscape is TRUE)

**Usage**

```
mogamun_postprocess(
  ExperimentDir = ".",
  LoadedData = LoadedData,
  JaccardSimilarityThreshold = 70,
  VisualizeInCytoscape = TRUE
)
```

**Arguments**

**ExperimentDir** folder containing the results to be processed. It is the same folder specified as **ResultsDir** in `mogamun_run`  
**LoadedData** list returned by `mogamun_load_data()`  
**JaccardSimilarityThreshold** subnetworks over this Jaccard similarity threshold are merged in a single sub-network  
**VisualizeInCytoscape** TRUE if you wish to visualize the accumulated Pareto front in Cytoscape, FALSE otherwise

**Value**

None

**Examples**

```

DEGPath <- system.file("extdata/DE/Sample_DE.csv", package = "MOGAMUN")
NodesScoresPath <-
  system.file("extdata/DE/Sample_NodesScore.csv", package = "MOGAMUN")
LayersPath <-
  paste0(system.file("extdata/LayersMultiplex", package = "MOGAMUN"), "/")
EvolutionParameters <- mogamun_init(Generations = 1, PopSize = 10)
LoadedData <-
  mogamun_load_data(
    EvolutionParameters = EvolutionParameters,
    DifferentialExpressionPath = DEGPath,
    NodesScoresPath = NodesScoresPath,
    NetworkLayersDir = LayersPath,
    Layers = "23"
  )
ResultsDir <- system.file("SampleResults", package="MOGAMUN")
mogamun_run(
  LoadedData = LoadedData,
  Cores = 1,
  NumberOfRunsToExecute = 1,
  ResultsDir = ResultsDir
)
mogamun_postprocess(
  ExperimentDir = ResultsDir,
  LoadedData = LoadedData,
  JaccardSimilarityThreshold = 70,
  VisualizeInCytoscape = FALSE
)

```

---

`mogamun_run`

*mogamun\_run*

---

**Description**

Run the algorithm with the specified values for the evolution parameters

**Usage**

```
mogamun_run(LoadedData, Cores = 1, NumberOfRunsToExecute = 1, ResultsDir = ".")
```

**Arguments**

LoadedData      list returned by mogamun\_load\_data()  
 Cores            to run MOGAMUN in parallel on the given number of cores (in line with the number of physical processor cores) (default = 1)  
 NumberOfRunsToExecute      number of runs (default = 1)  
 ResultsDir      outputs the results in the specified folder

**Value**

None

**Examples**

```
DEGPath <- system.file("extdata/DE/Sample_DE.csv", package = "MOGAMUN")
NodesScoresPath <-
  system.file("extdata/DE/Sample_NodesScore.csv", package = "MOGAMUN")
LayersPath <-
  paste0(system.file("extdata/LayersMultiplex", package = "MOGAMUN"), "/")
EvolutionParameters <- mogamun_init(Generations = 1, PopSize = 10)
LoadedData <-
  mogamun_load_data(
    EvolutionParameters = EvolutionParameters,
    DifferentialExpressionPath = DEGPath,
    NodesScoresPath = NodesScoresPath,
    NetworkLayersDir = LayersPath,
    Layers = "23"
  )
ResultsDir <- system.file("SampleResults", package="MOGAMUN")
mogamun_run(
  LoadedData = LoadedData,
  Cores = 1,
  NumberOfRunsToExecute = 1,
  ResultsDir = ResultsDir
)
```

# Index

mogamun\_init, 2  
mogamun\_load\_data, 3  
mogamun\_postprocess, 4  
mogamun\_run, 5