Package ‘ClusterSignificance’

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

Version  1.2.3

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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.

Depends  R (>= 3.3.0)

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

License  GPL-3

LazyData  true

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

VignetteBuilder  knitr

biocViews  Clustering, Classification, PrincipalComponent,
            StatisticalMethod

NeedsCompilation  no

Collate  'ClusterSignificance-package.R' 'All-classes.R'
         'classifier-methods.R' 'initialize-methods.R' 'mlpMatrix.R'
         'pcpMatrix.R' 'permutation-methods.R' 'plot-methods.R'
         'projection-methods.R' 'show-methods.R'

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R topics documented:

ClusterSignificance-package ........................................... 2
ClassifiedPoints-class ................................................ 2
Mlp-class ..................................................................... 4
mlpMatrix .................................................................... 6
The ClusterSignificance package provides tools to assess if clusters have a separation different from random or permuted data.

Details

Package: ClusterSignificance
Type: Package
Version: 1.0
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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.

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,
  group.color)

## S4 method for signature 'ClassifiedPoints,missing'
plot(x, y, comparison = "all",
  group.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)
- `group.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.
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)
groups <- rownames(pcpMatrix)

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

gdata accessor
gdata(cl)

gdata accessor specific
gdata(cl, "scores")

# plot result
plot(cl)
```

Mlp-class

Projection of points into one dimension.

Description

Project points onto the mean based line.

Usage

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

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

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

mlp(mat, ...)

## S4 method for signature 'matrix'
mlp(mat, groups, group.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
- **groups**: 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
- **group.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
```
getData(prj, "line")

#plot result
plot(prj)

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

pcp(mat, ...)

## S4 method for signature 'matrix'
pcp(mat, groups, df = NULL, group.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
- **groups**: 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
- **group.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)
groups <- rownames(pcpMatrix)

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

# getData accessor
data(prj)

# getData accessor specific
data(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], groups)
plot(prj2)
```

---

**Description**

Pcp demonstration matrix.

**Usage**

`pcpMatrix`

**Format**

Matrix

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

**Value**

simulated matrix

**Examples**

`pcpMatrix`
PermutationResults-class

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, ...)

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

permute(mat, ...)

## S4 method for signature 'matrix'
permute(mat, groups, 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()')
.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.
groups  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)
groups <- rownames(pcpMatrix)

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

#use mlp method
data(mlpMatrix)
groups <- rownames(mlpMatrix)
pe <- permute(
    mat=mlpMatrix,
    groups=groups,
    iter=iterations,
    projmethod="mlp"
)
PermutationResults-class

#getData accessor
ggetData(pe)

#getData accessor specific
ggetData(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

getData (Pcp-class), 6
ggetData (ClassifiedPoints-class), 2
ggetData, Mlp-method (Mlp-class), 4
ggetData, Pcp-method (Pcp-class), 6
ggetData, 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