Package ‘degenes’

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Type Package

Title Detection of differentially expressed genes.

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Description Detection of differentially expressed genes between two distinct groups of samples.

License GPL-2

LazyLoad yes

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Description

Detects differentially expressed genes between two distinct groups of samples.

Details
**Author(s)**

Klaus Jung

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

**References**


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**deg**  

*Detection of differentially expressed genes.*

**Description**

Detects differentially expressed genes between two distinct groups of samples.

**Usage**

`deg(treatment, control, alpha = 0.05)`

**Arguments**

- `treatment`  
  Matrix of normalized expression levels in the first group. Rows represent genes, columns represent samples.

- `control`  
  Matrix of normalized expression levels in the second group. Rows represent genes, columns represent samples.

- `alpha`  
  Global significance level.

**Details**

The function controls the FWER at the specified alpha-level.

**Value**

A vector with the row numbers of the genes detected as differentially expressed.
Author(s)
Klaus Jung

References

Examples
X1 = matrix(rnorm(2000, 0, 1), 200, 10)
X2 = matrix(rnorm(2000, 0, 1), 200, 10)
index = sample(1:200, 5, replace=FALSE)
X2[index,] = X2[index,] + 5
D = deg(X1, X2)
PD = pdeg(X1, X2)
PDa = p.adjust(PD, method="bonferroni")
sort(index)
D
which(PDa<0.05)
which(PD<0.05)

kern
Kernel density estimation.

Description
Determines the density of the test statistics by kernel estimation.

pdeg
Detection of differentially expressed genes.

Description
Calculated gene-specific unadjusted p-values for the comparison of samples from two distinct groups.

Usage
pdeg(treatment, control, alpha = 0.05)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>treatment</td>
<td>Matrix of normalized expression levels in the first group. Rows represent genes, columns represent samples.</td>
</tr>
<tr>
<td>control</td>
<td>Matrix of normalized expression levels in the second group. Rows represent genes, columns represent samples.</td>
</tr>
<tr>
<td>alpha</td>
<td>Global significance level.</td>
</tr>
</tbody>
</table>
Value

A vector with the gene-specific unadjusted p-values.

Author(s)

Klaus Jung

References


Examples

```r
X1 = matrix(rnorm(2000, 0, 1), 200, 10)
X2 = matrix(rnorm(2000, 0, 1), 200, 10)
index = sample(1:200, 5, replace=FALSE)
X2[index,] = X2[index,] + 5
D = deg(X1, X2)
PD = pdeg(X1, X2)
PDa = p.adjust(PD, method="bonferroni")
sort(index)
D
which(PDa<0.05)
which(PD<0.05)
```

*z.b* Calculation of test statistic.

Description

Calculates test statistics for the functions 'deg' and 'pdeg'.

*z.s* Calculation of test statistic.

Description

Calculates test statistics for the functions 'deg' and 'pdeg'.
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