Package ‘Mulcom’

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R topics documented:

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Description

Affy Dataset

Author(s)

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

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AffyIlmn  cross mapping table

Description

cross mapping table

Author(s)

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

**Description**

Computes harmonic means across groups replicate Should not be called directly

**Usage**

```
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>

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### Illumina

**Description**

Illumina Dataset

**Author(s)**

Claudio Isella, <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**

*MulCom Calculation*

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

**Usage**
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

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

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

**mulCAND**

*Identify the Mulcom candidate feature selection*

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

**Usage**
mulCAND(eset, Mulcom_P, m, t, ese = "T")
**Arguments**

- `eset`: an `AffyBatch`  
- `Mulcom_P`: an object of class MULCOM  
- `m`: a numeric vector corresponding to log 2 ratio correction  
- `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**

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

---

**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**

```r
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**

```r
mulDELTA(vector, index)
```

**Arguments**

- `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**

```r
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**

```r
mulDiff(eset, Mulcom_P, m, t, ind)
```
**mulFSG**

### Arguments

- `eset` An ExpressionSet object from package affy
- `Mulcom_P` An object of class Mulcom_P
- `m` the m values for the analysis
- `t` the t values for the analysis
- `ind` and index referring to the comparison, should be numeric

### Value

- `eset` An ExpressionSet object from package affy
- `Mulcom_P` An object of class Mulcom_P
- `m` the m values for the analysis
- `t` the t values for the analysis
- `ind` and index referring to the comparison, should be numeric

### Author(s)

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

### Examples

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

---

**mulFSG**  
**MulCom False Significant Genes**

### Description

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

### Usage

```r
mulFSG(Mulcom_P, m, t)
```

### Arguments

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

### 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**

```r
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>
### mulOptPars

**MulCom Parameter Optimization**

**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))
```

**Description**

Function to optimize Mulcom parameter for maximum number of genes with a user defined FDR

**Usage**

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

**Arguments**

- `opt`: an MulCom optimization object
- `ind`: index corresponding to the comparison
- `ths`: a threshold for the FDR optimization, default is 0.05

**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

**MulCom optimization Plot**

**Description**

MulCom optimization Plot to identify best configuration parameters

**Usage**

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

**Arguments**

- **M.Opt**: an MulCom optimization object
- **ind**: index corresponding to the comparison to plot
- **th**: a threshold for the FDR plot
- **smooth**: indicates whether the FDR plot will show a significant threshold or will be continuous.

**Details**

`mulOptPlot MulCom optimization Plot`

**Value**

- a numeric vector

**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))
mulOptPlot(mulcom_opt, 1, 0.05)
```

---

**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**

```r
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
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

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

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 paramatheres 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>
Examples

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

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

```r
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>

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**samIlmnSymbols**

significant gene list with SAM in Illumina

**Description**

significant gene list with SAM in Illumina

**Author(s)**

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

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

**Usage**

```r
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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