# Package ‘GeneMeta’

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**Title**  MetaAnalysis for High Throughput Experiments  

**Version**  1.46.0  

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**Description**  A collection of meta-analysis tools for analysing high throughput experimental data  

**Maintainer**  Bioconductor Package Maintainer  

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**License**  Artistic-2.0  

**Depends**  R (>= 2.10), methods, Biobase (>= 2.5.5), genefilter  

**Imports**  methods, Biobase (>= 2.5.5)  

**Suggests**  RColorBrewer  

**LazyLoad**  yes  

**biocViews**  Sequencing, GeneExpression, Microarray  

**NeedsCompilation**  no

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**Description**  

Plots for meta-analysis
Usage

IDRplot(m,CombineExp=1:(length(grep("zSco_Ex",colnames(m)))),colPos="black",colNeg="red",pchPos="*",pchNeg="*",type="b",ylab="IDR",xlab="z threshold",...)

CountPlot(kkk,cols,Score=c("FDR","zSco"),kindof=c("two.sided","pos","neg"),type="b",pch="*",ylab="Number of genes",xlab="FDR threshold",...)

Arguments

m               result matrix of the function zScores
type            plot parameter
ylab            plot parameter
xlab            plot parameter
pch             plot parameter
colPos          color for positive z scores
colNeg          color for negative z scores
pchPos          symbol for positive z scores
pchNeg          symbol for negative z scores
CombineExp      vector of integer- which experiments should be combined-default:all experiments
kkk             result object of function zScoreFDR
cols            vector of cols, one for each experiment, and one for the combination
Score           should the FDR or the zScore be plotted
kindof          "pos", "neg" or "two.sided"
...             additional plot parameter

Details

IDRplot produces a plot described in Choi et al.

Author(s)

M.Ruschhaupt

References

Choi et al, Combining multiple microarray studies and modeling interstudy variation. Bioinformatics, 2003, i84-i90.

dstar

Tools for Meta-analysis of gene expression data.

Description

A small number of meta-analysis functions for comparing two gene expression experiments are provided.
**Usage**

```r
dstar(d, n)
getdF(data, categ)
sigmad(d, ng1, ng2)
```

**Arguments**

- **d**: A vector of t-statistics, i.e. the output of `getdF`.
- **n**: The number of t-statistics.
- **data**: The data used to compute t-statistics, either a `matrix` or an `ExpressionSet`.
- **categ**: A vector of 0’s and 1’s indicating group membership.
- **ng1**: The number of samples in group 1.
- **ng2**: The number of samples in group 2.

**Details**

The functions `getdF` compute t-test statistics for the input data and group membership (note that group membership must be indicated by a vector of 0’s and 1’s).

The function `dstar` computes an unbiased estimate of the t-test. The function `sigmad` computes the variance estimate of `dstar`.

**Value**

The different functions have different return values, but generally they are vectors of the requested quantities.

**Author(s)**

L. Lusa, R. Gray and R. Gentleman

**References**

Choi et al, Combining multiple microarray studies and modeling interstudy variation. Bioinformatics, 2003, i84-i90.

**Examples**

```r
x = matrix(rnorm(1000), ncol=10)
ds = getdF(x, rep(c(0,1), c(5,5)))
dst = dstar(ds, ncol(x))
sgd = sigmad(ds, 5, 5)
```
Compute Cochran’s Q statistic

Description
Compute Cochran’s Q statistic for testing whether a fixed effects or a random effects model will be appropriate.

Usage
f.Q(dadj, varadj)

Arguments
- dadj: A matrix, each row is a gene, each column a study, of the estimated t-statistics.
- varadj: A matrix, each row is a gene, each column a study, of the estimated, adjusted variances of the t-statistics.

Details
A straightforward computation of Cochran’s Q statistic. If the null hypothesis that the data are well modeled by a fixed effects design is true then the estimate Q values will have approximately a chi-squared distribution with degrees of freedom equal to the number of studies minus one.

Value
A vector of length equal to the number of rows of dadj with the Q statistics.

Author(s)
L. Lusa and R. Gentleman

References
Choi et al, Combining multiple microarray studies and modeling interstudy variation. Bioinformatics, 2003, i84-i90.

See Also
dstar, sigmad

Examples
# none now, this requires a pretty elaborate example
**Nevins**

Intensity data for 46 Affymetrix slides with tissue samples of breast tumors. See vignette Nevins.pdf in the /scripts directory for details of the processing.

**Usage**

```r
data(Nevins)
```

**Format**

Nevins is an ExpressionSet containing the data from 46 Affymetrix chips.

**Source**

http://data.cgt.duke.edu/west.php

**References**


**Examples**

```r
data(Nevins)
Nevins
```

---

**tau2.DL**

*estimating my and tau in a REM*

**Description**

tau2.DL is an estimation of tau in a random effects model (REM) using Cochran’s Q statistic.

**Usage**

```r
tau2.DL(Q, num.studies, my.weights)
mu.tau2(my.d, my.vars.new)
var.tau2(my.vars.new)
```
Arguments

- **Q**: A vector of Cochran’s Q statistics.
- **num.studies**: The number of studies used for the meta-analysis.
- **my.weights**: A matrix with one column for each experiment containing the variances of the effects that should be combined.
- **my.d**: A matrix, with one column for each experiment, containing the effects that should be combined.
- **my.vars.new**: A matrix, with one column for each experiment, containing the variances of the effects that should be combined.

Author(s)

L. Lusa and R. Gentleman

References

Choi et al, Combining multiple microarray studies and modeling interstudy variation. Bioinformatics, 2003, i84-i90.

See Also

dstar, sigmad

Examples

# please have a look at the vignette

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zScores

Tools for Meta-analysis of gene expression data.

Description

A small number of meta-analysis functions for computing zScores for FEM and REM and computing FDR.

Usage

zScores(esets, classes, useREM=TRUE, CombineExp=1:length(esets))
zScorePermuted(esets, classes, useREM=TRUE, CombineExp=1:length(esets))
zScoreFDR(esets, classes, useREM=TRUE, nperm=1000, CombineExp=1:length(esets))
multExpFDR(theScores, thePermScores, type="pos")

Arguments

- **esets**: A list of ExpressionSets, one expression set per experiment. All experiments must have the same variables (genes).
- **classes**: A list of class memberships, one per experiment. Each list can only contain 2 levels.
- **useREM**: A logical value indicating whether or not to use a REM, TRUE, or a FEM, FALSE, for combining the z scores.
**Details**

The function `zScores` implements the approach of Choi et al. for a set of `ExpressionSet`s. The function `zScorePermuted` applies `zScore` to a single permutation of the class labels. The function `zScoreFDR` computes a FDR for each gene, both for each single experiment and for the combined experiment. The FDR is calculated as described in Choi et al. Up to now ties in the zscores are not taken into account in the calculation. The function might produce incorrect results in that case. The function also computes `zScores`, both for the combined experiment and for each single experiment.

**Value**

A matrix with one row for each probe(set) and the following columns:

- `zSco_Ex_` For each single experiment the standardized mean difference, \( \text{Effect}_{Ex.} \), divided by the estimated standard deviation, the square root of the `EffectVar_Ex_` column.
- `MUvals` The combined standardized mean difference (using a FEM or REM)
- `MUsds` The standard deviation of the `MUvals`.
- `zSco` The z statistic - the `MUvals` divided by their standard deviations, `MUsds`.
- `Qvals` Cochran’s Q statistic for each gene.
- `df` The degree of freedom for the Chi-square distribution. This is equal to the number of combined experiments minus one.
- `Qpvalues` The probability that a Chi-square random variable, with \( df \) degrees of freedom) has a higher value than the value from the Q statistic.
- `Chisq` The probability that a Chi-square random variate (with 1 degree of freedom) has a higher value than the value of \( zSco^2 \).
- `Effect_Ex_` The standardized mean difference for each single experiment.
- `EffectVar_Ex_` The variance of the standardized mean difference for each single experiment.

Note that the three column names that end in an underscore are replicated, once for each experiment that is being analyzed.

**Author(s)**

M. Ruschhaupt

**References**

Choi et al, Combining multiple microarray studies and modeling interstudy variation. Bioinformatics, 2003, i84-i90.
Examples

data(Nevins)

###Splitting

```r
thestatus <- Nevins$ER.status
group1 <- which(thestatus=="pos")
group2 <- which(thestatus=="neg")
rrr <- c(sample(group1, floor(length(group1)/2)),
      sample(group2, ceiling(length(group2)/2)))
Split1 <- Nevins[,rrr]
Split2 <- Nevins[,-rrr]
```

#obtain classes

```r
Split1.ER <- as.numeric(Split1$ER.status) - 1
Split2.ER <- as.numeric(Split2$ER.status) - 1
```

```r
esets <- list(Split1, Split2)
classes <- list(Split1.ER, Split2.ER)
theScores <- zScores(esets, classes, useREM=FALSE)
theScores[1:2,]
```
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