Package ‘ClusterSignificance’

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Title The ClusterSignificance package provides tools to assess if class clusters in dimensionality reduced data representations have a separation different from permuted data

Version 1.4.0

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Description The ClusterSignificance package provides tools to assess if class clusters in dimensionality reduced data representations have a separation different from permuted data. The term class clusters here refers to, clusters of points representing known classes in the data. This is particularly useful to determine if a subset of the variables, e.g. genes in a specific pathway, alone can separate samples into these established classes. ClusterSignificance accomplishes this by, projecting all points onto a one dimensional line. Cluster separations are then scored and the probability of the seen separation being due to chance is evaluated using a permutation method.

Depends R (>= 3.3.0)

Imports methods, pracma, princurve, scatterplot3d, RColorBrewer, grDevices, graphics, utils, stats

License GPL-3

LazyData true

Suggests knitr, rmarkdown, testthat, BiocStyle, ggplot2, plsgenomics

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biocViews Clustering, Classification, PrincipalComponent, StatisticalMethod

NeedsCompilation no


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The ClusterSignificance package provides tools to assess if clusters have a separation different from random or permuted data.

Description

The ClusterSignificance package provides tools to assess if clusters have a separation different from random or permuted data. ClusterSignificance investigates clusters of two or more groups by first, projecting all points onto a one dimensional line. Cluster separations are then scored and the probability of the seen separation being due to chance is evaluated using a permutation method.

Details

Package: ClusterSignificance
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Author(s)

Author: Jason T. Serviss, Jesper R. Gadin

References

Reference to published application note (work in progress)

Classification of the one dimensional points in a Pcp or Mlp object.

Description

Classification based on ROC params (TN TP FP FN).
## Usage

```r
## S4 method for signature 'ClassifiedPoints'
getData(x, n = NULL)

classify(x, ...)

## S4 method for signature 'Pcp'
classify(x, ...)

## S4 method for signature 'Mlp'
classify(x, ...)

## S4 method for signature 'ClassifiedPoints'
initialize(.Object, ..., scores,
  scores.points = scores.points, scores.index = scores.index, ROC, AUC,
  class.color)

## S4 method for signature 'ClassifiedPoints,missing'
plot(x, y, comparison = "all",
  class.color = NULL, ...)

## S4 method for signature 'ClassifiedPoints'
show(object)
```

### Arguments

- `x`: Pcp or Mlp Object for the function classify otherwise it is a ClassifiedPoints object
- `n`: data to extract from ClassifiedPoints (NULL gives all)
- `...`: additional arguments to pass on
- `.Object`: internal object
- `scores`: final scores
- `scores.points`: sorted points
- `scores.index`: index of sorted points
- `ROC`: parameters (TN, TP, FN and FP)
- `AUC`: area under the curve
- `class.color`: user assigned group coloring scheme
- `y`: default plot param, which should be set to NULL
- `comparison`: Specify a comparison i.e. ("grp1 vs grp2") and plot only that comparison.
- `object`: ClassifiedPoints Object

### Details

Tests all possible discrimination lines and picks the one with highest score based on a score which is simply calculated by the formula \((TP - FP) + (TN - FN)\).

The plot shows the distribution of scores for different discrimination lines. Each line is a separator that has a score for the separation of the two groups, and the height of the line marks the score for this separation.
Value

The classify function returns an object of class ClassifiedPoints

Author(s)

Jesper R. Gadin and Jason T. Serviss

Examples

```r
# use demo data
data(pcpMatrix)
classes <- rownames(pcpMatrix)

# run function
prj <- pcp(pcpMatrix, classes)
c1 <- classify(prj)

# getData accessor
gData(c1)

# getData accessor specific
gData(c1, "scores")

# plot result
plot(c1)
```

Mlp-class

Projection of points into one dimension.

Description

Project points onto the mean based line.

Usage

```r
## S4 method for signature 'Mlp'
getData(x, n = NULL)

## S4 method for signature 'Mlp'
initialize(.Object, ..., classes, points.orig, line,
          points.onedim, class.color)

## S4 method for signature 'Mlp,missing'
plot(x, y, steps = "all", ...)

mlp(mat, ...)

## S4 method for signature 'matrix'
mlp(mat, classes, class.color = NULL, ...)

## S4 method for signature 'Mlp'
show(object)
```
**Arguments**

- `x`: matrix object for the function `mlp` otherwise it is a `Mlp` object
- `n`: data to extract from `Mlp` (NULL gives all)
- `.Object`: internal object
- `...`: additional arguments to pass on
- `classes`: vector in same order as rows in matrix
- `points.orig`: multidimensional points describing the original data
- `line`: multidimensional points describing a line
- `points.onedim`: a vector of points
- `class.color`: user assigned group coloring scheme
- `y`: default plot param, which should be set to NULL (default: NULL)
- `steps`: 1, 2, 3, 4, 5, 6 or "all"
- `mat`: matrix with samples on rows, PCs in columns. Ordered PCs, with PC1 to the left.
- `object`: `Mlp` object

**Details**

Projection of the points onto a line between the mean of two groups. `Mlp` is the abbreviation for 'mean line projection'. The function accepts, at the moment, only two groups and two PCs at a time.

An object containing results from a mean line projection reduction to one dimension.

The group and the one dimensional points are the most important information to carry out a classification using the `classify()` function. As a help to illustrate the details of the dimension reduction, the information from some critical steps are stored in the object. To visually explore these there is a dedicated plot method for `Mlp` objects, use `plot()`.

**Value**

The `mlp` function returns an object of class `Mlp`

**Author(s)**

Jesper R. Gadin and Jason T. Serviss

**Examples**

```r
# use demo data
data(mlpMatrix)
groups <- rownames(mlpMatrix)

# run function
prj <- mlp(mlpMatrix, groups)

# getData accessor
data(prj)

# getData accessor specific
```
mlpMatrix

Simulated data used to demonstrate the Mlp method.

Description

Mlp demonstration matrix.

Usage

mlpMatrix

Format

Matrix

rownames Groups

colnames dimension number

Value

simulated matrix

Examples

mlpMatrix

Pcp-class

Projection of points into one dimension.

Description

Project points onto a principal curve.

Usage

getData(x, ...)

## S4 method for signature 'Pcp'
getData(x, n = NULL)

## S4 method for signature 'Pcp'
initialize(.Object, ..., classes, points.orig, line,
points.onedim, index, class.color)
## S4 method for signature 'Pcp,missing'
plot(x, y, steps = "all", class.color = NULL, ...)

pcp(mat, ...)

## S4 method for signature 'matrix'
pcp(mat, classes, df = NULL, class.color = NULL, ...)

## S4 method for signature 'Pcp'
show(object)

### Arguments

- **x**: matrix object for the function pcp otherwise it is a Pcp object
- **...**: additional arguments to pass on
- **n**: data to extract from Pcp (NULL gives all)
- **.Object**: internal object
- **classes**: vector in same order as rows in matrix
- **points.orig**: multidimensional points describing the original data
- **line**: multidimensional points describing a line
- **points.onedim**: a vector of points
- **index**: internal index from the projection
- **class.color**: user assigned group coloring scheme
- **y**: default plot param, which should be set to NULL
- **steps**: 1,2,3,4,5,6 or "all"
- **mat**: matrix with samples on rows, PCs in columns. Ordered PCs, with PC1 to the left.
- **df**: degrees of freedom, passed to smooth.spline
- **object**: Pcp object

### Details

The resulting Pcp object containing results from a principal curve reduction to one dimension. The group and the one dimensional points will be the information needed to carry out a classification using the classify() function. As a help to illustrate the details of the dimension reduction, the information from some critical steps is stored in the object. To visually explore these there is a dedicated plot method for Pcp objects, use plot().

### Value

The pcp function returns an object of class Pcp

### Author(s)

Jesper R. Gadin and Jason T. Serviss
Examples

```r
# use demo data
data(pcpMatrix)
classes <- rownames(pcpMatrix)

# run function
prj <- pcp(pcpMatrix, classes)

# getData accessor
getData(prj)

# getData accessor specific
getData(prj, "line")

# plot the result (if dim > 2, then plot in 3d)
plot(prj)

# plot the result (if dim=2, then plot in 2d)
prj2 <- pcp(pcpMatrix[,1:2], classes)
plot(prj2)
```

### pcpMatrix

Simulated data used to demonstrate the Pcp method.

**Description**

Pcp demonstration matrix.

**Usage**

pcpMatrix

**Format**

Matrix

- **rownames**: Groups
- **colnames**: dimension number

**Value**

simulated matrix

**Examples**

pcpMatrix
Description

Test how the classification performs compared to random (eg. permuted) data.

Usage

## S4 method for signature 'PermutationResults'
getData(x, n = NULL)

## S4 method for signature 'PermutationResults'
c(x, ..., recursive = FALSE)

pvalue(x, ...)

## S4 method for signature 'PermutationResults'
pvalue(x, ...)

conf.int(x, ...)

## S4 method for signature 'PermutationResults'
conf.int(x, conf.level = 0.99, ...)

## S4 method for signature 'PermutationResults'
initialize(.Object, ..., scores.real, scores.vec)

permute(mat, ...)

## S4 method for signature 'matrix'
permute(mat, classes, projmethod = "pcp", iter = 100,
    user.permutations = NULL, seed = 3, df = NULL, verbose = TRUE, ...)

## S4 method for signature 'PermutationResults,missing'
plot(x, y, comparison = "all", ...)

## S4 method for signature 'PermutationResults'
show(object)

Arguments

x          matrix for the function permute, otherwise it is a PermutationResults object
n          data to extract from ClassifiedPoints (NULL gives all)
...         arguments to pass on
recursive   dont use (belongs to default generic of combine 'c()')
conf.level  confidence level for the returned confidence interval
.Object     internal object
scores.real  the real score
scores.vec   all permuted scores
mat          matrix with samples on rows, PCs in columns. Ordered PCs, with PC1 to the left.
classes     vector in same order as rows in matrix
projmethod  'pcp' or 'mlp'
iter        integer number of iterations to be performed.
user.permutations user defined permutation matrix
seed        random seed to be used by the internal permutation
df          degrees of freedom, passed to smooth.spline
verbose     makes function more talkative
y            default plot param, which should be set to NULL
comparison  Specify a comparison i.e. ("grp1 vs grp2") and plot only that comparison.
object      ClassifiedPoints Object

Details

This is a test suit and will return a summarized object. The default of the parameter 'iter' is set quite low, and in principle the more iterations the better, or until the pvalue converges to a specific value. If no pre-permuted data has been supplied by the user, then the internal permutation method will perform a sampling without replacement within each dimension.

Value

The permute function returns an object of class PermutationResults

Author(s)

Jesper R. Gadin and Jason T. Serviss

Examples

#use pcp method
data(pcpMatrix)
classes <- rownames(pcpMatrix)

#run function
iterations <- 10
pe <- permute(
    mat=pcpMatrix,
    classes=classes,
    iter=iterations,
    projmethod="pcp"
)

#use mlp method
data(mlpMatrix)
classes <- rownames(mlpMatrix)
pe <- permute("pcp")
PermutationResults-class

```r
mat=mlpMatrix,
classes=classes,
iter=iterations,
projmethod="mlp"
)

#getData accessor
data(pe)

#getData accessor specific
data(pe, "scores.vec")

# get pvalue
pvalue(pe)

# plot result
plot(pe)

# combine three (parallel) jobs on the same matrix
pe2 <- c(pe, pe, pe)
```
Index

* Topic **classification**
  ClassifiedPoints-class, 2

* Topic **package**
  ClusterSignificance-package, 2

* Topic **permutation**
  PermutationResults-class, 9

* Topic **projection**
  Mlp-class, 4
  Pcp-class, 6
  ClassifiedPoints
    (ClassifiedPoints-class), 2
  Mlp (Mlp-class), 4
  Pcp (Pcp-class), 6
  PermutationResults
    (PermutationResults-class), 9

classified,PermutationResults-method
  (PermutationResults-class), 9

ClassifiedPoints
  (ClassifiedPoints-class), 2
ClassifiedPoints-class, 2
classify (ClassifiedPoints-class), 2
classify,Mlp-method
  (ClassifiedPoints-class), 2
classify,Pcp-method
  (ClassifiedPoints-class), 2
ClusterSignificance
  (ClusterSignificance-package), 2
ClusterSignificance-package, 2
conf.int (PermutationResults-class), 9
conf.int,PermutationResults-method
  (PermutationResults-class), 9

getData (Pcp-class), 6
data,ClassifiedPoints-method
  (ClassifiedPoints-class), 2
data,Mlp-method (Mlp-class), 4
data,Pcp-method (Pcp-class), 6
data,PermutationResults-method
  (PermutationResults-class), 9
initialize,ClassifiedPoints-method
  (ClassifiedPoints-class), 2
initialize,Mlp-method (Mlp-class), 4
initialize,Pcp-method (Pcp-class), 6
initialize,PermutationResults-method
  (PermutationResults-class), 9

Mlp (Mlp-class), 4
mlp (Mlp-class), 4
mlp,matrix-method (Mlp-class), 4
Mlp-class, 4
mlpMatrix, 6

Pcp (Pcp-class), 6
pcp (Pcp-class), 6
pcp,matrix-method (Pcp-class), 6
Pcp-class, 6
pcpMatrix, 8
PermutationResults-class, 9
permute (PermutationResults-class), 9
permute,matrix-method
  (PermutationResults-class), 9
plot,ClassifiedPoints,missing-method
  (ClassifiedPoints-class), 2
plot,Mlp,missing-method (Mlp-class), 4
plot,Pcp,missing-method (Pcp-class), 6
plot,PermutationResults,missing-method
  (PermutationResults-class), 9
pvalue (PermutationResults-class), 9
pvalue,PermutationResults-method
  (PermutationResults-class), 9

show,ClassifiedPoints-method
  (ClassifiedPoints-class), 2
show,Mlp-method (Mlp-class), 4
show,Pcp-method (Pcp-class), 6
show,PermutationResults-method
  (PermutationResults-class), 9