

Package ‘GARS’

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

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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.

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Encoding UTF-8

LazyData true

VignetteBuilder knitr

RoxygenNote 6.1.1

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Imports DaMiRseq, MLSeq, stats, methods, SummarizedExperiment

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

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

<code>data</code>	A SummarizedExperiment object or a matrix or a data.frame. In case of matrix or data.frame: • Rows and Cols have to be, respectively, observations and features. The variables are typically genes; • GARS also accept other -omic features as well as any continuous or factorial variables (e.g. sex, age, cholesterol level,...); • Usually the number of observation is « than the number of features ,
<code>chr.len</code>	The length of chromosomes. This value corresponds to the desired length of the feature set.
<code>chr.num</code>	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

*RNA-seq dataset for testing GARS***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

*Separate chromosome on the basis of the Fitness Scores***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

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
fitn.values	A numeric vector where each element corresponds to the fitness score of each chromosome in 'chr.pop'
n.elit	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	<i>This function implements the Fitness Function of GARS</i>
-------------	--

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	A SummarizedExperiment object or a matrix or a data.frame. In case of matrix or data.frame: • Rows and Cols have to be, respectively, observations and features. The variables are typically genes; • GARS also accept other -omic features as well as any continuous or factorial variables (e.g. sex, age, cholesterol level,...); • Usually the number of observation is « than the number of features
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

Description

This function allows the users to run all GARS function 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

data	A SummarizedExperiment object or a matrix or a data.frame. In case of matrix or data.frame: • Rows and Cols have to be, respectively, observations and features. The variables are typically genes; • GARS also accept other -omic features as well as any continuous or factorial variables (e.g. sex, age, cholesterol level,...); • Usually the number of observation is « than the number of features
classes	The class vector
chr.num	The number of chromosomes to generate. Default is 1000
chr.len	The length of chromosomes. This value corresponds to the desired length of the feature set
generation	The maximum number of generations. Default is 1000
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
mut.rate	The probability to apply a random mutation to each element. It must be between 0 and 1. Default is 0.01
n.elit	The number of best chromosomes to be selected by elitism. This number must be even. Default is 10
type.sel	The type of selection method; Roulette Wheel ("RW") and Tournament Selection ("TS") are allowed. Default is "RW"
type.co	The type of crossover method; one-point ("one.p") and two-point ("two.p") are allowed. Default is "one.p"
type.one.p.co	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"
n.gen.conv	The number of consecutive generations with the same maximum fitness score.
plots	If graphs have to be plotted; "yes" or "no" are allowed. Default is "yes"
n.Feat_plot	The number of features to be plotted
verbose	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

Perform the Mutation step

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

<code>chr.pop</code>	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
<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>totFeats</code>	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

<code>popul.list</code>	A SummarizedExpression object
<code>allFeat</code>	A character vector containing the list of the all features name. Often, it corresponds to the columns name of the data matrix.
<code>nFeat</code>	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	<i>RNA-seq dataset for testing GARS</i>
------------	---

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

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

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
type	The type of selection method; Roulette Wheel ("RW") and Tournament Selection ("TS") are allowed. Default is "RW"
fitn.values	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)
```

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