Package ‘GeneMeta’

March 27, 2024

Title MetaAnalysis for High Throughput Experiments
Version 1.74.0
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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
git_url https://git.bioconductor.org/packages/GeneMeta
git_branch RELEASE_3_18
git_last_commit 476eb5e
git_last_commit_date 2023-10-24
Repository Bioconductor 3.18
Date/Publication 2024-03-27

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CountPlot

Plots for Meta-analysis of gene expression data.

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

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result matrix of the function zScores

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result matrix of the function zScores

m
result matrix of the function zScores

type
plot parameter

ylog
plot parameter

xlab
plot parameter

pch
plot parameter

colPos
color for positive z scores

colNeg
color for negative z scores

cpchPos
symbol for positive z scores

cpchNeg
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.
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

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

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)
```

Description

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

Usage

```r
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

```r
# none now, this requires a pretty elaborate example
```

---

### Nevins

**Intensity data for 46 Affymetrix slides with tissue samples of breast tumors**

Description

Intensity data for 46 Affymetrix hu6800 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](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

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,sigmat

Examples

# please have a look at the vignette
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))
multiExpFDR(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.
theScores A vector of scores (e.g. t-statistics or z scores)
thePermScores A vector of permuted scores (e.g. t-statistics or z scores)
type "pos", "neg" or "two.sided"
nperm number of permutations to calculate the FDR
CombineExp vector of integer- which experiments should be combined-default:all experiments

Details

The function zScores implements the approach of Choi et al. for for a set of ExpressionSets. 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 combines 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, 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

Examples
data(Nevins)

#Splitting
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
Split1.ER <- as.numeric(Split1$ER.status) - 1
Split2.ER <- as.numeric(Split2$ER.status) - 1

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