Package ‘ABSSeq’

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Type Package

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

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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.

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ABSDataSet

**Description**

ABSDataSet object and constructors

**Usage**

```r
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 constructs 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

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

Description

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

Usage

```r
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`: default is 'BH', method for p-value adjusted, see `p.adjust.methods` for details.
- `replaceOutliers`: default is TRUE, switch for outlier replacement.
- `useaFold`: default 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 binomial 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, shrunked (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, adjusted 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 design.

**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, ...)
**ABSSeqlm**

**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 resprresents the saturated 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`.
- **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 (saturated model - reduced model). Saturated model includes all factors in design matrix and reduced model includes factors in condA+condB. if saturated 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**: default 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, adjusted 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). Saturated 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
callDEs

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 stabilized counts and basemean

Note
This function should run after normalFactors.

Examples

```r
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]])
```

Description
Testing the differential expression by counts difference

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>an ABSDataSet object.</td>
</tr>
<tr>
<td>adjmethod</td>
<td>the method for adjusting p-value, default is 'BH'. For details, see p.adjust.methods.</td>
</tr>
<tr>
<td>useaFold</td>
<td>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.</td>
</tr>
</tbody>
</table>

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: shrunk 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**

```r
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.
callParameterwithoutReplicates

Note

This function should run after `normalFactors` or providing size factors.

Examples

```r
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)
```

Description

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

Usage

```r
callParameterwithoutReplicates(object)
```

Arguments

- `object` A `ABSDataSet` object.

Details

building 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$count[,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$count, groups=factor(simuN5$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

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

```r
## 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 normalized (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

```r
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 based 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

ncounts  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

```r
## 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

```r
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

### Description

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

### Usage

```r
## 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
maxRates

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 estimation.

See Also
callParameter,ABSDataSet
minimalDispersion

Accessors for the 'minDispersion' slot of a ABSDataSet object.

### Description

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

### Usage

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

```r
## 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

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

```r
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 estimation.

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 estimating 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 estimates the size factors by selected method. It also 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

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

Description

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

Usage

```r
## 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

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

Description

Plot absolute differences 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, default 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 differences 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)
qaTotalNormalized

Estimating size factors from the reads count table via ranking

Description

Function of qaTotal for estimating size factors

Usage

qaTotalNormalized(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 estimates the size factors by qaTotal 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
qaTotalNormalized(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")))
Accessor functions for the result from a `ABSDataSet`

**Description**

Accessor functions for the result from a `ABSDataSet` by given names

**Usage**

```r
## 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 vector 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 `pbinom` '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 `cnames`.

**See Also**

`ABSSeq`

**Examples**

```r
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)
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/

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