# Package ‘tweeDEseq’

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compareCountDist

Description

Compares the empirical and estimated distributions for different count data models.

Usage

```
compareCountDist(x, plot=TRUE, ...
```

Arguments

- `x`: numeric vector containing the read counts.
- `plot`: If `TRUE` (the default) then the plot with the ECDF function for the counts and the three different Poisson-Tweedie distributions is produced, otherwise no graphical output is given and this only makes sense if one is interested in the returned value (see value section below).
- `...`: Further arguments to be passed to the plot function.

Details

This function serves the purpose of comparing a empirical distribution of counts with three Poisson-Tweedie distributions arising from estimating mean, dispersion and setting \( a = 1 \) for comparing against a Poisson, \( a = 0 \) for comparing against a negative binomial and estimating the shape parameter \( a \) from data too. The legend shows the values of the \( a \) parameter and the P-value of the likelihood ratio test on whether the expression profile follows a negative binomial distribution (\( H_0 : a = 0 \)).

Value

List with the following components:

- `a`: shape parameter estimated from the input data \( x \).
- `p.value`: P-value for the test that the data follows a negative binomial distribution, i.e., \( H_0 : a = 0 \).

References


See Also

`qqchisq`, `testShapePT`
Examples

```r
# Generate 500 random counts following a Poisson Inverse Gaussian
# distribution with mean = 20 and dispersion = 5
randomCounts <- rPT(n = 500, mu = 20, D = 5, a = 0.5)

xx <- compareCountDist(randomCounts, plot=FALSE)
xx
```

The Poisson-Tweedie family of distributions

Description

Density function and random generation for the Poisson-Tweedie family of distributions.

Usage

```r
dPT(x, mu, D, a, tol = 1e-15)
rPT(n, mu, D, a, max = 10*sqrt(mu*D), tol = 1e-4)
```

Arguments

- `x` an object of class `mlePT` or a non-negative vector containing the integers in which the distribution should be evaluated.
- `mu` numeric positive scalar giving the mean of the distribution.
- `D` numeric positive scalar giving the dispersion of the distribution.
- `a` numeric scalar smaller than 1 giving the shape parameter of the distribution.
- `tol` numeric scalar giving the tolerance.
- `n` integer scalar giving number of random values to return.
- `max` numeric scalar containing the maximum number of counts to be used in the sampling process.

Value

If 'x' is of class 'mlePT', 'dPT' will return the Poisson-Tweedie distribution with parameters equal to the ones estimated by 'mlePoissonTweedie' evaluated on the data that was used to estimate the parameters. If 'x' is a numeric vector, 'dPT' will return the density of the specified Poisson-Tweedie distribution evaluated on 'x'.

'rPT' generates random deviates.

References

See Also

`compareCountDist` `testShapePT`

Examples

```r
# To compute the density function in 1:100 of the Polya-Aeppli
# distribution with mean = 20 and dispersion = 5
dPT(x = 1:100, mu = 20, D = 5, a = -1)

# To generate 100 random counts of the same distribution with same
# parameters
rPT(n = 100, mu = 20, D = 5, a = -1)
```

Description

Filter count data to remove lowly expressed genes.

Usage

`filterCounts(counts, cpm.cutoff=0.5, n.samples.cutoff=2, mean.cpm.cutoff=0, lib.sizes=NULL)`

Arguments

counts numeric data.frame or matrix containing the count data.
cpm.cutoff expression level cutoff defined as the minimum number of counts per million.
By default this is set to 0.5 counts per million.
n.samples.cutoff minimum number of samples where a gene should meet the counts per million
cutoff (cpm.cutoff) in order to be kept as part of the count data matrix. When
n.samples.cutoff is a number between 0 and 1, then it is interpreted as the
fraction of samples that should meet the counts per million cutoff (cpm.cutoff).
mean.cpm.cutoff minimum mean of counts per million cutoff that a gene should meet in order to
be kept. When the value of this argument is larger than 0 then it overrules the
other arguments cpm.cutoff and n.samples.cutoff.
lib.sizes vector of the total number of reads to be considered per sample/library. If
lib.sizes=NULL (default) then these quantities are estimated as the column
sums in the input matrix of counts.

Details

This function removes genes with very low expression level defined in terms of a minimum number
of counts per million occurring in a minimum number of samples. Such a policy was described
by Davis McCarthy in a message at the bioc-sig-sequencing mailing list. By default, this function
keeps genes that are expressed at a level of 0.5 counts per million or greater in at least two samples.
Alternatively, one can use the mean.cpm.cutoff to set a minimum mean expression level through
all the samples.
**glmPT**

**Value**

A matrix of filtered genes.

**Author(s)**

J.R. Gonzalez and R. Castelo

**References**


**See Also**

normalizeCounts

**Examples**

```r
# Generate a random matrix of counts
counts <- matrix(rPT(n=1000, a=0.5, mu=10, D=5), ncol = 40)
dim(counts)

# Filter genes with requiring the minimum expression level on every sample
filteredCounts <- filterCounts(counts, n.samples.cutoff=dim(counts)[2])
dim(filteredCounts)
```

---

**glmPT**

Fit Poisson-Tweedie generalized linear model.

**Description**

’glmPT’ is used to fit generalized linear models for the Poisson-Tweedie family of distributions.

**Usage**

tweeDEglm(formula, counts, data, mc.cores = 1, a = NULL, offset = NULL, ...)
glmPT(formula, data, offset = NULL, a = NULL, ...)

**Arguments**

- **formula**: an object of class ‘formula’: a symbolic description of the model to be fitted.
- **counts**: Matrix or data.frame of counts for the ’tweeDEglm’.
- **data**: an optional data frame, list or environment containing the variables in the model. If not found in ’data’, the variables are taken from ’environment(formula)’, typically the environment from which ’glm’ is called.
- **mc.cores**: number of cpu cores to be used. This option is only available when the ’multicore’ package is installed and loaded first. In such a case, if the default value of ’mc.cores=1’ is not changed, all available cores will be used.
offset

this can be used to specify an _a priori_ known component to be included in the
linear predictor during fitting.

a

numeric vector (for 'tweeDEglm') or numeric scalar (for 'glmPT') smaller than
1. If specified the PT shape parameter will be fixed. For 'tweeDEglm', if the
provided 'a' is a scalar this value will be used for all rows of 'counts' (genes).

... additional arguments to be passed to the 'optim' 'control' options.

Value

An object of class 'glmPT' containing the following information:

call

the matched call.

contrasts

(where relevant) the contrasts used.

convergence

A character string giving any additional information returned by the optimizer,
or 'NULL'.

counts

A two-element integer vector giving the number of calls to 'fn' and 'gr' respec-
tively. This excludes those calls needed to compute the Hessian, if requested,
and any calls to 'fn' to compute a finite-difference approximation to the gradient.

df

Number of estimated parameters.

fitted.values

The fitted mean values, obtained by transforming the linear predictors by the
inverse of the link function.

hessian

A symmetric matrix giving an estimate of the Hessian at the solution found.

message

A character string giving any additional information returned by the optimizer,
or 'NULL'.

ncov

An integer giving the number of variables in the model.

par

A vector giving the estimated parameters.

residuals

The residuals in the final iteration of the IWLS fit.

se

A vector giving the standard error of the estimated parameters.

value

Value of the log-likelihood of the model in the last iteration.

...

Further arguments to be passed to the 'glm.fit' function.

Author(s)

Mikel Esnaola <mesnaola@creal.cat>

Examples

counts <- matrix(rPT(n = 1000, a = 0.5, mu = 10, D = 5), ncol = 40)
g <- factor(rep(c(0,1), 20))
mod1 <- glmPT(counts[,1]-g)
mod1

summary(mod1)

anova(mod1)

mod2 <- tweeDEglm(~ g, counts)
mod2
gofTest

Test the goodness of fit of every row in a matrix of counts

Description

Function to test the goodness of fit of every row in a matrix of counts

Usage

gofTest(counts, a = 0, mc.cores = 1)

Arguments

- **counts**: matrix of counts
- **a**: numeric scalar smaller than 1. The function will test whether the shape parameter is equal to the introduced ‘a’ (default is 0).
- **mc.cores**: number of cpu cores to be used. This option is only available when the ‘multi-core’ package is installed and loaded first. In such a case, if the default value of mc.cores=1 is not changed, all available cores will be used.

Details

By default \( a = 0 \), and therefore the function tests for every row of the input matrix of counts whether the count data follows a Negative-Binomial distribution. In this case, a Likelihood Ratio Test is performed. When the given value for ‘\( a \)’ is different from 0, a Wald test is performed. This function calls `testShapePT`.

Value

A vector of statistics that follows a \( \chi^2 \) distribution with one degree of freedom under the null hypothesis.

References


See Also

testShapePT
## Generate a random matrix of counts
```r
counts <- matrix(rPT(n=2000, a=0.5, mu=10, D=5), nrow=20)
```

## Perform the goodness-of-fit tests for every row in the matrix
```r
chi2gof <- gofTest(counts)
```

## Calculate and sort the corresponding P-values for the null hypothesis that counts follow a negative binomial distribution
```r
sort(pchisq(chi2gof, df=1, lower.tail=FALSE))
```

### Description
print, extract loglikelihood or compute confidence interval for an object of class 'mlePT'.

### Usage
```r
## S3 method for class 'mlePT'
print(x, digits = 3, ...)
## S3 method for class 'mlePT'
logLik(object, ...)
## S3 method for class 'mlePT'
confint(object, parm, level = 0.95, ...)
```

### Arguments
- `x` object of class 'mlePT'.
- `object` object of class 'mlePT'.
- `digits` integer scalar giving the number of digits to be rounded the solution.
- `parm` a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
- `level` the confidence level required (default is 0.95).
- `...` additional arguments.

### Value
- 'logLik' returns the loglikelihood of the selected model.
- 'confint' returns a matrix (or vector) with columns giving lower and upper confidence limits for each parameter.

### See Also
- `mlePoissonTweedie`
Examples

# Load and aggregate the 'seizure' database
data(seizure)
aggCounts <- aggregate(x = cbind(seizure$count, seizure$trx), by =
  list(seizure$id), FUN = sum)

# Estimate the parameters
mleSeizure <- mlePoissonTweedie(x = aggCounts[,2], a.ini = 0, D.ini =
10)

# Print
mleSeizure

# Extract loglikelihood
logLik(mleSeizure)

# Compute confidence interval
confint(mleSeizure)

mlePoissonTweedie  
Maximum likelihood estimation of the Poisson-Tweedie parameters

Description

Maximum likelihood estimation of the Poisson-Tweedie parameters using L-BFGS-B quasi-Newton
method.

Usage

mlePoissonTweedie(x, a, D.ini, a.ini, maxit = 100, loglik=TRUE,
maxCount=20000, w = NULL, ...)
getParam(object)

Arguments

x  numeric vector containing the read counts.
a  numeric scalar smaller than 1, if specified the PT shape parameter will be fixed.
D.ini  numeric positive scalar giving the initial value for the dispersion.
a.ini  numeric scalar smaller than 1 giving the initial value for the shape parameter
(ignored if 'a' is specified).
maxit  numeric scalar providing the maximum number of 'L-BFGS-B' iterations to be
performed (default is '100').
loglik  is log-likelihood computed? The default is TRUE
object  an object of class 'mlePT'.
maxCount  if max(x) > maxCount, then moment method is used to estimate model param-
ters to reduce computation time. The default is 20000.
w  vector of weights with length equal to the length of 'x'.
...  additional arguments to be passed to the 'optim' 'control' options.
Details

The L-BFGS-B quasi-Newton method is used to calculate iteratively the maximum likelihood estimates of the three Poisson-Tweedie parameters. If 'a' argument is specified, this parameter will be fixed and the method will only estimate the other two.

Value

An object of class 'mlePT' containing the following information:
par: numeric vector giving the estimated mean ('mu'), dispersion ('D') and shape parameter 'a'.
se: numeric vector containing the standard errors of the estimated parameters 'mu', 'D' and 'a'.
loglik: numeric scalar providing the value of the loglikelihood for the estimated parameters.
iter: numeric scalar giving the number of performed iterations.
paramZhu: numeric vector giving the values of the estimated parameters in the Zhu parameterization 'a', 'b' and 'c'.
paramHou: numeric vector giving the values of the estimated parameters in the Hougaard parameterization 'alpha', 'delta' and 'theta'.
skewness: numeric scalar providing the estimate of the skewness given the estimated parameters.
x: numeric vector containing the count data introduced as the 'x' argument by the user.
convergence: A character string giving any additional information returned by the optimizer, or 'NULL'.

References


See Also
testShapePT print.mlePT

Examples

# Generate 500 random counts following a Poisson Inverse Gaussian
# distribution with mean = 20 and dispersion = 5
randomCounts <- rPT(n = 500, mu = 20, D = 5, a = 0.5)

# Estimate all three parameters
res1 <- mlePoissonTweedie(x = randomCounts, a.ini = 0, D.ini = 10)
res1
getParam(res1)

# Fix 'a = 0.5' and estimate the other two parameters
res2 <- mlePoissonTweedie(x = randomCounts, a = 0.5, D.ini = 10)
normalizeCounts

res2
getParam(res2)

normalizeCounts Count data normalization

Description

Normalize count data to remove systematic technical effects.

Usage

normalizeCounts(counts, group=rep.int(1,ncol(counts)), method=c("TMM", "cqn"),
common.disp = FALSE, prior.df=8, annot=NULL, lib.sizes=NULL, verbose=TRUE)

Arguments

counts numeric data.frame or matrix containing the count data.
group vector giving the experimental group/condition for each sample/library. This argument is only relevant when method="cqn".
method specific method to use in order to normalize the input matrix of counts. By default this is set to TMM (Robinson and Oshlack, 2010) using the implementation available in the edgeR package. The other option is cqn (Hansen, Irizarry and Wu, 2012).
common.disp logical indicating whether a common or tagwise (default) dispersions should be estimated and employed when adjusting counts. This argument is only relevant when method="TMM".
prior.df argument provided to the call of estimateTagwiseDisp which defines the prior degrees of freedom. It is used in calculating 'prior.n' which, in turn, defines the amount of shrinkage of the estimated tagwise dispersions to the common one. By default prior.df=8 thus assuming no shrinkage toward that common dispersion. This argument is not used if common.disp=TRUE. This argument is only relevant when method="TMM".
annot matrix or data frame with row names matching at least part of the row names in the counts input matrix, containing feature/tag/gene lengths in bp on its first column, and a second covariate, such as G+C content, on its second column. These two pieces of information are provided to arguments lengths and x when calling cqn. This argument is only relevant when method="TMM".
lib.sizes vector of the total number of reads to be considered per sample/library. If lib.sizes=NULL (default) then these quantities are estimated as the column sums in the input matrix of counts.
verbose logical indicating whether progress should be reported.

Details

This function encapsulates calls to RNA-seq normalization procedures available in the edgeR and cqn packages in order to try to remove systematic technical effects from raw counts. By default, the TMM method described in Robinson and Oshlack (2010) is employed to calculate normalization factors which are applied to estimate effective library sizes, then common and tagwise (only when...
the argument common.disp=TRUE) dispersions are calculated (Robinson and Smyth, Bioinformatics 2007) and finally counts are adjusted so that library sizes are approximately equal for the given dispersion values (Robinson and Smyth, Biostatistics 2008). Setting the argument method="cqn", conditional quantile normalization (Hansen, Irizarry and Wu, 2012) is applied which aims at adjusting for tag/feature/gene length and other covariate such as G+C content. This information should be provided through the annot argument. This procedure calculates, for every gene and every sample, an offset to apply to the log2 reads per million (RPM) and the function normalizeCounts() adds this offset to the log2 RPM values calculated from the input count data matrix, unwlogs them and rolls back these normalized RPM values into integer counts. Details on these two normalization procedures are given in the documentation of the edgeR and cqn Bioconductor packages.

Value

A matrix of normalized counts.

Author(s)

J.R. Gonzalez and R. Castelo

References


See Also

filterCounts

Examples

# Generate a random matrix of counts
counts <- matrix(rPT(n=1000, a=0.5, mu=10, D=5), ncol = 40)

colSums(counts)
counts[1:5, 1:5]

# Normalize counts
normCounts <- normalizeCounts(counts, rep(c(1,2), 20))

colSums(normCounts)
normCounts[1:5, 1:5]
qqchisq

Chi-square quantile-quantile plot

Description

Make a chi-square quantile-quantile plot.

Usage

qqchisq(stat, df=1, normal=FALSE, rangeExpected=FALSE,
obsQuantiles=c(0.50, 0.75, 0.95), ylim = NULL, ...)

Arguments

stat vector of $\chi^2$ statistics.
df degrees of freedom of stat.
normal logical; set to TRUE if the $\chi^2$ statistics in stat should be transform into normal z-scores in order to improve the display of lower quantiles. For this purpose, this function uses the zscoreGamma function from the limma package. Default is set to FALSE.
rangeExpected logical; set to TRUE if the displayed range of the observed $\chi^2$ statistics is restricted to the range of their expected values. Default is set to FALSE.
obsQuantiles observed quantiles to indicate by horizontal dash lines. By default, these are set to 50%, 75% and 95%.
ylim they y limits of the plot. If 'NULL' (default), these will be obtained from the data.
... further arguments to pass to the plot function.

Details

The main purpose of this function in the tweeDEseq package is to provide means to assess the goodness of fit of count data to the negative binomial distribution. The main input argument stats should be the output of gofTest.

Value

It returns invisibly a list with two components x and y corresponding to the coordinates of the plotted statistics.

References


See Also

cmpareCountDist testShapePT
Examples

```r
## Generate a random matrix of counts
counts <- matrix(rPT(n=2000, a=0.5, mu=10, D=5), nrow=20)

## Perform the goodness-of-fit tests for every row in the matrix
chi2gof <- gofTest(counts)

## Not run:
qqchisq(chi2gof)

## End(Not run)
```

seizure

### Epileptic seizure counts

**Description**

Data on seizure counts for 59 epileptics.

**Usage**

```r
data(seizure)
```

**Format**

A data frame with 236 observations on the following 6 variables.

- `id` a numeric vector, identification number for each patient
- `count` a numeric vector, seizure counts
- `visit` a numeric vector, visit number
- `trx` a numeric vector, treatment: progabide (1) or placebo (0)
- `baseline` a numeric vector, baseline 8 week seizure count
- `age` a numeric vector, age of patient

**Details**

The data are from a placebo-controlled clinical trial of 59 epileptics. Patients with partial seizures were enrolled in a randomized clinical trial of the anti-epileptic drug, progabide. Participants in the study were randomized to either progabide or a placebo, as an adjuvant to the standard anti-epileptic chemotherapy. Progabide is an anti-epileptic drug whose primary mechanism of action is to enhance gamma-aminobutyric acid (GABA) content; GABA is the primary inhibitory neurotransmitter in the brain. Prior to receiving treatment, baseline data on the number of epileptic seizures during the preceding 8-week interval were recorded. Counts of epileptic seizures during 2-week intervals before each of four successive post-randomization clinic visits were recorded.

**Source**

testShapePT

References

See Also
testPoissonTweedie mlePoissonTweedie

Examples
# Although this is not a differential expression dataset, it is appropriate # to illustrate the application of the Poisson-Tweedie in # epidemiological studies
data(seizure)
summary(seizure)
# Aggregate
aggCounts <- aggregate(x = cbind(seizure$count, seizure$trx), by =
list(seizure$id), FUN = sum)
# Estimation of the three parameters for all individuals
mleSeizure <- mlePoissonTweedie(x = aggCounts[,2], a.ini = 0, D.ini = 10)
mleSeizure
#Poisson-Tweedie test
testPoissonTweedie(x = aggCounts[,2], group = aggCounts[,3])

testShapePT

Test shape parameter of PT

Description
Function to test whether the shape parameter is equal to a given value.

Usage
testShapePT(x, a = 0)

Arguments
x object of class 'mlePT'.
a numeric scalar smaller than 1. The function will test whether the shape parameter is equal to the introduced 'a' (default is 0).

Details
By default a = 0, and therefore the function tests whether the count data follows a Negative-Binomial distribution or not. In this case, a Likelihood Ratio Test is performed. When the given value for 'a' is different from 0, a Wald test is performed.
If a = 1, the function tests whether the count data follows a Poisson distribution or not.
If \( a = 0.5 \), the function tests whether the count data follows a Poisson-inverse Gaussian distribution or not.

If \( a = -1 \), the function tests whether the count data follows a Polya-Aeppli distribution or not.

Value

numeric p-value of the test.

References


See Also

gofTest mlePoissonTweedie compareCountDist

Examples

# Generate a random matrix of counts
counts <- rPT(n=1000, a=0.5, mu=10, D=5)

# Maximum likelihood estimation of the Poisson-Tweedie parameters
mleEstimate <- mlePoissonTweedie(x = counts, a.ini = 0, D.ini = 10)

# Test whether data comes from Negative-Binomial distribution
testShapePT(mleEstimate)

# Test whether data comes from Poisson-inverse Gaussian
testShapePT(mleEstimate, a = 0.5)
MAplot(x, log2fc.cutoff=0, highlight=NULL, ...)  
Vplot(x, log2fc.cutoff=0, pval.adjust.cutoff=1, highlight=NULL, ylab=expression(paste(-log[10], " Raw P-value")), ...)

Arguments

- **object**: a data.frame or a matrix of RNA-seq counts.
- **group**: vector giving the experimental group/condition for each sample/library.
- **mc.cores**: number of cpu cores to be used. This option is only available when the 'multicore' package is installed and loaded first. In such a case, if the default value of mc.cores=1 is not changed, all available cores will be used.
- **pair**: vector of two elements containing the representants of each of the two groups (default is 'NULL').
- **a**: for 'tweeDE' function, numerical vector with values strictly less than 1. It allows to fix the shape parameter 'a' during differential expression tests for each of the genes (rows of 'object'). for 'testPoissonTweedie' function, numeral value strictly less than 1 which fixes the shape parameter 'a' for the test.
- **n**: maximum number of genes printed.
- **sort.by**: character string, indicating whether genes should be ranked by their P-value (pval), which is the default setting, or by absolute log2 fold-change (log2fc).
- **log2fc.cutoff**: cutoff on the minimum value of the log2 fold change.
- **pval.adjust.cutoff**: cutoff on the maximum adjusted P-value (FDR).
- **print**: logical; it indicates whether the output should be printed on the terminal.
- **highlight**: list of arguments to the points() plotting function in order to highlight genes in the MA or volcano plots. A component called genes is expected to have the identifiers of the genes to be highlighted.
- **ylab**: label on the y-axis of the volcano plot set by default to -log10 of the raw P-value which is what this plot displays on that axis.
- **x**: object returned by the function tweeDE in the case of print and vector of count data in the case of testPoissonTweedie.
- **saveModel**: logical indicating whether the results of fitting the model should be saved or not (default is 'FALSE').
- **log**: logical (default is FALSE). If FALSE, the tested Null Hypothesis states that the difference between the means is 0 while, if TRUE, it states that the quotient between the logarithm of means is equal to 1. For this last case, the standard error is computed using the Delta Method.
- **...**: additional arguments.

Details

'testPoissonTweedie' performs the test for a vector of counts.

'tweeDE' performs the test for a whole 'data.frame'. The P-values are then corrected using the Benjamini and Hochberg method.
Value

'testPoissonTweedie' returns a list with:
'mean': means for each group 'pvalue': p-value for the test
'tweeDE' returns a 'data.frame' with columns
'overallMean': overall mean counts 'meanA': mean counts of the first group 'meanB': mean counts of the second group 'log2fc': logarithm (base 2) of the fold-change (second group vs. first group) 'pval': p-value for the test 'pval.adjust': adjusted p-value using Benjamini-Hochberg method

References


See Also

normalizeCounts mlePoissonTweedie

Examples

# Generate a random matrix of counts
counts <- matrix(rPT(n = 1000, a = 0.5, mu = 10, D = 5), ncol = 40)

# Test for differences between the two groups
tweeDE(counts, group = rep(c(1,2),20))

tweeDExact

Exact test for differences between two Poisson-Tweedie groups

Description

Carry out an exact test for differences between two Poisson-Tweedie populations.

Usage

tweeDExact(counts, group, tol = 1e-15, mc.cores = 1)
eXactTestPT(counts, group, tol = 1e-15, threshold = 150e3)

Arguments

counts The RNA-seq counts. An object of type 'matrix' or 'data.frame' for 'tweeDExact', or an object of type 'vector' for 'exactTest'.
group vector giving the experimental group/condition for each sample/library.
tol Tolerance for the Poisson-Tweedie probability computations. The probabilities under the 'tol' value will automatically considered as 0.
tweeDEexact

threshold

an integer (default is 50e3). If the sum of all counts in a certain gene exceeds this value 'testPoissonTweedie' will be called instead of 'exactTest'. Larger values will result in a longer computing time.

mc.cores

number of cpu cores to be used. This option is only available when the 'multicore' package is installed and loaded first. In such a case, if the default value of 'mc.cores=1' is not changed, all available cores will be used.

Details

'exactTest' performs the exact test for a vector of counts.
'tweeDEexact' performs the test for a whole 'data.frame'. The P-values are then corrected using the Benjamini and Hochberg method.

Value

'exactTest' returns the p-value resulting from the exact test between two different Poisson-Tweedie populations, as well as the method that was used to compute it.
'tweeDEexact' returns a 'data.frame'. Each row corresponds to a gene and it contains the following information:
- In the first columns the mean of counts in each of the subgroups.
- In the third column the p-value of the test for differential expression between the two subgroups.
- In the fourth column the p-value corrected for multiple comparisons using the Benjamini-Hochberg FDR procedure.
- In the last (fifth) column the method that was used to compute the p-value.

Author(s)

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References


See Also

testPoissonTweedie tweeDEexact

Examples

counts <- matrix(rPT(n = 1000, a = 0.5, mu = 10, D = 5), ncol = 40)
tweeDEexact(counts, group = rep(c(1,2),20))
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