

Package ‘Mulcom’

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Type Package

Title Calculates Mulcom test

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Depends R (>= 2.10), fields, Biobase

Imports graphics, grDevices, stats, methods

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

License GPL-2

LazyLoad yes

biocViews StatisticalMethod, MultipleComparison, Microarray, DifferentialExpression, GeneExpression

NeedsCompilation yes

R topics documented:

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Affy

Affy Dataset

Description

Affy Dataset

Author(s)

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

AffyIlmn

cross mapping table

Description

cross mapping table

Author(s)

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

| | |
|--------------|-----------------------------|
| harmonicMean | <i>MulCom Harmonic Mean</i> |
|--------------|-----------------------------|

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>

| | |
|----------|-------------------------|
| Illumina | <i>Illumina Dataset</i> |
|----------|-------------------------|

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 | <i>MulCom Calculation</i> |
|---------|---------------------------|

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 | 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

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

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

| | |
|---------|--|
| mulCAND | <i>Identify the Mulcom candidate feature selection</i> |
|---------|--|

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 | 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)
```

mulcomGeneListIlimn *significant gene list with limma in Illumina*

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 permuted 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 permuted 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)
```


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 refeing to te 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 refeing to te comparison, should be numeric |

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 False Significant Genes

Description

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

Usage

```
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

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())
```

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

```
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

*MulCom Parameter Optimization***Description**

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

Usage

```
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

```
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 paramters

Usage

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

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

```
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

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

Arguments

| | |
|-------|--|
| perm | a object with permuted 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 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>

Examples

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

| | |
|----------|---------------------------|
| mulPermC | <i>MulCom Permutation</i> |
|----------|---------------------------|

Description

R pipe to C function not called directly by user that reiterate MulCom Test on permuted 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 | <i>MulCom Score Calculation</i> |
|-----------|---------------------------------|

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 | <i>MulCom Sum of Square Error</i> |
|--------|-----------------------------------|

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>

samIlnnSymbols *significant gene list with SAM in Illumina*

Description

significant gene list with SAM in Illumina

Author(s)

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

`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

| | |
|------------------|--------------------------------------|
| <code>opt</code> | an Sam optimization object |
| <code>ths</code> | a threshold for the FDR optimization |

Value

a numeric vector

Author(s)

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

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