Package ‘Mulcom’

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Description Identification of differentially expressed genes and false discovery rate (FDR) calculation by Multiple Comparison test
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NeedsCompilation yes

R topics documented:

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AffyIlmn
cross mapping table

Description
cross mapping table

Author(s)
Claudio Isella, <claudio.isella@ircc.it>

Affy Ilmn
cross mapping table

Description
cross mapping table

Author(s)
Claudio Isella, <claudio.isella@ircc.it>
**Description**

Computes harmonic means across groups replicate. Should not be called directly.

**Usage**

```r
harmonicMean(index)
```

**Arguments**

- `index` a numeric vector with the groups labels of the samples. 0 are the control samples. Number must be progressive.

**Details**

`harmonicMean` calculates harmonic means across groups replicate for the estimation of Mulcom Test.

**Value**

a numeric vector.

**Author(s)**

Claudio Isella, <claudio.isella@ircc.it>

**References**

<claudio.isella@ircc.it>
**Ilmn**

*Ilmn Dataset*

**Description**

Ilmn Dataset

**Author(s)**

Claudio Isella, <claudio.isella@ircc.it>

**limmaAffySymbols**

*significant gene list with limma in Affymetrix*

**Description**

significant gene list with limma in Affymetrix

**Author(s)**

Claudio Isella, <claudio.isella@ircc.it>

**limmaIlmnSymbols**

*significant gene list with limma in Illumina*

**Description**

significant gene list with limma in Illumina

**Author(s)**

Claudio Isella, <claudio.isella@ircc.it>
mulCalc  

### Description
Calculates MulCom test score for given m and t parameters

### Usage
```r
mulCalc(Mulcom_P, m, t)
```

### Arguments
- **Mulcom_P**: an object of class MULCOM
- **m**: a numeric value corresponding to log 2 ratio correction for MulCom Test
- **t**: a numeric value corresponding to T values for MulCom Test

### Details
- mulCalc Calculate the Mulcom Score with m and t defined by the user
- **Mulcom_P**: an object of class MULCOM_P
- **m**: a number corresponding to log 2 ratio correction for MulCom Test
- **t**: a number corresponding to T values for MulCom Test

### Author(s)
Claudio Isella, <claudio.isella@ircc.it>

### Examples
```r
data(benchVign)
mulcom_scores <- mulScores(Affy, Affy$Groups)
mulcom_calc <- mulCalc(mulcom_scores, 0.2, 2)
```

---

mulCAND  

### Description
Identify the Mulcom candidate feature selection by the m and T defined by the user

### Usage
```r
mulCAND(eset, Mulcom_P, m, t, ese = "T")
```
Arguments

eset an AffyBatch
Mulcom_P an object of class MULCOM
m m: a numeric vector corresponding to log 2 ratio correction
t t: a numeric vector corresponding to the MulCom T values
ese True or False

Details

mulCAND Identify the Mulcom candidate feature selection by the m and T defined by the user

Author(s)

Claudio Isella, <claudio.isella@ircc.it>

Examples

data(benchVign)
mulcom_perm <- mulPerm(Affy, Affy$Groups, 10, 2)
mulcom_cand <- mulCAND(Affy, mulcom_perm, 0.2, 2)

MULCOM-class Class MulCom

Description

This is a class representation MulCom test scores

Objects from the Class

Objects can be created using the function mulScores on ExpressionSet.

Slots

FC: Object of class numeric representing difference between all experimental groups and the reference groups
HM: Object of class numeric representing the harmonic means in all subgroups
MSE_Corrected: Object of class numeric representing the MulCom test estimation of mean square error as described in the formula of the Dunnett’s t-test

Author(s)

Claudio Isella

Examples

data(benchVign)
mulcom_scores <- mulScores(Affy, Affy$Groups)
mulcomGeneListIlmn

Description

significant gene list with limma in Illumina

Author(s)

Claudio Isella, <claudio.isella@ircc.it>

MULCOM_P-class

Class MulCom Permutation

Description

This is a class representation MulCom test scores permutation

Objects from the Class

Objects can be created using the function `mulScores` on ExpressionSet.

Slots

FC: Object of class numeric representing delta between all experimental groups and the reference groups

MSE_Corrected: Object of class numeric representing the MulCom test estimation of mean square error as described in the formula of the Dunnett's t-test

FCp: Object of class numeric representing delta between all experimental groups and the reference groups in permutated data

MSE_Correctedp: Object of class numeric representing the MulCom test estimation of mean square error as described in the formula of the Dunnett's t-test in permutated data

Author(s)

Claudio Isella

Examples

data(benchVign)
mulcom_scores <- mulScores(Affy, Affy$Groups)
mulDELTA  MulCom Delta

Description
Computes Delta for all the experimental points in the datasets in respect to control Should not be called directly

Usage
mulDELTA(vector, index)

Arguments
vector  vector: numeric vector with data measurements
index   a numeric vector with the labels of the samples. 0 are the control samples. number must be progressive

Details
mulDELTA An internal function that should not be called directly. It calculates differential expression in the groups defined in the index class vector, in respect to the 0 groups

Value
vector  a numeric vector with data measurements
index   a numeric vector with the labels of the samples. 0 are the control samples. number must be progressive

Author(s)
Claudio Isella, <claudio.isella@ircc.it>

Examples
data(benchVign)
mulcom_delta <- mulDELTA(exprs(Affy[,1]),Affy$Groups)

mulDiff  MulCom Test Differential analysis

Description
Identify the differentially expressed features for a specific comparison with given m and t value

Usage
mulDiff(eset, Mulcom_P, m, t, ind)
mulFSG

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>eset</td>
<td>An ExpressionSet object from package affy</td>
</tr>
<tr>
<td>Mulcom_P</td>
<td>An object of class Mulcom_P</td>
</tr>
<tr>
<td>m</td>
<td>the m values for the analysis</td>
</tr>
<tr>
<td>t</td>
<td>the t values for the analysis</td>
</tr>
<tr>
<td>ind</td>
<td>and index referring to the comparison, should be numeric</td>
</tr>
</tbody>
</table>

Value

<table>
<thead>
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<th>Argument</th>
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</tr>
</thead>
<tbody>
<tr>
<td>eset</td>
<td>An ExpressionSet object from package affy</td>
</tr>
<tr>
<td>Mulcom_P</td>
<td>An object of class Mulcom_P</td>
</tr>
<tr>
<td>m</td>
<td>the m values for the analysis</td>
</tr>
<tr>
<td>t</td>
<td>the t values for the analysis</td>
</tr>
<tr>
<td>ind</td>
<td>and index referring to the comparison, should be numeric</td>
</tr>
</tbody>
</table>

Author(s)

Claudio Isella, <claudio.isella@ircc.it>

Examples

data(benchVign)
mulcom_perm <- mulPerm(Affy, Affy$Groups, 10, 7)
mulcom_diff <- mulDiff(Affy, mulcom_perm, 0.2, 2)

mulFSG(Mulcom_P, m, t)

Description

Calculate the False Significant Genes for m and t defined by the user

Usage

mulFSG(Mulcom_P, m, t)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mulcom_P</td>
<td>an object of class MULCOM</td>
</tr>
<tr>
<td>m</td>
<td>m: a numeric value corresponding to log 2 ratio correction for MulCom Test</td>
</tr>
<tr>
<td>t</td>
<td>t: a numeric value corresponding to t values for MulCom Test</td>
</tr>
</tbody>
</table>

Details

mulFDR evaluate the False Significant genes on the Mulcom_P object according to specific m and t parameters. For each permutation it is calculated the number of positive genes. An estimation of the false called genes is evaluated with the median for each experimental subgroups.
mulIndex

Author(s)
Claudio Isella, <claudio.isella@ircc.it>

Examples
data(benchVign)
mulcom_perm <- mulPerm(Affy, Affy$Groups, 10, 7)
mulcom_fsg <- mulFSG(mulcom_perm, 0.2, 2)

mulIndex

Mulcom Index for Monte Carlo Simulation

Description
Random assembly of the groups indices for Monte Carlo Simulation

Usage
mulIndex(index, np, seed)

Arguments
index the vector with the groups of analysis, must be numeric and 0 correspond to the reference.
np number of permutation in the simulation
seed seed for permutations

Details
'mulIndex' generates random index for the function mulPerm, it is not directly called by the user.

Value
A matrix with all indices permutations

Author(s)
Claudio Isella, <claudio.isella@ircc.it>

Examples
data(benchVign)
mulcom_scores <- mulIndex(Affy$Groups, 5, 7)
**mulInt**

*generates a consensus matrix from list of genes*

---

**Description**

generates a consensus matrix from list of genes

**Usage**

mulInt(...)

**Arguments**

...  
the function requires vector files as inputs

**Details**

mulCAND generates a consensus matrix from list of genes

**Author(s)**

Claudio Isella, <claudio.isella@ircc.it>

**Examples**

data(benchVign)
mulcom_perm <- mulPerm(Affy, Affy$Groups, 10,2)
mulcom_opt <- mulOpt(mulcom_perm, vm = seq(0,0.5, 0.1), vt = seq(1,3, 0.1))

h1_opt <- mulParOpt(mulcom_perm, mulcom_opt, ind = 1, th = 0.05)
h2_opt <- mulParOpt(mulcom_perm, mulcom_opt, ind = 1, th = 0.05)

int <- mulInt(h1_opt, h2_opt)

---

**mulMSE**

*MulCom Mean Square Error*

---

**Description**

Computes Mean Square Error for all the experimental points in the datasets in respect to control
Should not be called directly

**Usage**

mulMSE(vector, index, tmp = vector())
mulOpt

Arguments

vector a numeric vector with data measurements
index a numeric vector with the labels of the samples. 0 are the control samples.
    number must be progressive
tmp a vector

Details

mulMSE An internal function that should not be called directly. It calculates within group means
square error for the values defined in the x vector according to the index class vector

Value

vector a numeric vector with data measurements
index a numeric vector with the labels of the samples. 0 are the control samples.
    number must be progressive
tmp a vector

Author(s)

Claudio Isella, <claudio.isella@ircc.it>

---

mulOpt MulCom optimization

Description

The function systematically performs the calculation of significant genes and corresponding FDR
for all the combination of given list of m and t values.

Usage

mulOpt(Mulcom_P, vm, vt)

Arguments

Mulcom_P an object of class Mulcom_P
vm a vector of m values to test
vt a vector of t values to test

Details

mulOpt The function systematically performs the calculation of significant genes and corresponding
FDR for all the combination of given list of m and t values.

Author(s)

Claudio Isella, <claudio.isella@ircc.it>
Examples

```r
data(benchVign)
mulcom_perm <- mulPerm(Affy, Affy$Groups, 10, 7)
mulcom_opt <- mulOpt(mulcom_perm, seq(0.1, 0.5, 0.1), seq(1, 3, 0.1))
```

mulOptPars  

| mulOptPars | MulCom Parameter Optimization |

Description

Function to optimize Mulcom parameter for maximim nuber of genes with a user defined FDR

Usage

```r
mulOptPars(opt, ind, ths)
```

Arguments

<table>
<thead>
<tr>
<th>opt</th>
<th>an MulCom optimization object</th>
</tr>
</thead>
<tbody>
<tr>
<td>ind</td>
<td>index corresponding to the comparison</td>
</tr>
<tr>
<td>ths</td>
<td>a threshold for the FDR optimization, default is 0.05</td>
</tr>
</tbody>
</table>

Details

mulOptPars MulCom optimization function to identify best parameters

Author(s)

Claudio Isella, <claudio.isella@ircc.it>

Examples

```r
data(benchVign)
mulcom_perm <- mulPerm(Affy, Affy$Groups, 10, 7)
#mulcom_opt <- mulOpt(mulcom_perm, seq(0.1, 0.5, 0.1), seq(1, 3, 0.1))
#optThs <- mulOptPars(mulcom_opt, 1, 0.05)
```

mulOptPlot  

| mulOptPlot | MulCom optimization Plot |

Description

MulCom optimization Plot to identify best configuration paramters

Usage

```r
mulOptPlot(M.Opt, ind, th, smooth = "NO")
```
mulParOpt

MulCom Parameters Optimization

Description

MulCom parameter optimization function to identify best combination of t and m providing maximum number of genes at a given FDR

Usage

mulParOpt(perm, M.Opt, ind, th, image = "T")

Arguments

perm a object with permutated MulCom Scores
M.Opt an MulCom optimization object
ind index corresponding to the comparison to plot
th a threshold for the FDR plot
image default = "T", indicates is print the MulCom optimization plot
**mulPerm**

**Details**

`mulParOpt` The function `mulParOpt` is designed to identify the optimal m and t values combination leading to the maximum number of differentially regulated genes satisfying an user define FDR threshold. In case of equal number of genes, the combination of m and t with the lower FDR will be prioritized. In case of both identical number of genes and FDR, the function will chose the highest t. The function optionally will define a graphical output to visually inspect the performance of the test at given m and t parameters for a certain comparison.

**Author(s)**

Claudio Isella, <claudio.isella@ircc.it>

**Examples**

```r
data(benchVign)
mulcom_perm <- mulPerm(Affy, Affy$Groups, 10,2)
mulcom_opt <- mulOpt(mulcom_perm, vm=seq(0.1, 0.5, 0.1), vt=seq(1, 3,1))
mulParOpt(mulcom_perm, mulcom_opt, 1, 0.05)
```

---

**mulPerm**  *MulCom Permutation*

**Description**

Reiterate MulCom Test on permutated data to perform Montecarlo simulation

**Usage**

```r
mulPerm(eset, index, np, seed, segm = "F")
```

**Arguments**

- `eset` An an `AffyBatch` object, each row of must correspond to a variable and each column to a sample.
- `index` a numeric vector of length ncol(data) with the labels of the samples. 0 are the reference samples.
- `np` a numeric values indicating the number of permutation to perform. It is set as default to 10
- `seed` set the seed of the permutaton, default is 1
- `segm` a default set to F. This parametheres requires to be setted to avoid segmentation fault of C subroutin in the case of very large datasets.

**Details**

`mulPerm`

**Author(s)**

Claudio Isella, <claudio.isella@ircc.it>
mulPermC

MulCom Permutation

Description

R pipe to C function not called directly by user that reiterate MulCom Test on permutated data to perform Monte Carlo simulation

Usage

mulPermC(eset, index, means, mse, n, m, nump, ngroups, reference)

Arguments

eset An an AffyBatch object, each row of must correspond to a variable and each column to a sample.
index a numeric vector of length ncol(data) with the labels of the samples. 0 are the reference samples.
means entry for the means output.
mse entry for the mean square errors output
n number of rows in obext of class eset
m number of columns
nump number of permutation to perform
ngroups a number corresponding to the number of groups in the analysis.
reference reference for the comparisons. typically it is 0

Details

mulPerm

Author(s)

Claudio Isella, <claudio.isella@ircc.it>

Examples

data(benchVign)
mulScores

MulCom Score Calculation

Description
Computes the scores for the MulCom test. The function calculates the numerator and the denominator of the test without the parameters \( m \) and \( t \).

Usage
mulScores(eset, index)

Arguments
- **eset**: An an AffyBatch object, each row of must correspond to a variable and each column to a sample.
- **index**: A numeric vector of length `ncol(data)` with the labels of the samples. 0 are the reference samples.

Details
'mulScore' computes the scores for the MulCom test for multiple point profile. The Mulcom test is designed to compare each experimental mean with the control mean and it is derived from the "Dunnett’s test". Dunnett’s test controls the Experiment-wise Error Rate and is more powerful than tests designed to compare each mean with each other mean. The test is conducted by computing a modified t-test between each experimental group and the control group.

Value
An Object of class MULCOM from Mulcom package

Author(s)
Claudio Isella, <claudio.isella@ircc.it>

Examples
```
data(benchVign)
mulcom_scores <- mulScores(Affy, Affy$Groups)
```

mulSSE

MulCom Sum of Square Error

Description
Computes sum of square errors for all the experimental points in the datasets Should not be called directly.

Usage
mulSSE(vec, index)
Arguments

- **vec**: a numeric vector with data measurements
- **index**: a numeric vector with the labels of the samples. 0 are the control samples. number should be progressive

Details

**mulSSE**: An internal function that should not be called directly. It calculates sum of square error in the groups defined in the index class vector.

Value

- **vec**: a numeric vector with data measurements
- **index**: a numeric vector with the labels of the samples. 0 are the control samples. number must be progressive

Author(s)

Claudio Isella, <claudio.isella@ircc.it>

---

**samAffySymbols**: significant gene list with SAM in Affymetrix

Description

significant gene list with SAM in Affymetrix

Author(s)

Claudio Isella, <claudio.isella@ircc.it>

---

**samIlmnSymbols**: significant gene list with SAM in Illumina

Description

significant gene list with SAM in Illumina

Author(s)

Claudio Isella, <claudio.isella@ircc.it>
samOptPars

samOptPars

sam Parameter Optimization

Description

Function to optimize Sam parameter for maximum number of genes with a user-defined FDR.

Usage

```
samOptPars(opt, ths)
```

Arguments

- `opt` an `sam` optimization object
- `ths` a threshold for the FDR optimization

Value

a numeric vector

Author(s)

Claudio Isella, `<claudio.isella@ircc.it>`
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