

# 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** 1.37.0

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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)

**URL** <https://github.com/jasonserviss/ClusterSignificance/>

**BugReports** <https://github.com/jasonserviss/ClusterSignificance/issues>

**Imports** methods, pracma, princurve (>= 2.0.5), scatterplot3d, RColorBrewer, grDevices, graphics, utils, stats

**License** GPL-3

**LazyData** true

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

**VignetteBuilder** knitr

**biocViews** Clustering, Classification, PrincipalComponent, StatisticalMethod

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

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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.

**Details**

Package: ClusterSignificance  
Type: Package  
Version: 1.0  
Date: 2016-02-28  
License: GPL-3

**Author(s)**

Author: Jason T. Serviss, Jesper R. Gadin

**References**

Reference to published application note (work in progress)

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ClassifiedPoints-class

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

---

**Description**

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

**Usage**

```
## 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**

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

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

#getData accessor
getData(cl)

#getData accessor specific
getData(cl, "scores")

#plot result
plot(cl)
```

---

Mlp-class

*Projection of points into one dimension.*


---

**Description**

Project points onto the mean based line.

**Usage**

```
## 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

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

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

#getData accessor
getData(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, ..., 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, warn = TRUE,
  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                                     |

|        |                                                                                                               |
|--------|---------------------------------------------------------------------------------------------------------------|
| warn   | logical indicating if a change in the default df argument should generate a warning. mostly for internal use. |
| 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

```
#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

---

PermutationResults-class*Permutation test*

---

**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

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

#getData accessor
getData(pe)

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

#get pvalue
pvalue(pe)

#plot result
plot(pe)

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

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