

Package ‘TCC’

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Type Package

Title TCC: Differential expression analysis for tag count data with robust normalization strategies

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Author Jianqiang Sun, Tomoaki Nishiyama, Kentaro Shimizu, and Koji Kadota

Maintainer Jianqiang Sun <wukong@bi.a.u-tokyo.ac.jp>, Tomoaki Nishiyama <tomoakin@staff.kanazawa-u.ac.jp>

Description This package provides a series of functions for performing differential expression analysis from RNA-seq count data using robust normalization strategy (called DEGES). The basic idea of DEGES is that potential differentially expressed genes or transcripts (DEGs) among compared samples should be removed before data normalization to obtain a well-ranked gene list where true DEGs are top-ranked and non-DEGs are bottom ranked. This can be done by performing a multi-step normalization strategy (called DEGES for DEG elimination strategy). A major characteristic of TCC is to provide the robust normalization methods for several kinds of count data (two-group with or without replicates, multi-group/multi-factor, and so on) by virtue of the use of combinations of functions in other sophisticated packages (especially edgeR, DESeq, and baySeq).

Depends R (>= 2.15), methods, DESeq, edgeR, baySeq, ROC

Imports EBSeq, samr

Suggests RUnit, BiocGenerics

Enhances snow

biocViews HighThroughputSequencing, DifferentialExpression, RNAseq

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R topics documented:

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| | |
|------|-------------------------------------|
| arab | <i>Arabidopsis RNA-Seq data set</i> |
|------|-------------------------------------|

Description

This dataset was imported from NBPSeq package and the following explanation is verbatim copy of their explanation:

An RNA-Seq dataset from a pilot study of the defense response of *Arabidopsis* to infection by bacteria. We performed RNA-Seq experiments on three independent biological samples from each of the two treatment groups. The matrix contains the frequencies of RNA-Seq reads mapped to genes in a reference database. Rows correspond to genes and columns correspond to independent biological samples.

Usage

```
data(arab)
```

Format

A 26222 by 6 matrix of RNA-Seq read frequencies.

Details

This dataset was imported from NBPSeq package and the following explanation is verbatim copy of their explanation:

We challenged leaves of *Arabidopsis* with the defense-eliciting $\Delta hrcC$ mutant of *Pseudomonas syringae* pathovar *tomato* DC3000. We also infiltrated leaves of *Arabidopsis* with 10mM MgCl₂ as a mock inoculation. RNA was isolated 7 hours after inoculation, enriched for mRNA and prepared for RNA-Seq. We sequenced one replicate per channel on the Illumina Genome Analyzer (<http://www.illumina.com>). The length of the RNA-Seq reads can vary in length depending on user preference and the sequencing instrument. The dataset used here are derived from a 36-cycle sequencing reaction, that we trimmed to 25mers. We used an in-house computational pipeline to process, align, and assign RNA-Seq reads to genes according to a reference database we developed for *Arabidopsis*.

References

Di Y, Schafer DW, Cumbie JS, and Chang JH (2011): "The NBP Negative Binomial Model for Assessing Differential Gene Expression from RNA-Seq", *Statistical Applications in Genetics and Molecular Biology*, 10 (1).

Examples

```
data(arab)
```

calcAUCValue

Calculate AUC value from a TCC-class object

Description

This function calculates AUC (Area under the ROC curve) value from a [TCC-class](#) object for simulation study.

Usage

```
calcAUCValue(tcc)
```

Arguments

tcc [TCC-class](#) object having values in both `stat$rank` and `simulation$trueDEG` fields.

Details

This function is generally used after the [estimateDE](#) function that estimates p -values (and the derivatives such as the q -values and the ranks) for individual genes based on the statistical model for differential expression (DE) analysis. In case of the simulation analysis, we know which genes are DEGs or non-DEGs in advance and the information is stored in the `simulation$trueDEG` field

of the **TCC-class** object `tcc` (i.e., `tcc$simulation$trueDEG`). The `calcAUCValue` function calculates the AUC value between the ranked gene list obtained by the `estimateDE` function and the truth obtained by the `simulateReadCounts` function. A well-ranked gene list should have a high AUC value (i.e., high sensitivity and specificity).

Value

numeric scalar.

Examples

```
# Analyzing a simulation data for comparing two groups
# (G1 vs. G2) with biological replicates.
# the first 200 genes are DEGs, where 180 are up in G1.
# The DE analysis is performed by an exact test in edgeR coupled
# with the DEGES/edgeR normalization factors.
tcc <- simulateReadCounts(Ngene = 1000, PDEG = 0.2,
                        DEG.assign = c(0.9, 0.1),
                        DEG.foldchange = c(4, 4),
                        replicates = c(3, 3))
tcc <- calcNormFactors(tcc, norm.method = "tmm", test.method = "edgeR",
                    iteration = 1, FDR = 0.1, floorPDEG = 0.05)
tcc <- estimateDE(tcc, test.method = "edgeR", FDR = 0.1)
calcAUCValue(tcc)

# Analyzing a simulation data for comparing two groups
# (G1 vs. G2) without replicates.
# the levels of DE are 3-fold in G1 and 7-fold in G2
# The DE analysis is performed by a negative binomial test in
# DESeq coupled with the DEGES/DESeq normalization factors.
tcc <- simulateReadCounts(Ngene = 1000, PDEG = 0.2,
                        DEG.assign = c(0.9, 0.1),
                        DEG.foldchange = c(3, 7),
                        replicates = c(1, 1))
tcc <- calcNormFactors(tcc, norm.method = "deseq", test.method = "deseq",
                    iteration = 1, FDR = 0.1, floorPDEG = 0.05)
tcc <- estimateDE(tcc, test.method = "deseq", FDR = 0.1)
calcAUCValue(tcc)
```

calcNormFactors

Calculate normalization factors

Description

This function calculates normalization factors using a specified multi-step normalization method from a **TCC-class** object. The procedure can generally be described as the *STEP1* – (*STEP2* – *STEP3*)_{*n*} pipeline.

Usage

```
## S4 method for signature TCC
calcNormFactors(tcc, norm.method = NULL, test.method = NULL,
                iteration = TRUE, FDR = NULL, floorPDEG = 0.05,
                increment = FALSE, ...)
```

Arguments

| | |
|-------------|---|
| tcc | TCC-class object. |
| norm.method | character specifying a normalization method used in both the STEP1 and STEP3. Possible values are "tmm" for the TMM normalization method implemented in the edgeR package, "edger" (same as "tmm"), and "deseq" for the method implemented in the DESeq package. The default is "tmm" when analyzing the count data with multiple replicates (i.e., $\min(\text{table}(\text{tcc}\$group[, 1])) > 1$) and "deseq" when analyzing the count data without replicates (i.e., $\min(\text{table}(\text{tcc}\$group[, 1])) == 1$). |
| test.method | character specifying a method for identifying differentially expressed genes (DEGs) used in STEP2: one of "edger", "deseq", "bayseq", "ebseq", "samseq", and "wad". See the "Details" filed in estimateDE for detail. The default is "edger" when analyzing the count data with multiple replicates (i.e., $\min(\text{table}(\text{tcc}\$group[, 1])) > 1$) and "deseq" when analyzing the count data without replicates (i.e., $\min(\text{table}(\text{tcc}\$group[, 1])) == 1$). |
| iteration | logical or numeric value specifying the number of iteration (n) in the proposed normalization pipeline: the $STEP1 - (STEP2 - STEP3)_n$ pipeline. If FALSE or 0 is specified, the normalization pipeline is performed only by the method in STEP1. If TRUE or 1 is specified, the three-step normalization pipeline is performed. Integers higher than 1 indicate the number of iteration in the pipeline. |
| FDR | numeric value (between 0 and 1) specifying the threshold for determining potential DEGs after STEP2. |
| floorPDEG | numeric value (between 0 and 1) specifying the minimum value to be eliminated as potential DEGs before performing STEP3. |
| increment | logical value. if increment = TRUE, the DEGES pipeline will perform again from the current iterated result. |
| ... | arguments to identify potential DEGs at STEP2. See the "Arguments" field in estimateDE for details. |

Details

The [calcNormFactors](#) function is the main function in the TCC package. Since this pipeline employs the DEG identification method at STEP2, our multi-step strategy can eliminate the negative effect of potential DEGs before the second normalization at STEP3. To fully utilize the DEG elimination strategy (DEGES), we strongly recommend not to use `iteration = 0` or `iteration = FALSE`. This function internally calls functions implemented in the other R packages according to the specified value.

- `norm.method = "tmm"`

The [calcNormFactors](#) function implemented in edgeR is used for obtaining the TMM normalization factors at both STEP1 and STEP3.

- norm.method = "deseq"

The `estimateSizeFactors` function implemented in DESeq is used for obtaining the size factors at both STEP1 and STEP3. The size factors are internally converted to normalization factors that are comparable to the TMM normalization factors.

Value

After performing the `calcNormFactors` function, the calculated normalization factors are populated in the `norm.factors` field (i.e., `tcc$norm.factors`). Parameters used for DEGES normalization (e.g., potential DEGs identified in STEP2, execution times for the identification, etc.) are stored in the `DEGES` field (i.e., `tcc$DEGES`) as follows:

| | |
|-----------------------------|--|
| <code>iteration</code> | the iteration number n for the STEP1 - (STEP2 - STEP3)_n pipeline . |
| <code>pipeline</code> | the DEGES normalization pipeline. |
| <code>threshold</code> | it stores (i) the type of threshold (<code>threshold\$type</code>), (ii) the threshold value (<code>threshold\$input</code>), and (iii) the percentage of potential DEGs actually used (<code>threshold\$PDEG</code>). These values depend on whether the percentage of DEGs identified in STEP2 is higher or lower to the value indicated by <code>floorPDEG</code> . Consider, for example, the execution of <code>calcNormFactors</code> function with " <code>FDR = 0.1</code> and <code>floorPDEG = 0.05</code> ". If the percentage of DEGs identified in STEP2 satisfying <code>FDR = 0.1</code> was 0.14 (i.e., higher than the <code>floorPDEG</code> of 0.05), the values in the threshold fields will be <code>threshold\$type = "FDR"</code> , <code>threshold\$input = 0.1</code> , and <code>threshold\$PDEG = 0.14</code> . If the percentage (= 0.03) was lower than the predefined <code>floorPDEG</code> value of 0.05, the values in the threshold fields will be <code>threshold\$type = "floorPDEG"</code> , <code>threshold\$input = 0.05</code> , and <code>threshold\$PDEG = 0.05</code> . |
| <code>potDEG</code> | numeric binary vector (0 for non-DEG or 1 for DEG) after the evaluation of the percentage of DEGs identified in STEP2 with the predefined <code>floorPDEG</code> value. If the percentage (e.g., 2%) is lower than the <code>floorPDEG</code> value (e.g., 17%), 17% of elements become 1 as DEG. |
| <code>prePotDEG</code> | numeric binary vector (0 for non-DEG or 1 for DEG) before the evaluation of the percentage of DEGs identified in STEP2 with the predefined <code>floorPDEG</code> value. Regardless of the <code>floorPDEG</code> value, the percentage of elements with 1 is always the same as that of DEGs identified in STEP2. |
| <code>execution.time</code> | computation time required for normalization. |

Examples

```
data(hypoData)
group <- c(1, 1, 1, 2, 2, 2)

# calculating normalization factors using the DEGES/edgeR method
# (the TMM-edgeR-TMM pipeline)
tcc <- new("TCC", hypoData, group)
tcc <- calcNormFactors(tcc, norm.method = "tmm", test.method = "edgeR",
                      iteration = 1, FDR = 0.1, floorPDEG = 0.05)

tcc$norm.factors

# calculating normalization factors using the iterative DEGES/edgeR method
# (iDEGES/edgeR) with n = 3
```

```
tcc <- new("TCC", hypoData, group)
tcc <- calcNormFactors(tcc, norm.method = "tmm", test.method = "edger",
                      iteration = 3, FDR = 0.1, floorPDEG = 0.05)
tcc$norm.factors

# calculating normalization factors for simulation data without replicates
tcc <- simulateReadCounts(replicates = c(1, 1))
tcc <- calcNormFactors(tcc, norm.method = "deseq", test.method = "deseq",
                      iteration = 1, FDR = 0.1, floorPDEG = 0.05)
tcc$norm.factors
```

| | |
|--------|--|
| do_TbT | <i>Calculate normalization factors for raw tag count data using a multi-step normalization strategy called "TbT"</i> |
|--------|--|

Description

This method performs TMM normalization, baySeq, and again TMM normalization to infer a good normalization factor as described in Kadota et al. 2012, Algorithms Mol Biol 7:5. This function will be obsoleted. Please use [TCC-class](#) based methods.

Usage

```
do_TbT(data, data.cl, sample_num = 10000)
```

Arguments

| | |
|------------|--|
| data | The data matrix to be analysed. Numerical data only |
| data.cl | A vector describing the data class for columns in data |
| sample_num | Sample number for bayesian estimation |

See Also

[edgeR](#)

Examples

```
## Not run:
sample <- NBsample()
out <- do_TbT(sample$data, c(1, 1, 1, 2, 2, 2))

## End(Not run)
```

estimateDE

*Estimate degrees of differential expression (DE) for individual genes***Description**

This function calculates p -values (or the related statistics) for identifying differentially expressed genes (DEGs) from a [TCC-class](#) object. `estimateDE` internally calls a specified method implemented in other R packages.

Usage

```
estimateDE(tcc, test.method, FDR,
           dispersion, fit0, fit1, design,
           contrast, coef, comparison, samplesize, floor.value = 1, cl)
```

Arguments

| | |
|--------------------------|--|
| <code>tcc</code> | TCC-class object. |
| <code>test.method</code> | character string specifying a method for identifying DEGs: one of "edger", "deseq", "bayseq", "ebseq", "samseq", and "wad". See the "Details" field for detail. The default is "edger" when analyzing the count data with replicates (i.e., $\min(\text{table}(tcc\$group[, 1])) > 1$), "deseq" when analyzing the count data without replicates (i.e., $\min(\text{table}(tcc\$group[, 1])) == 1$). |
| <code>FDR</code> | numeric value (between 0 and 1) specifying the threshold for determining DEGs. |
| <code>dispersion</code> | numeric vector giving the dispersion of all genes for analyzing the count data without replicates when the <code>test.method = "edger"</code> is specified. See the exactTest function in edgeR for details. |
| <code>design</code> | numeric matrix giving the design matrix for the linear model. See the glmFit function in edgeR for details. |
| <code>contrast</code> | numeric vector specifying a contrast of the linear model coefficients to be tested equal to zero. See the glmLRT function in edgeR for details. |
| <code>coef</code> | integer or character vector indicating which coefficients of the linear model are to be tested equal to zero. See the glmLRT function in edgeR for details. |
| <code>fit0</code> | a formula for creating reduced model described in DESeq. The left hand side must be count, the right hand side can involve any column of <code>tcc\$group</code> is used as the model frame. See the fitNbinomGLMs function for details. |
| <code>fit1</code> | a formula for creating full model described in DESeq. The left hand side must be count, the right hand side can involve any column of <code>tcc\$group</code> is used as the model frame. See the fitNbinomGLMs function for details. |
| <code>comparison</code> | numeric or character string identifying the columns in the <code>tcc\$group[, 1]</code> for analysis. See the group argument in topCounts for details. |
| <code>samplesize</code> | integer specifying (i) the sample size for estimating the prior parameters if <code>test.method = "bayseq"</code> (defaults to 10000), (ii) the iteration number used in EM algorithm in EBSeq if <code>test.method = "ebseq"</code> (defaults to 5), and (iii) the number of permutation in samr if <code>test.method = "samseq"</code> (defaults to 10). |

| | |
|--------------------------|---|
| <code>floor.value</code> | numeric scalar (≥ 0) to replace the values higher than the <code>floor.value</code> if <code>test.method = "wad"</code> (defaults to 1). |
| <code>cl</code> | snow object when using multi processors if <code>test.method = "bayseq"</code> is specified. See the <code>getPriors.NB</code> function in <code>baySeq</code> for details. |

Details

`estimaetDE` function is generally used after performing the `calcNormFactors` function that calculates normalization factors. `estimateDE` constructs a statistical model for differential expression (DE) analysis with the calculated normalization factors and returns the p -values (or the derivatives). The individual functions in the other packages are internally called according to the specified `test.method` parameter.

- `test.method = "edger"`

There are two approaches (i.e., exact test and GLM) to identify DEGs in edgeR. The two approaches are implemented in TCC. As a default, the exact test approach is used for two-group data, and GLM approach is used for multi-group or multi-factor data. However, if `design` and the one of `coef` or `contrast` are given, the GLM approach will be used for two-group data. Currently, edgeR package does not support data without replicates.

If the exact test approach is used, `estimateCommonDisp`, `estimateTagwiseDisp`, and `exactTest` are internally called.

If the GLM approach is used, `estimateGLMCommonDisp`, `estimateGLMTrendedDisp`, `estimateGLMTagwiseDisp`, `glmFit`, and `glmLRT` are internally called.
- `test.method = "deseq"`

DESeq supports two approach (i.e. an exact test and GLM approach) for identifying DEGs. As a default, the exact test is used for two-group data, and GLM approach is used for multi-group or multi-factor data. However, if `fit0` and `fit1` are given, the GLM approach will be used for two-group data.

If the exact test is used, `estimateDispersions` and `nbinomTest` are internally called.

If the GLM approach is used, `estimateDispersions`, `fitNbinomGLMs`, and `nbinomGLMTest` are internally called.
- `test.method = "bayseq"`

`getPriors.NB` and `getLikelihoods.NB` in `baySeq` are internally called for identifying DEGs. Since `baySeq` outputs posterior likelihoods instead of p -values, the $(1 - \text{likelihood})$ values are stored in the corresponding field (i.e., `tcc$stat$p.value`).
- `test.method = "ebseq"`

`EBTest` and `EBMultiTest` are internally called for two-group and multi-group data with replicates, respectively. Currently, both functions does not support data without replicates. Since EBSeq only outputs q -value, the all values in `tcc$stat$p.value` are NA.
- `test.method = "samseq"`

`SAMseq` with `resp.type = "Two class unpaired"` argument in `samr` package is called to identify DEGs for two-group data, and `resp.type = "Multiclass"` for multi-group data. Since `SAMseq` outputs test statistics instead of p -values, the `tcc$stat$p.value` and `tcc$stat$q.value` are NA. Alternatively, the test statistics are stored in `tcc$stat$testStat` field.
- `test.method = "wad"`

The `WAD` implemented in TCC is used for identifying DEGs. Since `WAD` outputs test statistics

instead of p -values, the `tcc$stat$p.value` and `tcc$stat$q.value` are NA. Alternatively, the test statistics are stored in `tcc$stat$testStat` field.

Value

A `TCC-class` object containing following fields:

| | |
|-----------------------------|--|
| <code>stat\$p.value</code> | numeric vector of p -values. |
| <code>stat\$q.value</code> | numeric vector of q -values calculated based on the p -values using the <code>p.adjust</code> function with default parameter settings. |
| <code>stat\$testStat</code> | numeric vector of test statistics if <code>test.method = "samseq"</code> or <code>"wad"</code> is specified. |
| <code>stat\$rank</code> | gene rank in order of the p -values or test statistics. |
| <code>estimatedDEG</code> | numeric vector consisting of 0 or 1 depending on whether each gene is classified as non-DEG or DEG. The threshold for classifying DEGs or non-DEGs is preliminarily given as the FDR argument. |

Examples

```
# Analyzing a simulation data for comparing two groups
# (G1 vs. G2) with biological replicates
# The DE analysis is performed by an exact test in edgeR coupled
# with the DEGES/edgeR normalization factors.
# For retrieving the summaries of DE results, we recommend to use
# the getResult function.
data(hypoData)
group <- c(1, 1, 1, 2, 2, 2)
tcc <- new("TCC", hypoData, group)
tcc <- calcNormFactors(tcc, norm.method = "tmm", test.method = "edgeR",
                      iteration = 1, FDR = 0.1, floorPDEG = 0.05)
tcc <- estimateDE(tcc, test.method = "edgeR", FDR = 0.1)
head(tcc$stat$p.value)
head(tcc$stat$q.value)
head(tcc$estimatedDEG)
result <- getResult(tcc)

# Analyzing a simulation data for comparing two groups
# (G1 vs. G2) without replicates
# The DE analysis is performed by a negative binomial (NB) test
# in DESeq coupled with the DEGES/DESeq normalization factors.
data(hypoData)
group <- c(1, 2)
tcc <- new("TCC", hypoData[, c(1, 4)], group)
tcc <- calcNormFactors(tcc, norm.method = "deseq", test.method = "deseq",
                      iteration = 1, FDR = 0.1, floorPDEG = 0.05)
tcc <- estimateDE(tcc, test.method = "deseq", FDR = 0.1)
```

exactTestafterTbT *exactTest after TMM-baySeq-TMM procedure*

Description

This function perform exact test with edgeR after TMM-baySeq-TMM procedure via [do_TbT](#). This function will be obsolete. Use [TCC-class](#) based methods instead.

Usage

```
exactTestafterTbT(names, counts, group, sample_num = 10000)
```

Arguments

| | |
|------------|--|
| names | A vector containing the name of each element eg gene |
| counts | The data matrix to be analysed. Numerical data only |
| group | A vector describing the data class for columns in data |
| sample_num | Sample number for Bayesian estimation |

Value

This function return a list of data, `norm_f_TbT`, `counts`, and `group`. The data is a data frame containing the names and counts as the input, table output by the `exactTest()`, FDR calculated by `p.adjust()`, and rank by the FDR. `norm_f_TbT`, `Mval`, and `Aval` are calculated by `do_TbT()`. The counts and group are the copy of the input.

| | |
|------------|--|
| names | As in the input argument. |
| counts | As in the input argument. |
| table | As returned from <code>exactTest()</code> . |
| FDR | False discovery rate calculated by <code>p.adjust()</code> . |
| rank_edgeR | The rank of the above. |

See Also

[do_TbT](#) [exactTest](#) [p.adjust](#)

Examples

```
## Not run:
sample <- NBsample()
out <- exactTestafterTbT(paste("gene",1:nrow(sample$data), sep=""),
                        sample$data, c(1,1,1,2,2,2))

## End(Not run)
```

filterLowCountGenes *Filter genes from a TCC-class object*

Description

This function takes a TCC object and returns a new TCC object without genes having low count tags across samples. The threshold is configurable with `low.count` parameter.

Usage

```
filterLowCountGenes(tcc, low.count = 0)
```

Arguments

| | |
|------------------------|---|
| <code>tcc</code> | TCC-class object. |
| <code>low.count</code> | numeric value (≥ 0) specifying the threshold for filtering genes. The higher value indicates the more numbers of genes to be filtered out. |

Value

TCC-class object consisting of genes whose sum of the counts across samples is equal or higher than the `low.count` value.

Examples

```
# Filtering genes with zero counts across samples (default) from
# a hypothetical count dataset that originally has 1,000 genes
data(hypoData)
group <- c(1, 1, 1, 2, 2, 2)
tcc <- new("TCC", hypoData, group)
dim(tcc$count)
tcc <- filterLowCountGenes(tcc)
dim(tcc$count)

# Filtering genes with 10 counts across samples from hypoData
data(hypoData)
group <- c(1, 1, 1, 2, 2, 2)
tcc <- new("TCC", hypoData, group)
dim(tcc$count)
tcc <- filterLowCountGenes(tcc, low.count = 10)
dim(tcc$count)
```

getNormalizedData *Obtain normalized count data*

Description

This function generates normalized count data from both original count data and calculated normalization factors.

Usage

```
getNormalizedData(tcc)
```

Arguments

tcc [TCC-class](#) object.

Details

This function is generally used after the [calcNormFactors](#) function that calculates normalization factors. The normalized data is calculated using both the original count data stored in the count field and the normalization factors stored in the norm.factors field in the [TCC-class](#) object.

Value

A numeric matrix containing normalized count data.

Examples

```
# Note that the hypoData has non-DEGs at 201-1000th rows
nonDEG <- 201:1000
data(hypoData)
summary(hypoData[nonDEG, ])
group <- c(1, 1, 1, 2, 2, 2)

# Obtaining normalized count data after performing the
# DEGES/edgeR normalization method, i.e., DEGES/edgeR-normalized data
tcc <- new("TCC", hypoData, group)
tcc <- calcNormFactors(tcc, norm.method = "tmm", test.method = "edger",
                      iteration = 1, FDR = 0.1, floorPDEG = 0.05)
normalized.count <- getNormalizedData(tcc)
summary(normalized.count[nonDEG, ])

# Obtaining normalized count data after performing the
# TMM normalization method (Robinson and Oshlack, 2010),
# i.e., TMM-normalized data
tcc <- new("TCC", hypoData, group)
tcc <- calcNormFactors(tcc, norm.method = "tmm", iteration = 0)
normalized.count <- getNormalizedData(tcc)
summary(normalized.count[nonDEG, ])
```

| | |
|-----------|---|
| getResult | <i>Obtain the summaries of results after the differential expression analysis</i> |
|-----------|---|

Description

This function is generally used after the `estimateDE` function. It retrieves the summaries of differential expression (DE) results from `TCC-class` object. The retrieved information includes p -values, q -values, coordinates of M-A plot (i.e., M and A values), and so on.

Usage

```
getResult(tcc, sort = FALSE, floor = 0)
```

Arguments

| | |
|-------|---|
| tcc | <code>TCC-class</code> object |
| sort | logical. If TRUE, the retrieved results are sorted in order of the <code>stat\$rank</code> field in the <code>TCC-class</code> object. If FALSE, the results are retrieved by the original order. |
| floor | numeric scalar specifying a threshold for adjusting low count data. |

Value

A data frame object containing following fields:

| | |
|--------------|---|
| gene_id | character vector indicating the id of the count unit, usually gene. |
| a.value | numeric vector of average expression level on \log_2 scale (i.e., A-value) for each gene across the compared two groups. It corresponds to the x coordinate in the M-A plot. |
| m.value | numeric vector of fold-change on \log_2 scale (i.e., M-value) for each gene between the two groups compared. It corresponds to the y coordinate in the M-A plot. |
| p.value | numeric vector of p -values. |
| q.value | numeric vector of q -values calculated based on the p -values using the <code>p.adjust</code> function with default parameter settings. |
| rank | numeric vector of gene rank in order of the p -values. |
| estimatedDEG | numeric vector consisting of 0 or 1 depending on whether each gene is classified as non-DEG or DEG. The threshold for classifying DEGs or non-DEGs is preliminarily given when performing <code>estimateDE</code> . |

Examples

```
# Obtaining DE results by an exact test in edgeR coupled with
# the DEGES/edgeR normalization factors
data(hypoData)
group <- c(1, 1, 1, 2, 2, 2)
tcc <- new("TCC", hypoData, group)
tcc <- calcNormFactors(tcc, norm.method = "tmm", test.method = "edgeR",
                      iteration = 1, FDR = 0.1, floorPDEG = 0.05)
tcc <- estimateDE(tcc, test.method = "edgeR", FDR = 0.1)
result <- getResult(tcc, sort = TRUE)
head(result)

# Obtaining DE results by an negative binomial test in DESeq
# coupled with the iterative DEGES/DESeq normalization method
tcc <- new("TCC", hypoData, group)
tcc <- calcNormFactors(tcc, norm.method = "deseq", test.method = "deseq",
                      iteration = 1, FDR = 0.1, floorPDEG = 0.05)
tcc <- estimateDE(tcc, test.method = "deseq", FDR = 0.1)
result <- getResult(tcc, sort = TRUE)
head(result)
```

| | |
|----------|---|
| hypoData | <i>A simulation dataset for comparing two-group tag count data, focusing on RNA-seq</i> |
|----------|---|

Description

A simulation dataset, consisting of 1,000 rows (or genes) and 6 columns (or independent biological samples).

Usage

```
data(hypoData)
```

Format

hypoData is a matrix of dimension 1,000 times 6.

Details

This package typically start the differential expression analysis with a count table matrix such as hypoData where each row indicates the gene (or transcript), each column indicates the sample (or library), and each cell indicates the number of counts to the gene in the sample. The first three columns are produced from biological replicates of, for example, Group 1 and the remaining columns are from Group 2; i.e., G1_rep1, G1_rep2, G1_rep3 vs. G2_rep1, G2_rep2, G2_rep3. This data is generated by the [simulateReadCounts](#) function with default parameter settings. The first 200 genes are differentially expressed in the two groups. Of these, the first 180 genes are expressed at a higher level in Group 1 (G1) and the remaining 20 genes are expressed at a higher level in G2. Accordingly, the 201-1000th genes are not differentially expressed (non-DEGs). The levels of differential expression (DE) are four-fold in both groups.

Examples

```
# The hypoData is generated by following commands.
tcc <- simulateReadCounts(Ngene = 1000, PDEG = 0.2,
  DEG.assign = c(0.9, 0.1),
  DEG.foldchange = c(4, 4),
  replicates = c(3, 3))

hypoData <- tcc$count
```

| | |
|-------------|---|
| hypoData_mg | <i>A simulation dataset for comparing three-group tag count data, focusing on RNA-seq</i> |
|-------------|---|

Description

A simulation dataset, consisting of 1,000 rows (or genes) and 9 columns (or independent biological samples).

Usage

```
data(hypoData_mg)
```

Format

hypoData_mg is a matrix of dimension 1,000 times 9.

Details

The hypoData_mg, a matrix object, is a simulation dataset which consists of 1,000 rows (genes) and 9 columns (samples). Each cell of matrix indicates the number of counts to the gene in the sample. The first three columns are produced from biological replicates of, for example, Group 1, the next three columns are from Group 2 and the remaining columns are from Group 3; i.e., G1_rep1, G1_rep2, G1_rep3 vs. G2_rep1, G2_rep2, G2_rep3 vs. G3_rep1, G3_rep2, G3_rep3. This data is generated by the [simulateReadCounts](#) function with the following parameters (see Examples). The first 200 genes are differentially expressed among the three groups. Of these, the first 140 genes are expressed at a higher level only in Group 1 (G1), the next 40 genes are expressed at a higher level only in G2 and the last 20 genes are expressed at a higher level only in G3. Accordingly, the 201-1000th genes are not differentially expressed (non-DEGs). The levels of differential expression (DE) are four-fold in each group.

Examples

```
# The hypoData_mg is generated by following commands.
tcc <- simulateReadCounts(Ngene = 1000, PDEG = 0.2,
  DEG.assign = c(0.7, 0.2, 0.1),
  DEG.foldchange = c(4, 4, 4),
  replicates = c(3, 3, 3))

hypoData_mg <- tcc$count
```

`hypoData_ts`*A sample microarray data for detecting tissue-specific patterns.*

Description

A hypothetical microarray data consisting of eight rows (genes) and ten columns (tissues). The expression patterns are quite similar to those in figure 1 in Kadota et al., 2006.

Usage

```
data(hypoData_ts)
```

Format

`hypoData_ts` is a matrix of dimension eight times ten.

Details

The `hypoData_ts` is designed for explaining the performance of [ROKU](#) that identify tissue-specific expression patterns. The `hypoData_ts` contains a total of eight genes having various expression patterns across ten tissues: (1) 'up-type' genes selectively over-expressed in a small number of tissues but unexpressed ("gene1"), slightly expressed ("gene3"), and moderately expressed ("gene4"), (2) 'down-type' genes selectively under-expressed ("gene5"), and (3) 'mixed-type' genes selectively over- and under-expressed in some tissues ("gene6"). The other genes are not tissue-specific genes (i.e., "gene2", "gene7", and "gene8").

References

Kadota K, Ye J, Nakai Y, Terada T, Shimizu K: ROKU: a novel method for identification of tissue-specific genes. *BMC Bioinformatics* 2006, 7: 294.

Examples

```
data(hypoData_ts)
```

`MAplot`*plot a MA plot*

Description

This method plots a MA plot based on the `exactTest` after `TbT`. This function will be obsoleted.

Usage

```
MAplot(datalist, FDR_threshold = 0.01)
```

Arguments

`datalist` The output from `exactTestafterTbT`
`FDR_threshold` Points below the threshold will be plotted in red.

See Also

[edgeR](#)

Examples

```
## Not run:  
sample <- NBsample()  
out <- exactTestafterTbT(paste("gene",1:nrow(sample$data), sep=""),  
                          sample$data, c(1,1,1,2,2,2))  
MAplot(out)  
  
## End(Not run)
```

nakai

DNA microarray data set

Description

This is a \log_2 -transformed two-group microarray (Affymetrix GeneChip) data consisting of 31,099 probesets. A total of eight samples were taken from the rat liver: the first four samples are fed and the last four are 24-hour fasted. The original data can be obtained from NCBI Gene Expression Omnibus (GEO) with GSE7623. This is a subset.

Usage

```
data(nakai)
```

Format

`nakai` is a matrix of 31,099 rows (probesets) and 8 columns (samples or tissues).

References

Nakai Y, Hashida H., Kadota K, Minami M, Shimizu K, Matsumoto I, Kato H, Abe K., Up-regulation of genes related to the ubiquitin-proteasome system in the brown adipose tissue of 24-h-fasted rats. *Bioscience Biotechnology and Biochemistry* 2008, 72(1):139-148.

Examples

```
data(nakai)
```

| | |
|----------|---|
| NBsample | <i>Sampling from negative binomial distribution</i> |
|----------|---|

Description

This methods allow sampling from Negative Binomial distribution with specified proportion of differentially expressed genes having specified level of differential expression in terms of fold change. The proportion of upregulated are also specified. The distribution of original expression levels are generated by resampling real data of *Arabidopsis* RNA-seq data from [arab](#). This function will be obsoleted. Use [simulateReadCounts](#) instead.

Usage

```
NBsample(DEG_foldchange = 4, repA = 3, repB = 3,
          Ngene = 3000, PDEG = 0.15, PA = 0.2)
```

Arguments

| | |
|----------------|---|
| DEG_foldchange | Fold change value of differentially expressed genes |
| repA | Replicate number for sample A |
| repB | Replicate number for sample B |
| Ngene | Number of genes to produce |
| PDEG | Proportion of differentially expressed genes |
| PA | Proportion of upregulated genes in sample A among differentially expressed genes (DEGs) |

Examples

```
## Not run:
sample <- NBsample()

## End(Not run)
```

| | |
|------|--|
| plot | <i>Plot a log fold-change versus log average expression (so-called M-A plot)</i> |
|------|--|

Description

This function generates a scatter plot of log fold-change (i.e., $M = \log_2 G2 - \log_2 G1$ on the y -axis between Groups 1 vs. 2) versus log average expression (i.e., $A = (\log_2 G1 + \log_2 G2)/2$ on the x -axis) using normalized count data.

Usage

```
## S3 method for class TCC
plot(x, FDR = NULL, median.lines = FALSE, floor = 0,
     groups = NULL, col = NULL, col.tag = NULL, normalize = TRUE, ...)
```

Arguments

| | |
|---------------------------|---|
| <code>x</code> | <code>TCC-class</code> object. |
| <code>FDR</code> | numeric scalar specifying a false discovery rate (FDR) threshold for determining differentially expressed genes (DEGs) |
| <code>median.lines</code> | logical. If <code>TRUE</code> , horizontal lines specifying the median <code>M</code> values for non-DEGs (black), DEGs up-regulated in Group 1 (G1; blue), and G2 (red) are drawn. |
| <code>floor</code> | numeric scalar specifying a threshold for adjusting low count data. |
| <code>groups</code> | numeric vector consists two elements for specifying what two groups should be drawn when data contains more than three groups. |
| <code>col</code> | vector specifying plotting color. |
| <code>col.tag</code> | numeric vector specifying the index of <code>col</code> for coloring the points of the genes. |
| <code>normalize</code> | logical. If <code>FALSE</code> , the coordinates of M-A plot are calculated from the raw data. |
| <code>...</code> | further graphical arguments, see <code>plot.default</code> . |

Details

This function generates roughly three different M-A plots depending on the conditions for `TCC-class` objects. When the function is performed just after the new method, all the genes (points) are treated as non-DEGs (the default is black; see Example 1). The `simulateReadCounts` function followed by the `plot` function can classify the genes as *true* non-DEGs (black), *true* DEGs up-regulated in Group 1 (G1; blue), and *true* DEGs up-regulated in G2 (red) (see Example 2). The `estimateDE` function followed by the `plot` function generates *estimated* DEGs (magenta) and the remaining *estimated* non-DEGs (black).

Genes with normalized counts of 0 in any one group cannot be plotted on the M-A plot because those `M` and `A` values cannot be calculated (as $\log 0$ is undefined). Similar to the `plotSmear` function in edgeR package, `plot` function plots those points at the left side of the minimum `A` (i.e., log average expression) value. The `x` coordinate of those points is the minimum `A` value minus 1. The `y` coordinate is calculated as if the 0 count was the minimum observed non-0 count in each group.

Value

A scatter plot to the current graphic device.

Examples

```
# 1.
# M-A plotting just after constructing the TCC class object from
# hypoData. In this case, the plot is generated from hypoData
# that has been scaled in such a way that the library sizes of
# each sample are the same as the mean library size of the
```

```
# original hypoData. Note that all points are in black. This is
# because the information about DEG or non-DEG for each gene is
# not indicated.
data(hypoData)
group <- c(1, 1, 1, 2, 2, 2)
tcc <- new("TCC", hypoData, group)
plot(tcc)

normalized.count <- getNormalizedData(tcc)
colSums(normalized.count)
colSums(hypoData)
mean(colSums(hypoData))

# 2.
# M-A plotting of DEGES/edgeR-normalized simulation data.
# It can be seen that the median M value for non-DEGs approaches
# zero. Note that non-DEGs are in black, DEGs up-regulated in
# G1 and G2 are in blue and red.
tcc <- simulateReadCounts()
tcc <- calcNormFactors(tcc, norm.method = "tmm", test.method = "edger",
                      iteration = 1, FDR = 0.1, floorPDEG = 0.05)
plot(tcc, median.lines = TRUE)

# 3.
# M-A plotting of DEGES/edgeR-normalized hypoData after performing
# DE analysis.
data(hypoData)
group <- c(1, 1, 1, 2, 2, 2)
tcc <- new("TCC", hypoData, group)
tcc <- calcNormFactors(tcc, norm.method = "tmm", test.method = "edger",
                      iteration = 1, FDR = 0.1, floorPDEG = 0.05)
tcc <- estimateDE(tcc, test.method = "edger", FDR = 0.1)
plot(tcc)

# Changing the FDR threshold
plot(tcc, FDR = 0.7)
```

plotFCPseudocolor *Create a pseudo-color image of simulation data*

Description

This function creates a pseudo-color image of simulation data regarding the number of differentially expressed genes (DEGs) and the breakdowns for individual groups from a [TCC-class](#) object.

Usage

```
plotFCPseudocolor(tcc, main, xlab, ylab)
```

Arguments

| | |
|------|---|
| tcc | TCC-class object. |
| main | character string indicating the plotting title. |
| xlab | character string indicating the x-label title. |
| ylab | character string indicating the y-label title. |

Details

This function should be used after the `simulateReadCounts` function that generates simulation data with arbitrary defined conditions. The largest log fold-change (FC) values are in magenta and no-changes are in white.

Examples

```
# Generating a simulation data for comparing two groups
# (G1 vs. G2) with biological replicates.
# the first 200 genes are DEGs, where 180 are up in G1.
tcc <- simulateReadCounts(Ngene = 1000, PDEG = 0.2,
                          DEG.assign = c(0.9, 0.1),
                          DEG.foldchange = c(4, 4),
                          replicates = c(3, 3))

plotFCPseudocolor(tcc)

# Generating a simulation data for comparing three groups
# (G1 vs. G2 vs. G3) with biological replicates.
# the first 300 genes are DEGs, where the 70%, 20%, and 10% are
# up-regulated in G1, G2, G3, respectively. The levels of DE are
# 3-, 10, and 6-fold in individual groups.
tcc <- simulateReadCounts(Ngene = 1000, PDEG = 0.3,
                          DEG.assign = c(0.7, 0.2, 0.1),
                          DEG.foldchange = c(3, 10, 6),
                          replicates = c(3, 3, 3))

plotFCPseudocolor(tcc)
```

ROKU

detect tissue-specific (or tissue-selective) patterns from microarray data with many kinds of samples

Description

ROKU is a method for detecting tissue-specific (or tissue-selective) patterns from gene expression data for many tissues (or samples). ROKU (i) ranks genes according to their overall tissue-specificity using Shannon entropy after data processing and (ii) detects tissues specific to each gene if any exist using an Akaike's information criterion (AIC) procedure.

Usage

```
ROKU(data, upper.limit = 0.25, sort = FALSE)
```

Arguments

| | |
|--------------------------|--|
| <code>data</code> | numeric matrix or data frame containing microarray data (on log2 scale), where each row indicates the gene or probeset ID, each column indicates the tissue, and each cell indicates a (log2-transformed) expression value of the gene in the tissue. Numeric vector can also be accepted for a single gene expression vector. |
| <code>upper.limit</code> | numeric value (between 0 and 1) specifying the maximum percentage of tissues (or samples) as outliers to each gene. |
| <code>sort</code> | logical. If TRUE, results are sorted in descending order of the entropy scores. |

Details

As shown in Figure 1 in the original study of ROKU (Kadota et al., 2006), Shannon entropy H of a gene expression vector (x_1, x_2, \dots, x_N) for N tissues can range from zero to $\log_2 N$, with the value 0 for genes expressed in a single tissue and $\log_2 N$ for genes expressed uniformly in all the tissues. Researchers therefore rely on the low entropy score for the identification of tissue-specific patterns. However, direct calculation of the entropy for raw gene expression vector works well only for detecting tissue-specific patterns when over-expressed in a small number of tissues but unexpressed or slightly expressed in others: The H scores of tissue-specific patterns such as $(8, 8, 2, 8, 8, 8, 8, 8, 8, 8)$ for the 3rd tissue-specific down-regulation (see the Figure 1e) are close to the maximum value ($\log_2 N = 3.32$ when $N = 10$) and cannot identify such patterns as tissue-specific. To detect various kinds of tissue-specific patterns by low entropy score, ROKU processes the original gene expression vector and makes a new vector $(x_{1'}, x_{2'}, \dots, x_{N'})$. The data processing is done by subtracting the one-step Tukey biweight and by taking the absolute value. In case of the above example, ROKU calculates the H score from the processed vector $(0, 0, 6, 0, 0, 0, 0, 0, 0, 0)$, giving very low score (from $H = 3.26$ before processing to $H' = 0$ after processing). A major characteristic of ROKU is, therefore, to be able to rank various tissue-specific patterns by using the modified entropy scores.

Note that the modified entropy does not explain to which tissue a gene is specific, only measuring the degree of overall tissue specificity of the gene. ROKU employs an AIC-based outlier detection method (Ueda, 1996). Consider, for example, a hypothetical mixed-type of tissue-selective expression pattern $(1.2, 5.1, 5.2, 5.4, 5.7, 5.9, 6.0, 6.3, 8.5, 8.8)$ where we imagine a total of three tissues are specific (down-regulated in tissue1; up-regulated in tissues 9 and 10). The method first normalize the expression values by subtracting the mean and dividing by the standard deviation (i.e., z -score transformation), then sorted in order of increasing magnitude by $(-2.221, -0.342, -0.294, -0.198, -0.053, 0.043, 0.092, 0.236, 1.296, 1.441)$. The method evaluates various combinations of outlier candidates starting from both sides of the values: model1 for non-outlier, model2 for one outlier for high-side, model3 for two outliers for high-side, ..., model x for one outlier for down-side, ..., model y for two outliers for both up- and down sides, and so on. Then, it calculates AIC-like statistic (called U) for each combination of model and search the best combination that achieves the lowest U value and is termed the minimum AIC estimate (MAICE). Since the `upper.limit` value corresponds to the maximum number of the outlier candidates, it decides the number of combinations. The AIC-based method output a vector (1 for up-regulated outliers, -1 for down-regulated outliers, and 0 for non-outliers) that corresponds to the input vector. For example, the method outputs a vector $(-1, 0, 0, 0, 0, 0, 0, 0, 1, 1)$ when using `upper.limit = 0.5` and $(-1, 0, 0, 0, 0, 0, 0, 0, 0, 0)$ when using `upper.limit = 0.25` (as default). See the Kadota et al., 2007 for detailed discussion about the effect of different parameter settings.

Value

A list containing following fields:

| | |
|---------|---|
| outlier | A numeric matrix when the input data are data frame or matrix. A numeric vector when the input data are numeric vector. Both matrix or vector consist of 1, -1, and 0: 1 for over-expressed outliers, -1 for under-expressed outliers, and 0 for non-outliers. |
| modH | A numeric vector when the input data are data frame or matrix. A numeric scalar when the input data are numeric vector. Both vector or scalar consist of modified entropy (H') score(s) calculated from a processed gene expression vector. |
| H | A numeric vector when the input data are data frame or matrix. A numeric scalar when the input data are numeric vector. Both vector or scalar consist of original entropy (H) score(s) calculated from an original gene expression vector. |
| rank | A numeric vector or scalar consisting of the rank(s) of modH. |
| Tbw | a numeric vector or scalar consisting of one-step Tukey's biweight as an iteratively reweighted measure of central tendency. This value is in general similar to median value and the same as the output of <code>tukey.biweight</code> with default parameter settings in <code>affy</code> package. The data processing is done by subtracting this value for each gene expression vector and by taking the absolute value. |

References

- Kadota K, Konishi T, Shimizu K: Evaluation of two outlier-detection-based methods for detecting tissue-selective genes from microarray data. *Gene Regulation and Systems Biology* 2007, 1: 9-15.
- Kadota K, Ye J, Nakai Y, Terada T, Shimizu K: ROKU: a novel method for identification of tissue-specific genes. *BMC Bioinformatics* 2006, 7: 294.
- Kadota K, Nishimura SI, Bono H, Nakamura S, Hayashizaki Y, Okazaki Y, Takahashi K: Detection of genes with tissue-specific expression patterns using Akaike's Information Criterion (AIC) procedure. *Physiol Genomics* 2003, 12: 251-259.
- Ueda T. Simple method for the detection of outliers. *Japanese J Appl Stat* 1996, 25: 17-26.

Examples

```
data(hypoData_ts)

result <- ROKU(hypoData_ts)
```

simulateReadCounts *Generate simulation data from negative binomial (NB) distribution*

Description

This function generates simulation data with arbitrary defined experimental condition.

Usage

```
simulateReadCounts(Ngene = 10000, PDEG = 0.20, DEG.assign = NULL,
                  DEG.foldchange = NULL, replicates = NULL, group = NULL)
```

Arguments

| | |
|----------------|--|
| Ngene | numeric scalar specifying the number of genes. |
| PDEG | numeric scalar specifying the proportion of differentially expressed genes (DEGs). |
| DEG.assign | numeric vector specifying the proportion of DEGs up- or down-regulated in individual groups to be compared. The number of elements should be the same as that of replicates if replicates is specified. The indication of replicates means a single-factor experimental design. The number of elements in DEG.assign should be the same as the number of columns in DEG.foldchange. Both DEG.foldchange as data frame and group should simultaneously be specified and those indication means a multi-factor experimental design. |
| DEG.foldchange | numeric vector for single-factor experimental design and data frame for multi-factor experimental design. Both DEG.foldchange as numeric vector and replicates should simultaneously be specified for single-factor experimental design. The <i>i</i> -th element in DEG.foldchange vector indicates the degree of fold-change for Group <i>i</i> . The default is DEG.foldchange = c(4, 4), indicating that the levels of DE are four-fold in both groups. Both DEG.foldchange as data frame and group should simultaneously be specified for multi-factor experimental design. Numeric values in the DEG.foldchange object indicate the degree of fold-change for individual conditions or factors. |
| replicates | numeric vector indicating the numbers of (biological) replicates for individual groups compared. Ignored if group is specified. |
| group | data frame specifying the multi-factor experimental design. |

Details

The empirical distribution of read counts used in this function is calculated from a RNA-seq dataset obtained from *Arabidopsis* data (three biological replicates for both the treated and non-treated samples), the `arab` object, in `NBPSeq` package (Di et al., 2011). The overall design about the simulation conditions introduced can be viewed as a pseudo-color image by the `plotFCPseudocolor` function.

Value

A `TCC-class` object containing following fields:

| | |
|--------------|---|
| count | numeric matrix of simulated count data. |
| group | data frame indicating which group (or condition or factor) each sample belongs to. |
| norm.factors | numeric vector as a placeholder for normalization factors. |
| stat | list for storing results after the execution of the <code>calcNormFactors</code> (and <code>estimateDE</code>) function. |

`estimatedDEG` numeric vector as a placeholder for indicating which genes are up-regulated in particular group compared to the others. The values in this field will be populated after the execution of the `estimateDE` function.

`simulation` list containing four fields: `trueDEG`, `DEG.foldchange`, `PDEG`, and `params`. The `trueDEG` field (numeric vector) stores information about DEGs: 0 for non-DEG, 1 for DEG up-regulated in Group 1, 2 for DEG up-regulated in Group 2, and so on. The information for the remaining three fields is the same as those indicated in the corresponding arguments.

Examples

```
# Generating a simulation data for comparing two groups
# (G1 vs. G2) without replicates (single-factor experimental design).
# the levels of DE are 3-fold in G1 and 7-fold in G2
tcc <- simulateReadCounts(Ngene = 10000, PDEG = 0.2,
                        DEG.assign = c(0.9, 0.1),
                        DEG.foldchange = c(3, 7),
                        replicates = c(1, 1))

dim(tcc$count)
head(tcc$count)
str(tcc$simulation)
head(tcc$simulation>trueDEG)

# Generating a simulation data for comparing three groups
# (G1 vs. G2 vs. G3) with biological replicates
# (single-factor experimental design).
# the first 3000 genes are DEGs, where the 70%, 20%, and 10% are
# up-regulated in G1, G2, G3, respectively. The levels of DE are
# 3-, 10-, and 6-fold in individual groups.
tcc <- simulateReadCounts(Ngene = 10000, PDEG = 0.3,
                        DEG.assign = c(0.7, 0.2, 0.1),
                        DEG.foldchange = c(3, 10, 6),
                        replicates = c(2, 4, 3))

dim(tcc$count)
head(tcc$count)
str(tcc$simulation)
head(tcc$simulation>trueDEG)

# Generating a simulation data consisting of 10,000 rows (i.e., Ngene = 10000)
# and 8 columns (samples) for two-factor experimental design
# (condition and time). The first 3,000 genes are DEGs (i.e., PDEG = 0.3).
# Of the 3,000 DEGs, 40% are differentially expressed in condition (or GROUP) "A"
# compared to the other condition (i.e., condition "B"), 40% are differentially
# expressed in condition (or GROUP) "B" compared to the other condition
# (i.e., condition "A"), and the remaining 20% are differentially expressed at
# "10h" in association with the second factor: DEG.assign = c(0.4, 0.4, 0.2).
# The levels of fold-change are (i) 2-fold up-regulation in condition "A" for
# the first 40% of DEGs, (ii) 4-fold up-regulation in condition "B" for the
# second 40%, and (iii) 0.4- and 0.6-fold up-regulation at "10h" in "A" and
# 5-fold up-regulation at "10h" in "B".
```

```

group <- data.frame(
  GROUP = c("A", "A", "A", "A", "B", "B", "B", "B"),
  TIME = c("2h", "2h", "10h", "10h", "2h", "2h", "10h", "10h")
)
DEG.foldchange <- data.frame(
  FACTOR1.1 = c(2, 2, 2, 2, 1, 1, 1, 1),
  FACTOR1.2 = c(1, 1, 1, 1, 4, 4, 4, 4),
  FACTOR2 = c(1, 1, 0.4, 0.6, 1, 1, 5, 5)
)
tcc <- simulateReadCounts(Ngene = 10000, PDEG = 0.3,
  DEG.assign = c(0.4, 0.4, 0.2),
  DEG.foldchange = DEG.foldchange,
  group = group)

tcc

```

TCC

A package for differential expression analysis from tag count data with robust normalization strategies

Description

This package performs differential expression analysis from transcriptome data that are produced from high-throughput sequencing (HTS) and microarray technologies. A notable feature of this package is to provide robust normalization methods whose strategy is to remove data assigned as potential differentially expressed genes (DEGs) before performing normalization for RNA-seq count data (Kadota et al., 2012; Sun et al., 2013).

Details

TCC is a package for differential expression analysis from transcriptome data produced from RNA-seq and microarray data. This package implements some functions for calculating normalization factors, identifying DEGs, depicting so-called M-A plot, and generating simulation data.

To utilize this package, the count matrix coupled with label information should be stored to a **TCC-class** object using the new method. All functions, except for some legacy functions (i.e., `NBSample`, `do_TbT`, `exactTestafterTbT`, and `MAplot` for RNA-seq data) and for two recently added functions (i.e., `ROKU` and `WAD`) for microarray data, used in this package require this **TCC-class** object. Using this object, the `calcNormFactors` function calculates normalization factors and the `estimateDE` function estimates the degree of differential expression (DE) for individual genes. The estimated normalization factors obtained by using the `calcNormFactors` function are used within the statistical model for differential analysis in the `estimateDE` function. Both two functions internally call functions from other packages (`edgeR`, `DESeq`, `baySeq`, `EBSeq`, and `samr`) when specified. TCC also provides some useful functions: `simulateReadCounts` for generating simulation data with various experimental designs, `plot` for depicting a M-A plot, `plotFCPseudocolor` for depicting a pseudo-color image of simulation condition that the user specified, `WAD` for identifying DEGs from two-group microarray data (single-factor design), and `ROKU` for identifying tissue-specific genes from microarray data for many tissues.

See Also[TCC-class](#)**Examples**

```
data(hypoData)
group <- c(1, 1, 1, 2, 2, 2)
tcc <- new("TCC", hypoData, group)
show(tcc)
```

TCC-class

*A container for storing information used in TCC***Description**

This is a container class for TCC. This class initially contains count data matrix and some information for the analysis of count data. It also provides further fields that are populated during the analysis.

Details

This class is implemented as an R5 reference class. Functions calling such methods copies the object prior to calling the method to keep the semantics of functional programming. This class can be created by the generic `new` function with count data and associated information of experimental design.

The values (defaults to all 1) in the `norm.factors` field will be changed after performing the [calcNormFactors](#) function. The `DEGES` field stores information related to our DEGES-based normalization pipeline after performing the [calcNormFactors](#) function. The `stat` and `estimatedDEG` fields store results after performing the [estimateDE](#) function. The `simulation` field stores parameters used when performing the [simulateReadCounts](#) function.

Fields

This class contains the following fields:

count numeric matrix containing count data.

gene_id character vector indicating the identifier of the count unit, usually gene.

group data frame indicating information about experimental design.

norm.factors numeric vector containing normalization factors (default to 1).

stat list for storing results after the execution of the [calcNormFactors](#) and [estimateDE](#) functions.

estimatedDEG numeric vector as a placeholder for indicating either DEGs (flagged as "1") or non-DEGs (as "0") for individual genes. The values in this field will be populated after the execution of the [estimateDE](#) function.

simulation list. This field is only used for analyzing simulation data.

DEGES list for storing the information about normalization steps.

Examples

```
tcc <- simulateReadCounts(Ngene = 10000, PDEG = 0.2, DEG.assign = c(0.8, 0.2),
  DEG.foldchange = c(4, 4), replicates = c(3, 3))

# Check the TCC class object.
tcc

# Check the fields of TCC class object.
names(tcc)
head(tcc$count)

# Check the normalization factors.
tcc <- calcNormFactors(tcc, norm.method = "tmm", test.method = "edger",
  iteration = 1, FDR = 0.1, floorPDEG = 0.05)
tcc$norm.factors

# Check the p-values and q-values.
tcc <- estimateDE(tcc, test.method = "edger", FDR = 0.1)
tcc

# Compare the breakdowns of estimated DEGs with the truth.
head(tcc$estimatedDEG)
head(tcc$simulation$trueDEG)

# M-A plotting.
plot(tcc)
```

WAD

Calculate WAD statistic for individual genes

Description

This function performs WAD method to identify differentially expressed genes (DEGs) from two-group gene expression data. A high absolute value for the WAD statistic is evident of a high degree of differential expression.

Usage

```
WAD(data, group, log.scale = FALSE, floor.value = 1, sort = FALSE)
```

Arguments

| | |
|-------|--|
| data | numeric matrix or data frame containing count data or microarray data, where each row indicates the gene (or transcript or probeset ID), each column indicates the sample (or library), and each cell indicates the expression value (i.e., number of counts or signal intensity) of the gene in the sample. |
| group | numeric vector indicating the experimental group for each sample (or library). |

| | |
|--------------------------|---|
| <code>log.scale</code> | logical. If TRUE, the data are log scaled (base = 2) after performing the <code>floor.value</code> setting. The default is <code>log.scale = FALSE</code> . |
| <code>floor.value</code> | numeric scalar specifying a floor value for the data. The default is <code>floor.value = 1</code> , i.e., values less than 1 are replaced by 1. Ignored if <code>log.scale = FALSE</code> . |
| <code>sort</code> | logical. If TRUE, the retrieved results are sorted in order of the rank of absolute WAD statistic. If FALSE, the results are retrieved by the original order. |

Value

A numeric vector of WAD statistic for individual genes

References

Kadota K, Nakai Y, Shimizu K: A weighted average difference method for detecting differentially expressed genes from microarray data. *Algorithms Mol Biol.* 2008, 3: 8.

Examples

```
data(nakai)
group <- c(1, 1, 1, 1, 2, 2, 2, 2)

wad <- WAD(nakai, group,
           log.scale = TRUE, floor.value = 1, sort = TRUE)
```

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