

# Package: GARS (via r-universe)

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**Type** Package

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**Title** GARS: Genetic Algorithm for the identification of Robust Subsets of variables in high-dimensional and challenging datasets

**Version** 1.25.0

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**Description** Feature selection aims to identify and remove redundant, irrelevant and noisy variables from high-dimensional datasets. Selecting informative features affects the subsequent classification and regression analyses by improving their overall performances. Several methods have been proposed to perform feature selection: most of them relies on univariate statistics, correlation, entropy measurements or the usage of backward/forward regressions. Herein, we propose an efficient, robust and fast method that adopts stochastic optimization approaches for high-dimensional. GARS is an innovative implementation of a genetic algorithm that selects robust features in high-dimensional and challenging datasets.

**License** GPL (>= 2)

**Encoding** UTF-8

**LazyData** true

**VignetteBuilder** knitr

**RoxygenNote** 6.1.1

**biocViews** Classification, FeatureExtraction, Clustering

**Imports** DaMiRseq, MLSeq, stats, methods, SummarizedExperiment

**Suggests** BiocStyle, knitr, testthat

**Depends** R (>= 3.5), ggplot2, cluster

**Repository** <https://bioc.r-universe.dev>

**RemoteUrl** <https://github.com/bioc/GARS>  
**RemoteRef** HEAD  
**RemoteSha** 15b73554a629576db135c0b76b89e1d26dd697ef

**Contents**

AllPop . . . . .	2
FitScore . . . . .	3
GARS . . . . .	4
GarsSelectedFeatures-class . . . . .	4
GARS_classes . . . . .	5
GARS_create_rnd_population . . . . .	5
GARS_Crossover . . . . .	6
GARS_data_norm . . . . .	7
GARS_Elitism . . . . .	7
GARS_FitFun . . . . .	8
GARS_Fitness_score . . . . .	9
GARS_fit_list . . . . .	10
GARS_GA . . . . .	10
GARS_Mutation . . . . .	12
GARS_PlotFeaturesUsage . . . . .	13
GARS_PlotFitnessEvolution . . . . .	14
GARS_popul . . . . .	15
GARS_pop_list . . . . .	15
GARS_res_GA . . . . .	16
GARS_Selection . . . . .	16
LastPop . . . . .	17
MatrixFeatures . . . . .	18
<b>Index</b>	<b>19</b>

---

AllPop	<i>Accessors for the 'AllPop' slot of a GarsSelectedFeatures object.</i>
--------	--

---

**Description**

The AllPop slot contains the list of populations

**Usage**

```
AllPop(x)  
  
## S4 method for signature 'GarsSelectedFeatures'  
AllPop(x)
```

**Arguments**

x                      a GarsSelectedFeatures object

**Value**

a list containing all the populations

**Author(s)**

Mattia Chiesa, Luca Piacentini

**Examples**

```
data(GARS_res_GA)
ex_pop <- AllPop(GARS_res_GA)
```

---

FitScore

*Accessors for the 'FitScore' slot of a GarsSelectedFeatures object.*

---

**Description**

The FitScore slot contains the fitness values over the generations

**Usage**

```
FitScore(x)

## S4 method for signature 'GarsSelectedFeatures'
FitScore(x)
```

**Arguments**

x                      a GarsSelectedFeatures object

**Value**

a vector containing the fitness scores

**Author(s)**

Mattia Chiesa, Luca Piacentini

**Examples**

```
data(GARS_res_GA)
ex_pop <- FitScore(GARS_res_GA)
```

---

GARS

*GARS package for a robust feature selection of high-dimensional data*


---

### Description

The main function of GARS is [GARS\\_GA](#), which implements a clustering-based Genetic Algorithm to select Robust Subsets of features in high-dimensional datasets. The user can extract the results of [GARS\\_GA](#), exploiting the assessor methods: [MatrixFeatures](#), [LastPop](#), [AllPop](#) and [FitScore](#).

### Details

See the package vignette, by typing `vignette("GARS")` to discover all the [GARS\\_GA](#) functions.

### Author(s)

Mattia Chiesa, Giada Maioli, Luca Piacentini

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GarsSelectedFeatures-class

*The output class 'GarsSelectedFeatures'*


---

### Description

The output class for GARS\_GA function

### Slots

`data_red` a matrix containing the expression values for the selected feature  
`last_pop` a matrix containing the chromosome population of the last generation  
`pop_list` a list containing all the populations produced over the generations  
`fit_list` a vector containing the maximum fitness scores

### Examples

```
showClass("GarsSelectedFeatures")
```

GARS\_classes

*RNA-seq dataset for testing GARS***Description**

The class labels of the sample dataset

**Usage**

```
GARS_classes
```

**Format**

A vector of type "factor" with 58 elements: 29 labelled as "N" and 29 labelled as "T".

**Value**

An example data for testing GARS package

GARS\_create\_rnd\_population

*Create a random chromosomes population***Description**

This function creates the initial random population of chromosomes

**Usage**

```
GARS_create_rnd_population(data, chr.len, chr.num = 1000)
```

**Arguments**

data	<p>A SummarizedExperiment object or a matrix or a data.frame. In case of matrix or data.frame:</p> <ul style="list-style-type: none"> <li>• Rows and Cols have to be, respectively, observations and features. The variables are typically genes;</li> <li>• GARS also accept other -omic features as well as any continuous or factorial variables (e.g. sex, age, cholesterol level,...);</li> <li>• Usually the number of observation is « than the number of features</li> </ul>
chr.len	The length of chromosomes. This value corresponds to the desired length of the feature set.
chr.num	The number of chromosomes to generate. Default is 1000

**Value**

A matrix representing the chromosomes population: each column is a chromosome and each element correspond to the feature position in 'data'

**Author(s)**

Mattia Chiesa, Luca Piacentini

**Examples**

```
# use example data:
data(GARS_data_norm)
GARS_create_rnd_population(GARS_data_norm, chr.len=10, chr.num=100)
```

---

GARS\_Crossover

---

*Perform the one-point and the two-point Crossover*


---

**Description**

This function implements the one-point and the two-point cross-over.

**Usage**

```
GARS_Crossover(chr.pop, co.rate = 0.8, type = c("one.p", "two.p"),
  one.p.quart = c("I.quart", "II.quart", "III.quart"))
```

**Arguments**

chr.pop	A matrix or a data.frame representing the chromosomes population: each column is a chromosome and each element corresponds to the feature position in the data matrix
co.rate	The probability of each random couple of chromosomes to swap some parts. It must be between 0 and 1. Default is 0.8
type	The type of crossover method; one-point ("one.p") and two-point ("two.p") are allowed. Default is "one.p"
one.p.quart	The position of the cromosome where performing the crossover, if "one.p" is selected. The first quartile ("I.quart"), the second quartile ("II.quart", i.e. the median) and the third quartile ("III.quart") are allowed. Default is "I.quart"

**Value**

A matrix representing the "crossed" population. The dimensions of this matrix are the same of 'chr.pop'

**Author(s)**

Mattia Chiesa, Luca Piacentini

See Also

[GARS\\_Mutation](#), [GARS\\_Selection](#), [GARS\\_Elitism](#),

Examples

```
data(GARS_popul)
crossed_pop <- GARS_Crossover(GARS_popul, co.rate=0.9)
crossed_pop <- GARS_Crossover(GARS_popul, type="two.p")
crossed_pop <- GARS_Crossover(GARS_popul, type="one.p",
one.p.quart= "II.quart")
```

---

GARS_data_norm	<i>RNA-seq dataset for testing GARS</i>
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---

Description

An RNA-seq normalized matrix to test several GARS functions; this dataset was obtained using the DaMirseq package to normalize the raw count matrix present in MLSeq package.

Usage

```
GARS_data_norm
```

Format

A matrix of 157 genes (columns) and 58 samples (rows)

Value

An example data for testing GARS package

---

GARS_Elitism	<i>Separate chromosome on the basis of the Fitness Scores</i>
--------------	---

---

Description

This function splits the chromosome population in two parts allowing the best chromosomes to be preserved from the "evolutionary" steps: Selection, Crossover and Mutation.

Usage

```
GARS_Elitism(chr.pop, fitn.values, n.elit = 10)
```

**Arguments**

<code>chr.pop</code>	A matrix or a data.frame representing the chromosomes population: each column is a chromosome and each element corresponds to the feature position in the data matrix
<code>fitn.values</code>	A numeric vector where each element corresponds to the fitness score of each chromosome in 'chr.pop'
<code>n.elit</code>	The number of best chromosomes to be selected by elitism. This number must be even. Default is 10

**Value**

A list containing:

- The population of best chromosomes selected by elitism.
- The population of chromosomes not selected by elitism.
- The fitness values of best chromosomes selected by elitism.
- The fitness values of chromosomes not selected by elitism.

**Author(s)**

Mattia Chiesa, Luca Piacentini

**See Also**

[GARS\\_Mutation](#), [GARS\\_Selection](#), [GARS\\_Crossover](#), [GARS\\_FitFun](#),

**Examples**

```
data(GARS_popul)
data(GARS_Fitness_score)
pop_list <- GARS_Elitism(GARS_popul, GARS_Fitness_score)
```

---

GARS\_FitFun

---

*This function implements the Fitness Function of GARS*


---

**Description**

In GARS the Fitness Function consists in calculating the Averaged Silhouette Index after a Multi-Dimensional Scaling

**Usage**

```
GARS_FitFun(data, classes, chr.pop)
```



**Arguments**

data	<p>A SummarizedExperiment object or a matrix or a data.frame. In case of matrix or data.frame:</p> <ul style="list-style-type: none"> <li>• Rows and Cols have to be, respectively, observations and features. The variables are typically genes;</li> <li>• GARS also accept other -omic features as well as any continuous or factorial variables (e.g. sex, age, cholesterol level,...);</li> <li>• Usually the number of observation is « than the number of features</li> </ul>
classes	A vector of type "factor" with nrow(data) elements. Each element represents the class label for each observation.
chr.pop	A matrix or a data.frame representing the chromosomes population: each column is a chromosome and each element corresponds to the feature position in the expression data matrix

**Value**

A numeric vector where each element corresponds to the fitness score of each chromosome in 'chr.pop'

**Author(s)**

Mattia Chiesa, Luca Piacentini

**See Also**

[GARS\\_create\\_rnd\\_population](#)

**Examples**

```
# use example data:
data(GARS_data_norm)
data(GARS_classes)
data(GARS_popul)
fitness_scores <- GARS_FitFun(GARS_data_norm, GARS_classes, GARS_popul)
```

---

GARS_Fitness_score	<i>RNA-seq dataset for testing GARS</i>
--------------------	---

---

**Description**

A numeric vector with the fitness scores for each chromosome in a single generation

**Usage**

```
GARS_Fitness_score
```

**Format**

A numeric vector with 50 fitness scores

**Value**

An example data for testing GARS package

---

GARS_fit_list	<i>RNA-seq dataset for testing GARS</i>
---------------	---

---

**Description**

A numeric vector with the maximum fitness score for each iteration

**Usage**

GARS\_fit\_list

**Format**

A numeric vector with 100 fitness scores

**Value**

An example data for testing GARS package

---

GARS_GA	<i>The wrapper fuction to use GARS</i>
---------	--

---

**Description**

This function allows the users to run all GARS funtion at once. This is the easier and recommended way to use GARS.

**Usage**

```
GARS_GA(data, classes, chr.num = 1000, chr.len, generation = 500,
  co.rate = 0.8, mut.rate = 0.01, n.elit = 10, type.sel = c("RW",
    "TS"), type.co = c("one.p", "two.p"), type.one.p.co = c("I.quart",
    "II.quart", "III.quart"), n.gen.conv = 80, plots = c("yes", "no"),
  n.Feat_plot = 10, verbose = c("yes", "no"))
```

**Arguments**

<code>data</code>	A SummarizedExperiment object or a matrix or a data.frame. In case of matrix or data.frame: <ul style="list-style-type: none"> <li>• Rows and Cols have to be, respectively, observations and features. The variables are typically genes;</li> <li>• GARS also accept other -omic features as well as any continuous or factorial variables (e.g. sex, age, cholesterol level,...);</li> <li>• Usually the number of observation is « than the number of features</li> </ul>
<code>classes</code>	The class vector
<code>chr.num</code>	The number of chromosomes to generate. Default is 1000
<code>chr.len</code>	The length of chromosomes. This value corresponds to the desired length of the feature set
<code>generation</code>	The maximum number of generations. Default is 1000
<code>co.rate</code>	The probability of each random couple of chromosomes to swap some parts. It must be between 0 and 1. Default is 0.8
<code>mut.rate</code>	The probability to apply a random mutation to each element. It must be between 0 and 1. Default is 0.01
<code>n.elit</code>	The number of best chromosomes to be selected by elitism. This number must be even. Default is 10
<code>type.sel</code>	The type of selection method; Roulette Wheel ("RW") and Tournament Selection ("TS") are allowed. Default is "RW"
<code>type.co</code>	The type of crossover method; one-point ("one.p") and two-point ("two.p") are allowed. Default is "one.p"
<code>type.one.p.co</code>	The position of the chromosome where performing the crossover, if "one.p" is selected. The first quartile ("I.quart"), the second quartile ("II.quart", i.e. the median) and the third quartile ("III.quart") are allowed. Default is "I.quart"
<code>n.gen.conv</code>	The number of consecutive generations with the same maximum fitness score.
<code>plots</code>	If graphs have to be plotted; "yes" or "no" are allowed. Default is "yes"
<code>n.Feat_plot</code>	The number of features to be plotted
<code>verbose</code>	If statistics have to be printed; "yes" or "no" are allowed. Default is "yes"

**Value**

A GarsSelectedFeatures object, containing:

**data\_red** a matrix of selected features

**last\_pop** a matrix containing the last chromosome population

**pop\_list** a list containing all the populations produced over the generations

**fit\_list** a numeric vector containing the maximum fitness scores, computed in each generation

**Author(s)**

Mattia Chiesa, Luca Piacentini

Examples

```
# use example data:
data(GARS_data_norm)
data(GARS_classes)

res_ex <- GARS_GA(GARS_data_norm,
  GARS_classes,
  chr.num = 100,
  chr.len=10,
  generation = 5,
  co.rate = 0.8,
  mut.rate = 0.1,
  n.elit = 10,
  type.sel = "RW",
  type.co ="one.p",
  type.one.p.co = "II.quart",
  n.gen.conv = 80,
  plots = "no",
  verbose = "no")
```

---

GARS_Mutation	<i>Perform the Mutation step</i>
---------------	----------------------------------

---

Description

This function implements the mutation step in the GA. First, it checks and replace duplicate features in each chromosomes; then, random mutation are applied to the entire population.

Usage

```
GARS_Mutation(chr.pop, mut.rate = 0.01, totFeats)
```

Arguments

chr.pop	A matrix or a data.frame representing the chromosomes population: each column is a chromosome and each element correspond to the feature position in the data matrix
mut.rate	The probability to apply a random mutation to each element. It must be between 0 and 1. Default is 0.01
totFeats	The total number of features. Often, it corresponds to number of columns of the data matrix

Value

A matrix representing the "mutated" population. The dimensions of this matrix are the same of 'chr.pop'

**Author(s)**

Mattia Chiesa, Luca Piacentini

**See Also**

[GARS\\_Elitism](#), [GARS\\_Selection](#), [GARS\\_Crossover](#),

**Examples**

```
# use example data:
data(GARS_popul)
data(GARS_data_norm)

mutated_pop <- GARS_Mutation(GARS_popul, mut.rate=0.1,
  dim(GARS_data_norm)[2])
```

---

GARS\_PlotFeaturesUsage

*A bubble chart to assess the usage of each features*

---

**Description**

This function allows assessing visually how many times a feature is selected across the generations. In principle, a highly recurring feature is more likely to be important.

**Usage**

```
GARS_PlotFeaturesUsage(popul.list, allFeat, nFeat = length(allFeat))
```

**Arguments**

popul.list	A SummarizedExpression object
allFeat	A character vector containing the list of the all features name. Often, it corresponds to the columns name of the data matrix.
nFeat	The number of features which have to be plotted. Default is 'length(allFeat)'

**Value**

A bubble chart where each plotted feature is represented by a colored circle. A feature is important (i.e. conserved) if the size is wide and the color tends to red; the smaller the size, the lighter the color and less informative the feature.

**Author(s)**

Mattia Chiesa, Luca Piacentini

**See Also**[GARS\\_PlotFitnessEvolution](#)**Examples**

```
# use example data:
data(GARS_data_norm)
data(GARS_pop_list)
allfeat_names <- colnames(GARS_data_norm)
GARS_PlotFeaturesUsage(GARS_pop_list, allfeat_names, nFeat = 10)
```

---

`GARS_PlotFitnessEvolution`*Plot the maximum fitness scores for each generation*

---

**Description**

This function plots the maximum fitness scores for each generation

**Usage**

```
GARS_PlotFitnessEvolution(fitness.scores)
```

**Arguments**

`fitness.scores` A numeric vector where each element corresponds to the fitness score

**Value**

A plot which represent the evolution of the fitness score across the generations

**Author(s)**

Mattia Chiesa, Luca Piacentini

**See Also**[GARS\\_PlotFeaturesUsage](#)**Examples**

```
# use example data:
data(GARS_fit_list)
GARS_PlotFitnessEvolution(GARS_fit_list)
```

---

`GARS_popul`*RNA-seq dataset for testing GARS*

---

**Description**

A matrix to test several GARS functions, representing a chromosome population

**Usage**`GARS_popul`**Format**

A matrix of 20 rows (features) and 50 columns (chromosomes)

**Value**

An example data for testing GARS package

---

`GARS_pop_list`*RNA-seq dataset for testing GARS*

---

**Description**

A list containing 100 of consecutive chromosomes populations

**Usage**`GARS_pop_list`**Format**

A list with 100 consecutive chromosomes populations

**Value**

An example data for testing GARS package

---

GARS_res_GA	<i>A GarsSelectedFeatures object for testing GARS</i>
-------------	---

---

**Description**

An object representing the output of GARS\_GA

**Usage**

```
GARS_res_GA
```

**Format**

A GarsSelectedFeatures

**Value**

An example data for testing GARS package

---

GARS_Selection	<i>Perform the "Roulette Wheel" or the "Tournament" selection</i>
----------------	---

---

**Description**

This function implements two kind of GA Selection step: the "Roulette Wheel" and the "Tournament" selection.

**Usage**

```
GARS_Selection(chr.pop, type = c("RW", "TS"), fitn.values)
```

**Arguments**

<code>chr.pop</code>	A matrix or a data.frame representing the chromosomes population: each column is a chromosome and each element corresponds to the feature position in the data matrix
<code>type</code>	The type of selection method; Roulette Wheel ("RW") and Tournament Selection ("TS") are allowed. Default is "RW"
<code>fitn.values</code>	A numeric vector where each element corresponds to the fitness score of each chromosome in 'chr.pop'

**Value**

A matrix representing the "selected" population. The dimensions of this matrix are the same of 'chr.pop'.



**Author(s)**

Mattia Chiesa, Luca Piacentini

**See Also**

[GARS\\_Mutation](#), [GARS\\_Crossover](#), [GARS\\_Elitism](#),

**Examples**

```
# use example data:
data(GARS_popul)
data(GARS_Fitness_score)
selected_pop <- GARS_Selection(GARS_popul, "RW", GARS_Fitness_score)
```

---

LastPop

*Accessors for the 'LastPop' slot of a GarsSelectedFeatures object.*

---

**Description**

The LastPop slot contains the last chromosome population

**Usage**

```
LastPop(x)
```

```
## S4 method for signature 'GarsSelectedFeatures'
LastPop(x)
```

**Arguments**

x                      a GarsSelectedFeatures object

**Value**

a matrix containing the last population

**Author(s)**

Mattia Chiesa, Luca Piacentini

**Examples**

```
data(GARS_res_GA)
ex_pop <- LastPop(GARS_res_GA)
```

---

MatrixFeatures	<i>Accessors for the 'MatrixFeatures' slot of a GarsSelectedFeatures object.</i>
----------------	--

---

**Description**

The MatrixFeatures slot contains the reduced dataset

**Usage**

```
MatrixFeatures(x)
```

```
## S4 method for signature 'GarsSelectedFeatures'  
MatrixFeatures(x)
```

**Arguments**

x                      a GarsSelectedFeatures object

**Value**

a matrix with the reduced dataset

**Author(s)**

Mattia Chiesa, Luca Piacentini

**Examples**

```
data(GARS_res_GA)  
ex_matrix <- MatrixFeatures(GARS_res_GA)
```

# Index

## \* datasets

- GARS\_classes, [5](#)
- GARS\_data\_norm, [7](#)
- GARS\_fit\_list, [10](#)
- GARS\_Fitness\_score, [9](#)
- GARS\_pop\_list, [15](#)
- GARS\_popul, [15](#)
- GARS\_res\_GA, [16](#)

## \* package

- GARS, [4](#)

AllPop, [2](#), [4](#)

AllPop, GARS-AllPop (AllPop), [2](#)

AllPop, GarsSelectedFeatures-method  
(AllPop), [2](#)

FitScore, [3](#), [4](#)

FitScore, GARS-FitScore (FitScore), [3](#)

FitScore, GarsSelectedFeatures-method  
(FitScore), [3](#)

GARS, [4](#)

GARS-package (GARS), [4](#)

GARS\_classes, [5](#)

GARS\_create\_rnd\_population, [5](#), [9](#)

GARS\_Crossover, [6](#), [8](#), [13](#), [17](#)

GARS\_data\_norm, [7](#)

GARS\_Elitism, [7](#), [7](#), [13](#), [17](#)

GARS\_fit\_list, [10](#)

GARS\_FitFun, [8](#), [8](#)

GARS\_Fitness\_score, [9](#)

GARS\_GA, [4](#), [10](#)

GARS\_Mutation, [7](#), [8](#), [12](#), [17](#)

GARS\_PlotFeaturesUsage, [13](#), [14](#)

GARS\_PlotFitnessEvolution, [14](#), [14](#)

GARS\_pop\_list, [15](#)

GARS\_popul, [15](#)

GARS\_res\_GA, [16](#)

GARS\_Selection, [7](#), [8](#), [13](#), [16](#)

GarsSelectedFeatures-class, [4](#)

LastPop, [4](#), [17](#)

LastPop, GARS-LastPop (LastPop), [17](#)

LastPop, GarsSelectedFeatures-method  
(LastPop), [17](#)

MatrixFeatures, [4](#), [18](#)

MatrixFeatures, GARS-MatrixFeatures  
(MatrixFeatures), [18](#)

MatrixFeatures, GarsSelectedFeatures-method  
(MatrixFeatures), [18](#)