Package ‘RepeatedHighDim’

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Type Package

Title Global tests for expression data of high-dimensional sets of molecular features.

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Description Global tests for expression data of high-dimensional sets of molecular features.

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RepeatedHighDim-package

Global tests for expression data of high-dimensional sets of molecular features.

Description

Global tests for expression data of high-dimensional sets of molecular features.

Details

Package:	RepeatedHighDim
Type:	Package
Version:	2.0.0
Date:	2013-08-21
License:	GPL (>= 2)
LazyLoad:	yes

Global tests for expression data of high-dimensional sets of molecular features.

Author(s)

Klaus Jung <Klaus.Jung@ams.med.uni-goettingen.de>

Examples

```
### Global comparison of a set of 100 genes between two experimental groups.
X1 = matrix(rnorm(1000, 0, 1), 10, 100)
X2 = matrix(rnorm(1000, 0.1, 1), 10, 100)
RHD = RepeatedHighDim(X1, X2, paired=FALSE)
summary(RHD)

### Global comparison of a set of 100 proteins between two experimental groups,
### where (tau * 100) percent of expression levels are missing.
n1 = 10
n2 = 10
d = 100
tau = 0.1
X1 = t(matrix(rnorm(n1*d, 0, 1), n1, d))
X2 = t(matrix(rnorm(n2*d, 0.1, 1), n2, d))
X1[sample(1:(n1*d), tau * (n1*d))] = NA
X2[sample(1:(n2*d), tau * (n2*d))] = NA
GlobTestMissing(X1, X2, nperm=100)
```

GlobTestMissing *Detection of global group effect*

Description

Tests a global effect for a set of molecular features (e.g. genes, proteins,...) between the two groups of samples. Missing values are allowd in the expression data. Samples of the two groups are supposed to be unpaired.

Usage

```
GlobTestMissing(X1, X2, nperm = 100)
```

Arguments

X1	Matrix of expression levels in first group. Rows represent features, columns represent samples.
X2	Matrix of expression levels in second group. Rows represent features, columns represent samples.
nperm	Number of permutations.

Value

The p-value of a permutation test.

Author(s)

Klaus Jung <Klaus.Jung@ams.med.uni-goettingen.de>

Examples

```
### Global comparison of a set of 100 proteins between two experimental groups,
### where (tau * 100) percent of expression levels are missing.
n1 = 10
n2 = 10
d = 100
tau = 0.1
X1 = t(matrix(rnorm(n1*d, 0, 1), n1, d))
X2 = t(matrix(rnorm(n2*d, 0.1, 1), n2, d))
X1[sample(1:(n1*d), tau * (n1*d))] = NA
X2[sample(1:(n2*d), tau * (n2*d))] = NA
GlobTestMissing(X1, X2, nperm=100)
```

RepeatedHighDim *Detection of global group effect*

Description

Global test for a set of molecular features (e.g. genes, proteins,...) between two experimental groups. Paired or unpaired design is allowed.

Usage

```
RepeatedHighDim(X1, X2, paired = TRUE)
```

Arguments

X1	Matrix of expression levels in first group. Rows represent features, columns represent samples.
X2	Matrix of expression levels in second group. Rows represent features, columns represent samples.
paired	FALSE if samples are unpaired, TRUE if samples are paired.

Value

An object that contains the test results. Contents can be displayed by the summary function.

Author(s)

Klaus Jung <Klaus.Jung@ams.med.uni-goettingen.de>

References

- Brunner, E (2009) Repeated measures under non-sphericity. Proceedings of the 6th St. Petersburg Workshop on Simulation, 605-609.
- Jung K, Becker B, Brunner B and Beissbarth T (2011) Comparison of Global Tests for Functional Gene Sets in Two-Group Designs and Selection of Potentially Effect-causing Genes. Bioinformatics, 27: 1377-1383.

Examples

```
### Global comparison of a set of 100 genes between two experimental groups.
X1 = matrix(rnorm(1000, 0, 1), 10, 100)
X2 = matrix(rnorm(1000, 0.1, 1), 10, 100)
RHD = RepeatedHighDim(X1, X2, paired=FALSE)
summary(RHD)
```

`summary.RHD` *Summary of RepeatedHighDim function*

Description

Summarizes the test results obtained by the RepeatedHighDim function.

Usage

```
 ## S3 method for class 'RHD'
summary(object, ...)
```

Arguments

`object`	An object provided by the RepeatedHighDim function.
`...`	additional arguments affecting the summary produced.

Value

No value

Author(s)

Klaus Jung <Klaus.Jung@ams.med.uni-goettingen.de>

References

- Brunner, E (2009) Repeated measures under non-sphericity. Proceedings of the 6th St. Petersburg Workshop on Simulation, 605-609.
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Examples

```
### Global comparison of a set of 100 genes between two experimental groups.
X1 = matrix(rnorm(1000, 0, 1), 10, 100)
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RHD = RepeatedHighDim(X1, X2, paired=FALSE)
summary(RHD)
```

`TestStatSimple` *Calculation of test statistic*

Description

Calculates the test statistic for RepeatedHighDim in the case of paired samples.

Usage

```
TestStatSimple(Y, H)
```

Arguments

`Y`	Matrix with differences of paires. Rows represent features (e.g. genes, proteins,...), columns represent samples.
`H`	Hypothesis matrix.

Value

A list containing the following items:

`k`	Indicates whether the paired or unpaired case was tested.
`d`	Number of features.
`n1`	Number of samples in group 1.
`n2`	Number of samples in group 2.
`Fn`	Test statistic.
`f`	First degree of freedoms.
`f2`	Second degree of freedom.
`p`	p-value.

Author(s)

Klaus Jung <`Klaus.Jung@ams.med.uni-goettingen.de`>

References

- Brunner, E (2009) Repeated measures under non-sphericity. Proceedings of the 6th St. Petersburg Workshop on Simulation, 605-609.
- Jung K, Becker B, Brunner B and Beissbarth T (2011) Comparison of Global Tests for Functional Gene Sets in Two-Group Designs and Selection of Potentially Effect-causing Genes. Bioinformatics, 27: 1377-1383.

Examples

```
### Global comparison of a set of 100 genes between two experimental groups.
X1 = matrix(rnorm(1000, 0, 1), 10, 100)
X2 = matrix(rnorm(1000, 0.1, 1), 10, 100)
RHD = RepeatedHighDim(X1, X2, paired=FALSE)
summary(RHD)
```

`TestStatSP` *Calculation of test statistic*

Description

Calculates the test statistic for RepeatedHighDim in the case of unpaired samples.

Usage

```
TestStatSP(Y1, Y2)
```

Arguments

`Y1`	Matrix of expression levels in first group. Rows represent features (e.g. genes, proteins,...), columns represent samples.
`Y2`	Matrix of expression levels in second group. Rows represent features (e.g. genes, proteins,...), columns represent samples.

Value

A list containing the following items:

`k`	Indicates whether the paired or unpaired case was tested.
`d`	Number of features.
`n1`	Number of samples in group 1.
`n2`	Number of samples in group 2.
`Fn`	Test statistic.
`f`	First degree of freedoms.
`f2`	Second degree of freedom.
`p`	p-value.

Author(s)

Klaus Jung `<Klaus.Jung@ams.med.uni-goettingen.de>`

References

- Brunner, E (2009) Repeated measures under non-sphericity. Proceedings of the 6th St. Petersburg Workshop on Simulation, 605-609.
- Jung K, Becker B, Brunner B and Beissbarth T (2011) Comparison of Global Tests for Functional Gene Sets in Two-Group Designs and Selection of Potentially Effect-causing Genes. Bioinformatics, 27: 1377-1383.

Examples

```
### Global comparison of a set of 100 genes between two experimental groups.
X1 = matrix(rnorm(1000, 0, 1), 10, 100)
X2 = matrix(rnorm(1000, 0.1, 1), 10, 100)
RHD = RepeatedHighDim(X1, X2, paired=FALSE)
summary(RHD)
```

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