Package ‘RepeatedHighDim’

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Type Package

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

Version 2.0.0

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

Depends MASS, nlme

License GPL-2

Collate 'RepeatedHighDim.R'

NeedsCompilation no

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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)
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 allowed in the expression data. Samples of the two groups are supposed to be unpaired.

Usage
GlobTestMissing(x1, x2, nperm = 100)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>x1</td>
<td>Matrix of expression levels in first group. Rows represent features, columns represent samples.</td>
</tr>
<tr>
<td>x2</td>
<td>Matrix of expression levels in second group. Rows represent features, columns represent samples.</td>
</tr>
<tr>
<td>nperm</td>
<td>Number of permutations.</td>
</tr>
</tbody>
</table>

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.
```r
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**

```r
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**


**Examples**

```r
### 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 of RepeatedHighDim function

Description

Summarizes the test results obtained by the RepeatedHighDim function.

Usage

```r
## 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


Examples

```r
### 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)
```
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 pairs. 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.
F_n  Test statistic.
f  First degree of freedoms.
f_2  Second degree of freedom.
p  p-value.

Author(s)

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

References

Examples

```r
### 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)
```

### 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


Examples

```r
### 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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