Package 'ABSSeq'

November 5, 2025

Type Package

Title ABSSeq: a new RNA-Seq analysis method based on modelling absolute expression differences

Version 1.65.0

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Description Inferring differential expression genes by absolute counts difference between two groups, utilizing Negative binomial distribution and moderating fold-change according to heterogeneity of dispersion across expression level.

License GPL (>= 3)

biocViews DifferentialExpression

Imports locfit, limma

Depends R (>= 2.10), methods

Suggests edgeR

RoxygenNote 6.0.1

git_url https://git.bioconductor.org/packages/ABSSeq

git_branch devel

git_last_commit 3e159b8

git_last_commit_date 2025-10-29

Repository Bioconductor 3.23

Date/Publication 2025-11-05

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`ABSDataSet` *ABSDataSet object and constructors*

Description

ABSDataSet object and constructors

Usage

```
ABSDataSet(counts, groups, normMethod = c("user", "qtotal", "total", "quartile",
  "geometric", "TMM"), sizeFactor = 0, paired = FALSE, minDispersion = NULL, minRates = 0.1,
   maxRates = 0.3, LevelstoNormFC = 100)
```

Arguments

`counts`	a matrix or table with at least two columns and one row,
`groups`	a factor with two groups, whose length should be equal with sample size
`normMethod`	method for estimating the size factors, should be one of 'user', 'qtotal', 'total', 'quartile', 'geometric' and 'TMM'. See `normalFactors` for description.
`sizeFactor`	size factors for 'user' method, self-defined size factors by user.
`paired`	switch for differential expression detection in paired samples.
`minDispersion`	a positive double for user-defined penalty of dispersion estimation
`minRates`	low bounder rate of baseline estimation for counts difference, default is 0.1

maxRates	up bounder rate of baseline estimation for counts difference, default is 0.3. Setting minRates equal with maxRates will result in a testing on user-define rate,
LevelstoNormFC	maximal level of average standard deviation in fold-change normalization according to expression level, default is 100.

Details

The function contructs an ABSDataSet object with counts table and groups. It also checks the structure of counts and groups.The ABSDataSet is a class, used to store the input values, intermediate calculations and results of an analysis of differential expression. It also contains information for the running time of an analysis.

Value

An ABSDataSet object.

Examples

```
counts <- matrix(1:4,ncol=2)
groups <- factor(c("a","b"))
obj <- ABSDataSet(counts, groups)
obj <- ABSDataSet(counts, groups, paired=TRUE)
```

ABSSeq *Differential expression analysis based on the total counts difference.*

Description

This function performs a default analysis by calling, in order, the functions: normalFactors, callParameter, callDEs.

Usage

```
ABSSeq(object, adjmethod = "BH", replaceOutliers = TRUE, useaFold = FALSE,
  quiet = FALSE, ...)
```

Arguments

object	an ABSDataSet object, contains the reads count matrix, groups and normalization method.
adjmethod	defualt is 'BH', method for p-value adjusted, see p.adjust.methods for details
replaceOutliers	default is TRUE, switch for outlier replacement.
useaFold	defualt is FALSE, switch for DE detection through fold-change, see callDEs for details
quiet	default is FALSE, whether to print messages at each step
...	parameters passed to ReplaceOutliersByMAD and genAFold from callParameter

Details

The differential expression analysis models the total counts difference by a Negative binomal distribution

$$NB(\mu, r)$$

:

Value

an ABSDataSet object with additional elements, which can be retrieved by `results`: Amean and Bmean, mean of log2 normalized reads count for group A and B, foldChange, shrinked (expression level and gene-specific) log2 of fold-change, B - A, rawFC, raw log2 of fold-change, B-A (without shrinkage), lowFC, expression level corrected log2 fold-change, pvalue, pvalue from NB distribution model, adj.pvalue, adjuested p-value used p.adjust method.

Author(s)

Wentao Yang

References

Wentao Yang, Philip Rosenstiel & Hinrich Schulenburg: ABSSeq: a new RNA-Seq analysis method based on modelling absolute expression differences

Examples

```
data(simuN5)
obj <- ABSDataSet(counts=simuN5$counts, groups=factor(simuN5$groups))
obj <- ABSSeq(obj)
res <- results(obj,c("Amean","Bmean","foldChange","pvalue","adj.pvalue"))
head(res)
```

`ABSSeqlm` *Differential expression analysis for complex desgin.*

Description

This function performs a default analysis by calling, in order, the functions: `normalFactors`, `aFoldcomplexDesign`,

Usage

```
ABSSeqlm(object, design, condA, condB = NULL, lmodel = TRUE,
  preval = 0.05, qforkappa = 0, adjmethod = "BH", scale = FALSE,
  quiet = FALSE, ...)
```

Arguments

object	a ABSDataSet object (not need 'groups' information).
design	a numeric matrix for expriment, with samples and factors in rows and colnums, respectively. Design respresents the satuarated model.
condA	a vector of factors for DE analysis, which could be redundant, see aFoldcomplexDesign.
condB	a vector of factors for DE analysis, which could be redundant, default is null, if not provide, the DE analysis will switch to assess difference across factors in condA (analysis of variance). If provide, DE analysis will focus on contrast between condB and condA (condB-condA). See aFoldcomplexDesign. The unique factors in condA+condB represents the reduced model.
lmodel	switch of fit linear model from limma-lmFit under design, default is TRUE. If TRUE, a gene-specific residual varaince will be estimated from (satuarated model - reduced model). Satuarated model includes all factors in design matrix and reduced model includes factors in condA+condB. if satuarated model == reduced model, the DE analysis performs pairwise comparison or one-way analysis of variance. See aFoldcomplexDesign.
preval	parameter for aFoldcomplexDesign, prior value for controlling of variance scale in case over-scaled, default is 0.05,
qforkappa	parameter for aFoldcomplexDesign, quantile for estimating kappa(>=qforkappa), default is 0 (no trimming of data).
adjmethod	defualt is 'BH', method for p-value adjusted, see p.adjust.methods for details
scale	switch for scaling fold change according to common SD under log2 transformation, default is FALSE.
quiet	default is FALSE, whether to print messages at each step
...	parameters passed to lmFit in limma

Details

This function uses a linear model (limma-lmFit) to infer DE under complex design.

Value

a result table with additional elements, including: basemean, log of basemean, foldChange, shrinked (expression level and gene-specific) log2 of fold-change, B - A, or (SDs under log2 for analysis of variance) pvalue, pvalue from NB distribution model, p.adj, adjuested p-value used p.adjust method. scaledlogFC, scaled logFC if scale=TRUE.

Author(s)

Wentao Yang

References

Wentao Yang, Philip Rosenstiel & Hinrich Schulenburg: ABSSeq: a new RNA-Seq analysis method based on modelling absolute expression differences

Examples

```
data(simuN5)
groups=factor(simuN5$groups)
obj <- ABSDataSet(counts=simuN5$counts)
design <- model.matrix(~0+groups)
res <- ABSSeqlm(obj,design,condA=c("groups0"),condB=c("groups1"))
head(res)
```

`aFoldcomplexDesign` *Calculate parameters for differential expression test base on absolute counts differences*

Description

Calculate aFold for each gene and general sd

Usage

```
aFoldcomplexDesign(nncounts, design, condA, condB = NULL, lmodel = TRUE,
  preval = 0.05, qforkappa = 0, priorgenesd, ...)
```

Arguments

`nncounts`	matrix for read count.
`design`	a numeric matrix for expriment, with samples and factors in rows and colnums, respectively.
`condA`	a vector of factors for DE analysis, which could be redundant.
`condB`	a vector of factors for DE analysis, which could be redundant, default is null. If not provide, the DE analysis will switch to assess difference across factors in condA (analysis of variance). If provide, DE analysis will focus on contrast between condB and condA (condB-condA).
`lmodel`	switch of fit linear model from limma-lmFit under design, default is TRUE. If TRUE, a gene-specific residual varaince will be estimated from (satuarated model - reduced model). Satuarated model includes all factors in design matrix and reduced model includes factors in condA+condB.
`preval`	pre-defined scale control for variance normalization, default is 0.05, a large value generally increases the fold-changes (decreases penalty of variances) under low expression.
`qforkappa`	quantile for estimating kappa(>=qforkappa), default is 0 (without trimming of data). Please set up a value in [0,1) if you want to trim the low expressed data.
`priorgenesd`	prior value for general SD of fold change, if provided, the estimation of general SD will be replaced by this value.
`...`	parameters passed to lmFit in limma

Details

shifted and calculate a set of parameters from normalized counts table

Value

A list with log2 foldchange, general SD (gene-specific SD if lmodel is TRUE) for calculating pvalue, variance stablized counts and basemean

Note

This function should run after `normalFactors`.

Examples

```
data(simuN5)
groups=factor(simuN5$groups)
obj <- ABSDataSet(counts=simuN5$counts, groups=factor(simuN5$groups))
mtx <- counts(obj,TRUE)
design <- model.matrix(~0+groups)
aFold <- aFoldcomplexDesign(mtx,design,condA=c("groups0"),condB=c("groups1"))
hist(aFold[[1]])
```

---

callDEs *Testing the differential expression by counts difference*

Description

Using NB distribution to calculate p-value for each gene as well as adjust p-value

Usage

```
callDEs(object, adjmethod = "BH", useaFold = FALSE)
```

Arguments

`object`	an `ABSDataSet` object.
`adjmethod`	the method for adjusting p-value, default is 'BH'. For details, see `p.adjust.methods`.
`useaFold`	switch for DE detection through fold-change, which will use a normal distribution (N(0,sd)) to test the significance of log2 fold-change. The sd is estimated through a quantile function of gamma distribution at `callParameter`.

Details

This function firstly calls p-value used `pnbinom` to call pvalue based on sum of counts difference between two groups or used `pnorm` to call pvalue via log2 fold-change, then adjusts the pvalues via `p.adjust` method. In addition, it also shrink the log2 fold-change towards a common dispersion after pvalue calling.

Value

an ABSDataSet object with additional elements: shrinked log2 fold-change, pvalue and adjusted p-value, denoted by foldChange pvalue and adj-pvalue, respectively. Use the results method to get access it.

Note

this function should run after callParameter

Examples

```
data(simuN5)
obj <- ABSDataSet(counts=simuN5$counts, groups=factor(simuN5$groups))
obj <- normalFactors(obj)
obj <- callParameter(obj)
obj <- callDEs(obj)
head(results(obj))
```

---

callParameter *Calculate parameters for differential expression test base on absolute counts differences*

Description

Calculate parameters for each gene (the moderating basemean, dispersions, moderated fold-change and general sd)

Usage

```
callParameter(object, replaceOutliers = TRUE, ...)
```

Arguments

object	a ABSDataSet object.
replaceOutliers	switch for outlier replacement, default is TRUE.
...	parameters past to ReplaceOutliersByMAD

Details

shifted and calculate a set of parameters from normalized counts table before callDEs

Value

A ABSDataSet object with absolute differences, basemean, mean of each group, variance, log2 of foldchange, named as 'absD', 'baseMean', 'Amean', 'Bmean', 'Variance' and 'foldChange', respectively. Use the results to get access it and plotDifftoBase to plot it.

Note

This function should run after normalFactors or providing size factors.

Examples

```
data(simuN5)
obj <- ABSDataSet(counts=simuN5$counts, groups=factor(simuN5$groups))
obj <- normalFactors(obj)
obj <- callParameter(obj)
head(results(obj,c("foldChange","absD","baseMean")))
plotDifftoBase(obj)
```

---

callParameterwithoutReplicates

Calculate parameters for differential expression test base on absolute counts differences without replicates

---

Description

Calculate parameters for each gene (the moderating basemean and dispersions), without replicates

Usage

```
callParameterwithoutReplicates(object)
```

Arguments

object	a ABSDataSet object.

Details

buliding a pseudo group to esitimate parameter by mean difference. shifted and calculate a set of parameters from normalized counts table before callDEs

Value

A ABSDataSet object with absolute differences, basemean, mean of each group, variance, log2 of foldchange, named as 'absD', 'baseMean', 'Amean', 'Bmean', 'Variance' and 'foldChange', respectively. Use the results to get access it

Note

This function should run after normalFactors or providing size factors. This function firstly constructs an expression level depended fold-change cutoffs and then separate the data into two groups. The group with fold-change less than cutoffs is used to training the dispersion. However, the cutoff might be too small when applied on data set without or with less DEs. To avoid it, we set a prior value (0.5) to it.

Examples

```
data(simuN5)
obj <- ABSDataSet(counts=(simuN5$counts)[,c(1,2)], groups=factor(c(1,2)))
obj <- normalFactors(obj)
obj <- callParameterwithoutReplicates(obj)
obj <- callDEs(obj)
head(results(obj))
```

---

counts *Accessors for the 'counts' slot of a ABSDataSet object.*

Description

Accessors for the 'counts' slot of a ABSDataSet object, return a matrix

Usage

```
## S4 method for signature 'ABSDataSet'
counts(object,norm=FALSE)

## S4 replacement method for signature 'ABSDataSet,matrix'
counts(object)<-value
```

Arguments

object	a ABSDataSet object.
norm	logical indicating whether or not to normalize the counts before returning
value	an numeric matrix

Details

The counts slot holds the count data as a matrix of non-negative integer count values, rows and columns for genes and samples, respectively.

See Also

sFactors, normalFactors

Examples

```
data(simuN5)
obj <- ABSDataSet(counts=simuN5$counts, groups=factor(simuN5$groups))
head(counts(obj))
counts(obj) <- matrix(1:50,nrow=5,ncol=10)
head(counts(obj))
```

`estimateSizeFactorsForMatrix` *Low-level function to estimate size factors with robust regression.*

Description

This function is borrowed from DESeq.

Usage

```
estimateSizeFactorsForMatrix(counts, locfunc = median)
```

Arguments

`counts`	a matrix or data frame of counts, i.e., non-negative integer values
`locfunc`	a function to compute a location for a sample. By default, the median is used.

Details

Given a matrix or data frame of count data, this function estimates the size factors as follows: Each column is divided by the geometric means of the rows. The median (or, if requested, another location estimator) of these ratios (skipping the genes with a geometric mean of zero) is used as the size factor for this column. Typically, you will not call this function directly.

Value

a vector with the estimates size factors, one element per column

Author(s)

Simon Anders

References

Simon Anders, Wolfgang Huber: Differential expression analysis for sequence count data. Genome Biology 11 (2010) R106, http://dx.doi.org/10.1186/gb-2010-11-10-r106

Examples

```
data(simuN5)
dat <- simuN5
estimateSizeFactorsForMatrix(dat$counts)
```

excounts *Accessors for the 'excounts' slot of a ABSDataSet object.*

Description

Accessors for the 'excounts' slot of a ABSDataSet object, return a matrix

Usage

```
## S4 replacement method for signature 'ABSDataSet,matrix'
excounts(object)<-value
```

Arguments

object	a ABSDataSet object.
value	an numeric matrix

Details

The excounts slot holds the nomarlized (trimmed or not) count data as a matrix of non-negative integer count values, rows and columns for genes and samples, respectively.

See Also

ABSDataSet, ReplaceOutliersByMAD

Examples

```
data(simuN5)
obj <- ABSDataSet(counts=simuN5$counts, groups=factor(simuN5$groups))
obj <- normalFactors(obj)
obj <- ReplaceOutliersByMAD(obj)
head(excounts(obj))
```

genAFold *Calculate parameters for differential expression test base on absolute counts differences*

Description

Calculate aFold for each gene and general sd

Usage

```
genAFold(nncounts, cond, preval = 0.05, qforkappa = 0, pair = FALSE,
  priorgenesd)
```

Arguments

nncounts	matrix for read count.
cond	factor for conditions. If provide only one condition, fold-change estimation will be suppressed.
preval	pre-defined scale control for variance normalization, default is 0.05, a large value generally increases the fold-changes (decreases penalty of variances) under low expression.
qforkappa	quantile for estimating kappa(>=qforkappa), default is 0 (without trimming of data). Please set up a value in [0,1) if you want to trim the low expressed data.
pair	switch for paired samples, default is false
priorgenesd	prior value for general SD of fold change, if provided, the estimation of general SD will be replaced by this value.

Details

shifted and calculate a set of parameters from normalized counts table before callDEs

Value

A list with log2 foldchange, general SD for calculating pvalue, variance stabilized counts and expression level adjusted counts (used for PCA analysis)

Note

This function should run after normalFactors.

Examples

```
data(simuN5)
obj <- ABSDataSet(counts=simuN5$counts, groups=factor(simuN5$groups))
mtx <- counts(obj,TRUE)
aFold <- genAFold(mtx,factor(simuN5$groups))
hist(aFold[[1]])
```

---

groups *Accessors for the 'groups' slot of a ABSDataSet object.*

Description

Accessor functions for the 'groups' information in a ABSDataSet object.

Usage

```
## S4 method for signature 'ABSDataSet'
groups(object)

## S4 replacement method for signature 'ABSDataSet,factor'
groups(object)<-value
```

Arguments

object	an ABSDataSet object.
value	a factor object, includes two groups, equal with the number of samples

Details

The 'groups' is a factor object, contains the experiment design for differential expression analysis. Its length should be equal with the sample size.

Examples

```
data(simuN5)
obj <- ABSDataSet(counts=simuN5$counts, groups=factor(simuN5$groups))
groups(obj)
groups(obj) <- factor(rep(c("A","B"),c(5,5)))
groups(obj)
```

LevelstoNormFC *Accessors for the 'LevelstoNormFC' slot of a ABSDataSet object.*

Description

Accessor functions for the 'LevelstoNormFC' slot of a ABSDataSet object.

Usage

```
## S4 method for signature 'ABSDataSet'
LevelstoNormFC(object)

## S4 replacement method for signature 'ABSDataSet,numeric'
LevelstoNormFC(object)<-value
```

Arguments

object	an ABSDataSet object.
value	a positive numeric object

Details

The 'LevelstoNormFC' is maximal level of average standard deviation in fold-change normalization according to expression level.

See Also

ABSDataSet, callParameter

Examples

```
data(simuN5)
obj <- ABSDataSet(counts=simuN5$counts, groups=factor(simuN5$groups))
LevelstoNormFC(obj)
LevelstoNormFC(obj) <- 200
LevelstoNormFC(obj)
```

---

maxRates *Accessors for the 'maxRates' slot of a ABSDataSet object.*

Description

Accessor functions for the 'maxRates' slot of a ABSDataSet object.

Usage

```
## S4 method for signature 'ABSDataSet'
maxRates(object)

## S4 replacement method for signature 'ABSDataSet,numeric'
maxRates(object)<-value
```

Arguments

object	an ABSDataSet object.
value	a positive numeric object

Details

The 'maxRates' is the upper bound of rate for baseline of counts difference esitimation.

See Also

callParameter,ABSDataSet

Examples

```
data(simuN5)
obj <- ABSDataSet(counts=simuN5$counts, groups=factor(simuN5$groups))
maxRates(obj)
maxRates(obj) <- 0.4
maxRates(obj)
```

`minimalDispersion` *Accessors for the 'minDispersion' slot of a ABSDataSet object.*

Description

Accessor functions for the 'minDispersion' slot of a ABSDataSet object.

Usage

```
## S4 method for signature 'ABSDataSet'
minimalDispersion(object)

## S4 replacement method for signature 'ABSDataSet,numeric'
minimalDispersion(object)<-value
```

Arguments

`object`	an `ABSDataSet` object.
`value`	a positive numeric object

Details

The 'minimalDispersion' is the penalty of dispersion estimation. User can set the penalty of dispersion by this function

See Also

`callParameter`,`ABSDataSet`

Examples

```
data(simuN5)
obj <- ABSDataSet(counts=simuN5$counts, groups=factor(simuN5$groups))
minimalDispersion(obj)
minimalDispersion(obj) <- 0.2
minimalDispersion(obj)
```

minRates *Accessors for the 'minRates' slot of a ABSDataSet object.*

Description

Accessor functions for the 'minRates' slot of a ABSDataSet object.

Usage

```
## S4 method for signature 'ABSDataSet'
minRates(object)

## S4 replacement method for signature 'ABSDataSet,numeric'
minRates(object)<-value
```

Arguments

object	an ABSDataSet object.
value	a positive numeric object

Details

The 'minRates' is the lower bound of rate for baseline of counts difference esitimation.

See Also

callParameter,ABSDataSet

Examples

```
data(simuN5)
obj <- ABSDataSet(counts=simuN5$counts, groups=factor(simuN5$groups))
minRates(obj)
minRates(obj) <- 0.3
minRates(obj)
```

normalFactors *Estimating size factors from the reads count table*

Description

Function for esitmating size factors

Usage

```
normalFactors(object)
```

Arguments

object	a ABSSeq object with element of 'counts' and 'normMethod', see the constructor functions ABSDataSet.

Details

Given a matrix of count data, this function esitmates the size factors by selected method. It aslo provides four different methods for normalizing according to user-defined size factors, total reads, up quantile (75

Value

a ABSDataSet object with the estimates size factors, one element per column. Use the sFactors to show it.

Examples

```
data(simuN5)
obj <- ABSDataSet(counts=simuN5$counts, groups=factor(simuN5$groups))
obj <- normalFactors(obj)
sFactors(obj)
```

---

normMethod *Accessors for the 'normMethod' slot of a ABSDataSet object.*

Description

Accessor functions for the 'normMethod' information in a ABSDataSet object.

Usage

```
## S4 method for signature 'ABSDataSet'
normMethod(object)

## S4 replacement method for signature 'ABSDataSet,character'
normMethod(object)<-value
```

Arguments

object	an ABSDataSet object.
value	a character object, should be one of 'user', 'qtoatl', 'total', 'quartile' and 'geometric'. See normalFactors

Details

The 'normMethod' is the method for calculating the size factors. Currently, Four methods: 'user', 'qtoatl', 'total', 'quartile' and 'DESeq' are available.

Examples

```
data(simuN5)
obj <- ABSDataSet(counts=simuN5$counts, groups=factor(simuN5$groups))
normMethod(obj)
normMethod(obj) <- "geometric"
normMethod(obj)
```

---

paired *Accessors for the 'paired' slot of a ABSDataSet object.*

Description

Accessors for the 'paired' slot of a ABSDataSet object, return a logical value

Usage

```
## S4 method for signature 'ABSDataSet'
paired(object)

## S4 replacement method for signature 'ABSDataSet,logical'
paired(object)<-value
```

Arguments

object	a ABSDataSet object.
value	value a boolean object, should be either TRUE or FALSE.

Details

The 'paired' is the switch for differential expression detection among paired samples, with a boolean value: TRUE or FALSE (default). When "paired" is TRUE, the replicates in each group should be equal.

Examples

```
data(simuN5)
obj <- ABSDataSet(counts=simuN5$counts, groups=factor(simuN5$groups))
paired(obj)
paired(obj) <- TRUE
paired(obj)
```

`plotDifftoBase` *Plot absolute log2 fold-change against base mean of expression*

Description

Plot absolute differencs against expression levels

Usage

```
plotDifftoBase(object, foldname = "foldChange", adj.pcut = 0.05,
  cols = c("black", "red"), pch = 16, xlab = "log2 of Expression level",
  ylab = "log2 fold-change", ...)
```

Arguments

`object`	a ABSDataSet
`foldname`	indicates kind of fold-change in plotting, default is 'foldChange', see `results`
`adj.pcut`	cutoff for differential expressed genes, marked by different color, default is 0.05
`cols`	the colors to mark the non-DE and DE genes, defualt is black and red, respectively
`pch`	pch, default is 16
`xlab`	xlab, default is 'log2 of Expression level'
`ylab`	ylab, default is 'log2 fold-change'
`...`	further arguments to `plot`

Details

Plot absolute differencs against expression levels and mark the gene with a color at a given cutoff of fold-change

Examples

```
data(simuN5)
obj <- ABSDataSet(counts=simuN5$counts, groups=factor(simuN5$groups))
obj <- ABSSeq(obj)
plotDifftoBase(obj)
```

qtotalNormalized *Estimating size factors from the reads count table via ranking*

Description

Function of qtotal for esitmating size factors

Usage

```
qtotalNormalized(ma, qper = 0.95, qst = 0.1, qend = 0.95, qstep = 0.01,
  qbound = 0.05, mcut = 4, qcl = 1.5)
```

Arguments

ma	a count matrix
qper	quantile for assessing dispersion of data, default is 0.95, which serves to avoid outliers, should in (0,1]
qst	start of quantile for estimating cv ratio, should be in [0,1], default is 0.1
qend	end of quantile for estimating cv ratio, should be in [qbound,1-qbound], default is .95
qstep	step of quantile for estimating cv ratio (sliding window), should be in (0,1], default is 0.01
qbound	window size for estimating cv and shifted size factor, default is 0.05, a smaller window size is suitable if number of genes is large
mcut	cutoff of mean from sliding window to avoid abnormal cv, should >=0, default is 4
qcl	scale for outlier detection, should >=0, default is 1.5

Details

Given a matrix of count data, this function esitmates the size factors by qtotal method, which is based on assessing DE (CV) and ranking. The CV is estimated via sliding window.

Value

a vector with the estimates size factors, one element per column

Examples

```
data(simuN5)
counts <- simuN5$counts
qtotalNormalized(counts)
```

ReplaceOutliersByMAD *Replacing outliers by moderated MAD*

Description

Function for replacing the outliers by MAD

Usage

```
ReplaceOutliersByMAD(object, replaceOutlier = TRUE, cutoff = 2,
  baseMean = 100, limitMad = 0.707, spriors = 2, Caseon = TRUE, ...)
```

Arguments

object	a ABSSeq object with element of 'counts' and 'normMethod', see the constructor functions ABSDataSet.
replaceOutlier	switch for replacing, default is TRUE.
cutoff	cutoff of moderating MAD for outliers, default is 2
baseMean	parameter for limiting the trimming at low expression level by baseMean/(sample size), default is 100.
limitMad	the minimal prior for moderating MAD, default is set to 0.707, which is usually the highest standard deviation at expression level of 1
spriors	prior weight size for prior MAD, default is 2
Caseon	switch for dealing with outlier trimming at sample size of 2
...	reserved parameters

Details

Given a matrix of count data, this function replacing the outliers by MAD. Noticely, this function also provides part of parameters for DEs calling. It is called by callParameter

Value

a ABSDataSet object with normalized counts after trimming (replaceOutlier=TRUE) or not (replaceOutlier=FALSE). Use the excounts to show it. Use results with name 'trimmed' to view the trimming status.

Examples

```
data(simuN5)
obj <- ABSDataSet(counts=simuN5$counts, groups=factor(simuN5$groups))
obj <- normalFactors(obj)
obj <- ReplaceOutliersByMAD(obj)
head(excounts(obj))
head(results(obj,c("trimmed")))
```

results *Accessor functions for the result from a ABSDataSet*

Description

Accessor functions for the result from a ABSDataSet by given names

Usage

```
## S4 method for signature 'ABSDataSet'
results(object, cnames = c("Amean", "Bmean",
  "baseMean", "absD", "Variance", "rawFC", "lowFC", "foldChange", "pvalue",
  "adj.pvalue", "trimmed"))
```

Arguments

object	a ABSDataSet
cnames	a vecotr of names for output, which are among: 'Amean','Bmean', log2 of mean counts for group A and B, "baseMean', estimated mean for absolute counts difference (absD), used for mu in pnbinom 'absD', absolute counts difference in total 'Variance', pooled Variance for two groups 'rawFC','lowFC', 'foldChange', log2 fold-change of original (Bmean-Amean), corrected by expression level and corrected by both expression level and gene-specific dispersion 'pvalue','adj.pvalue', pvalue and adjusted pvalue 'trimmed', number of trimmed outliers

Details

This function returns the result of ABSSeq as a table or a vector depended on the given names, see ABSSeq

Value

a table according to canmes.

See Also

ABSSeq

Examples

```
data(simuN5)
obj <- ABSDataSet(counts=simuN5$counts, groups=factor(simuN5$groups))
obj <- normalFactors(obj)
obj <- callParameter(obj)
obj <- callDEs(obj)
head(results(obj))
```

sFactors *Accessors for the 'sizeFactor' slot of a ABSDataSet object.*

Description

Accessor functions for the 'sizeFactor' slot of a ABSDataSet object.

Usage

```
## S4 method for signature 'ABSDataSet'
sFactors(object)

## S4 replacement method for signature 'ABSDataSet,numeric'
sFactors(object)<-value
```

Arguments

object	an ABSDataSet object.
value	a numeric object, one for each sample

Details

The sizeFactors vector assigns to each sample a value, used to normalize the counts in each sample according to selected normMethod.

See Also

normalFactors

Examples

```
data(simuN5)
obj <- ABSDataSet(counts=simuN5$counts, groups=factor(simuN5$groups))
obj <- normalFactors(obj)
sFactors(obj)
sFactors(obj) <- runif(10,1,2)
sFactors(obj)
```

simuN5 *Simulated study with random outliers*

Description

Simulated study with random outliers, include five samples for two groups. It contains counts table, groups and defined differential expression genes.

Usage

```
data(simuN5)
```

Format

The format is: List of 3

$ counts: integer, reads count matrix

$ groups: two groups

$ DEs : differential expression genes

Details

Multiple each gene with a value from 5-10 by chance at pvalue of 0.05.

Source

http://bcf.isb-sib.ch/data/compcodeR/

References

Soneson C, Delorenzi M: A comparison of methods for differential expression analysis of RNA-seq data. BMC Bioinformatics 2013, 14(1):91.

Examples

```
data(simuN5)
```

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