Package 'singscore'

November 6, 2025

Type Package

Title Rank-based single-sample gene set scoring method

Version 1.31.0

Description A simple single-sample gene signature scoring method that uses rank-based statistics to analyze the sample's gene expression profile. It scores the expression activities of gene sets at a single-sample level.

biocViews Software, GeneExpression, GeneSetEnrichment

Depends R (>= 3.6)

Imports methods, stats, graphics, ggplot2, grDevices, ggrepel, GSEABase, plotly, tidyr, plyr, magrittr, reshape, edgeR, RColorBrewer, Biobase, BiocParallel, SummarizedExperiment, matrixStats, reshape2, S4Vectors

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.2.0

Roxygen list(markdown = TRUE)

Collate 'singscore.R' 'rankAndScoring.R' 'permuTest.R' 'generatNullGeneric.R' 'multiScoreGeneric.R' 'plot.R' 'plotRankDensityGeneric.R' 'rankGenesGeneric.R' 'simpleScoreGeneric.R' 'stableGenes.R'

Suggests pkgdown, BiocStyle, hexbin, knitr, rmarkdown, testthat, covr

VignetteBuilder knitr

URL https://davislaboratory.github.io/singscore

BugReports https://github.com/DavisLaboratory/singscore/issues

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

git_branch devel

git_last_commit c86aa46

git_last_commit_date 2025-10-29

Repository Bioconductor 3.23

Date/Publication 2025-11-05

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Contents

generateNull *Permutation test for the derived scores of each sample*

Description

This function generates a number of random gene sets that have the same number of genes as the scored gene set. It scores each random gene set and returns a matrix of scores for all samples. The empirical scores are used to calculate the empirical p-values and plot the null distribution. The implementation uses `BiocParallel::bplapply()` for easy access to parallel backends. Note that one should pass the same values to the `upSet`, `downSet`, `centerScore` and `bidirectional` arguments as what they provide for the `simpleScore()` function to generate a proper null distribution.

Usage

```
generateNull(
  upSet,
  downSet = NULL,
  rankData,
  subSamples = NULL,
  centerScore = TRUE,
  knownDirection = TRUE,
  B = 1000,
  ncores = 1,
  seed = sample.int(1e+06, 1),
  useBPPARAM = NULL
)

## S4 method for signature 'vector,ANY'
generateNull(
  upSet,
  downSet = NULL,
  rankData,
  subSamples = NULL,
  centerScore = TRUE,
  knownDirection = TRUE,
  B = 1000,
  ncores = 1,
  seed = sample.int(1e+06, 1),
  useBPPARAM = NULL
)

## S4 method for signature 'GeneSet,ANY'
generateNull(
  upSet,
  downSet = NULL,
  rankData,
  subSamples = NULL,
```

```
  centerScore = TRUE,
  knownDirection = TRUE,
  B = 1000,
  ncores = 1,
  seed = sample.int(1e+06, 1),
  useBPPARAM = NULL
)

## S4 method for signature 'vector,vector'
generateNull(
  upSet,
  downSet = NULL,
  rankData,
  subSamples = NULL,
  centerScore = TRUE,
  knownDirection = TRUE,
  B = 1000,
  ncores = 1,
  seed = sample.int(1e+06, 1),
  useBPPARAM = NULL
)

## S4 method for signature 'GeneSet,GeneSet'
generateNull(
  upSet,
  downSet = NULL,
  rankData,
  subSamples = NULL,
  centerScore = TRUE,
  knownDirection = TRUE,
  B = 1000,
  ncores = 1,
  seed = sample.int(1e+06, 1),
  useBPPARAM = NULL
)
```

Arguments

upSet	A GeneSet object or character vector of gene IDs of up-regulated gene set or a gene set where the nature of genes is not known
downSet	A GeneSet object or character vector of gene IDs of down-regulated gene set or NULL where only a single gene set is provided
rankData	A matrix object, ranked gene expression matrix data generated using the `rankGenes()` function (make sure this matrix is not modified, see details)
subSamples	A vector of sample labels/indices that will be used to subset the rankData matrix. All samples will be scored if not provided
centerScore	A Boolean, specifying whether scores should be centered around 0, default as TRUE. Note: scores never centered if `knownDirection = FALSE`

knownDirection	A boolean, determining whether the gene set should be considered to be directional or not. A gene set is directional if the type of genes in it are known i.e. up- or down-regulated. This should be set to TRUE if the gene set is composed of both up- AND down-regulated genes. Defaults to TRUE. This parameter becomes irrelevant when both upSet(Colc) and downSet(Colc) are provided.
B	integer, the number of permutation repeats or the number of random gene sets to be generated, default as 1000
ncores	integer, the number of CPU cores the function can use
seed	integer, set the seed for randomisation
useBPPARAM	the backend the function uses, if NULL is provided, the function uses the default parallel backend which is the first on the list returned by `BiocParallel::registered()` i.e `BiocParallel::registered()[[1]]` for your machine. It can be changed explicitly by passing a BPPARAM

Value

A matrix of empirical scores for all samples

Author(s)

Ruqian Lyu

See Also

Post about BiocParallel `browseVignettes("BiocParallel")`

Examples

```
ranked <- rankGenes(toy_expr_se)
scoredf <- simpleScore(ranked, upSet = toy_gs_up, downSet = toy_gs_dn)

# find out what backends can be registered on your machine
BiocParallel::registered()
# the first one is the default backend
# ncores = ncores <- parallel::detectCores() - 2
permuteResult = generateNull(upSet = toy_gs_up, downSet = toy_gs_dn, ranked,
centerScore = TRUE, B =10, seed = 1, ncores = 1 )
```

---

generateNull_intl *Permutation test for the derived scores of each sample*

Description

This function generates a number of random gene sets that have the same number of genes as the scored gene set. It scores each random gene set and returns a matrix of scores for all samples. The empirical scores are used to calculate the empirical p-values and plot the null distribution. The implementation uses `BiocParallel::bplapply()` for easy access to parallel backends. Note that one should pass the same values to the `upSet`, `downSet`, `centerScore` and `knownDirection` arguments as what they provide for the `simpleScore()` function to generate a proper null distribution.

Usage

```
generateNull_intl(
  upSet,
  downSet = NULL,
  rankData,
  subSamples = NULL,
  centerScore = TRUE,
  knownDirection = TRUE,
  B = 1000,
  ncores = 1,
  seed = sample.int(1e+06, 1),
  useBPPARAM = NULL
)
```

Arguments

downSet	A GeneSet object, down regulated gene set
rankData	matrix, outcome of function rankGenes()
centerScore	A Boolean, specifying whether scores should be centered around 0, default as TRUE
knownDirection	A boolean flag, it deterimines whether the scoring method should derive the scores in a directional mannar when the gene signature only contains one set of gene set (passing the gene set via upSet). It is default as TRUE but one can set the argument to be FALSE to derive the score for a single gene set in a undirectional way. This parameter becomes irrelevant when both upSet and downSet are provided.
B	integer, the number of permutation repeats or the number of random gene sets to be generated, default as 1,000
ncores	integer, the number of CPU cores the function can use
seed	integer, set the seed for randomisation
useBPPARAM	the backend the function uses, if NULL is provided, the function uses the default parallel backend which is the first on the list returned by BiocParallel::registered() i.e BiocParallel::registered()[[1]] for your machine. It can be changed explicitly by passing a BPPARAM

Value

A matrix of empirical scores for all samples

Author(s)

Ruqian Lyu

See Also

Post about BiocParallel browseVignettes("BiocParallel")

getPvals *Estimate the empirical p-values*

Description

With null distributions estimated using the generateNull() function, p-values are estimated using a one-tailed test. A minimum p-value of 1/B can be achieved with B permutations.

Usage

```
getPvals(permuteResult, scoredf, subSamples = NULL)
```

Arguments

permuteResult	A matrix, null distributions for each sample generated using the generateNull() function
scoredf	A dataframe, the scored results of samples under test generated using the simpleScore() function
subSamples	A vector of sample labels/indices that will be used to subset the score matrix. All samples will be scored if not provided

Value

Estimated p-values for enrichment of the signature in each sample. A p-value of 1/B indicates that the estimated p-value is less than or equal to 1/B.

Examples

```
ranked <- rankGenes(toy_expr_se)
scoredf <- simpleScore(ranked, upSet = toy_gs_up, downSet = toy_gs_dn)
# find out what backends can be registered on your machine
BiocParallel::registered()
# the first one is the default backend, and it can be changed explicitly.
# See vignette for more details
permuteResult = generateNull(upSet = toy_gs_up, downSet = toy_gs_dn, ranked,
B =10, seed = 1, useBPPARAM = NULL)

# call the permutation function to generate the empirical scores
# for B times.
pvals <- getPvals(permuteResult,scoredf)
```

getStableGenes *Get a list of stably expressed genes*

Description

Get a list of genes that are stably expressed in cancer and normal solid tissue.

Usage

```
getStableGenes(
  n_stable,
  type = c("carcinoma", "blood", "protein"),
  id = c("geneid", "ensembl")
)
```

Arguments

n_stable	numeric, number of stable genes to retrieve
type	character, type of stable genes requested, stable genes in "carcinoma" or stable genes in "blood"
id	character, gene identifier required. This can be either "geneid" for symbols or "ensembl" ensembl id)

Value

a character vector with gene IDs sorted by their expected expression levels in the requested tissue

Examples

```
getStableGenes(5)
getStableGenes(5, id = 'ensembl')
getStableGenes(5, type = 'blood')
```

multiScore *single-sample gene-set scoring method for multiple signatures*

Description

This function computes 'singscores' using a ranked gene expression matrix obtained from the rankGenes() function and a GeneSetCollection object or a list of GeneSet objects. It returns a list of two matrices containing the scores and dispersions. This function should be used when scoring needs to be performed for multiple signatures. It is faster than applying simpleScore() across the different signatures independently.

Usage

```
multiScore(
  rankData,
  upSetColc,
  downSetColc,
  subSamples = NULL,
  centerScore = TRUE,
  dispersionFun = mad,
  knownDirection = TRUE
)

## S4 method for signature 'matrix,GeneSetCollection,missing'
multiScore(
  rankData,
  upSetColc,
  downSetColc,
  subSamples = NULL,
  centerScore = TRUE,
  dispersionFun = mad,
  knownDirection = TRUE
)

## S4 method for signature 'matrix,GeneSetCollection,GeneSetCollection'
multiScore(
  rankData,
  upSetColc,
  downSetColc,
  subSamples = NULL,
  centerScore = TRUE,
  dispersionFun = mad,
  knownDirection = TRUE
)

## S4 method for signature 'matrix,list,missing'
multiScore(
  rankData,
  upSetColc,
  downSetColc,
  subSamples = NULL,
  centerScore = TRUE,
  dispersionFun = mad,
  knownDirection = TRUE
)

## S4 method for signature 'matrix,list,list'
multiScore(
  rankData,
  upSetColc,
```

```
  downSetColc,
  subSamples = NULL,
  centerScore = TRUE,
  dispersionFun = mad,
  knownDirection = TRUE
)
```

Arguments

rankData	A matrix object, ranked gene expression matrix data generated using the rankGenes() function (make sure this matrix is not modified, see details)
upSetColc	A GeneSetCollection object, a list of GeneSet objects, or a list of character vectors of up-regulated (or mixed, see simpleScore) gene sets.
downSetColc	A GeneSetCollection object, a list of GeneSet objects, or a list of character vectors of down-regulated gene sets. NULL otherwise. Names of gene sets within this collection/list should be the same as those of the upSetColc
subSamples	A vector of sample labels/indices that will be used to subset the rankData matrix. All samples will be scored if not provided
centerScore	A Boolean, specifying whether scores should be centered around 0, default as TRUE. Note: scores never centered if knownDirection = FALSE
dispersionFun	A function, dispersion function with default being mad
knownDirection	A boolean, determining whether the gene set should be considered to be directional or not. A gene set is directional if the type of genes in it are known i.e. up- or down-regulated. This should be set to TRUE if the gene set is composed of both up- AND down-regulated genes. Defaults to TRUE. This parameter becomes irrelevant when both upSet(Colc) and downSet(Colc) are provided.

Value

A list of two matrices containing the scores and dispersions

See Also

rank "GeneSet"

Examples

```
ranked <- rankGenes(toy_expr_se)
GSEABase::setName(toy_gs_up)  = "toy_gs_up"
GSEABase::setName(toy_gs_dn)  = "toy_gs_dn"
gslist <- list(toy_gs_up, toy_gs_dn)

gscolc <- GSEABase::GeneSetCollection(gslist)
scoredf <- multiScore(ranked, upSetColc = gscolc)
```

plotDispersion *Plot the score v.s. despersion for all samples*

Description

This function takes the output from the simpleScore() function and generates scatter plots of score vs. dispersion for the total score, the up score and the down score of samples. If you wish to use the plotting function but with some customized inputs (instead of outputs from `simpleScore` function), you need to make sure the formats are the same. To be specific, you need to have columns names "TotalScore" "TotalDispersion" "UpScore" "UpDispersion" "DownScore" "DownDispersion" and rows names as samples.

Usage

```
plotDispersion(
  scoredf,
  annot = NULL,
  annot_name = "",
  sampleLabels = NULL,
  alpha = 1,
  size = 1,
  textSize = 1.2,
  isInteractive = FALSE
)
```

Arguments

`scoredf`	data.frame, generated using the `simpleScore()` function
`annot`	any numeric, character or factor annotation provided by the user that needs to be plot. Alternatively, this can be a character specifying the column of scoredf holding the annotation. Annotations must be ordered in the same way as the scores
`annot_name`	character, legend title for the annotation
`sampleLabels`	vector of character, sample names to display, ordered in the same way as samples are ordered in the 'scoredf' data.frame and with labels for all samples. Samples whose labels should not be displayed should be left as empty strings or NAs. Default as NULL which means the projected points are not labelled.
`alpha`	numeric, set the transparency of points
`size`	numeric, set the size of each point
`textSize`	numeric, relative text sizes for title, labels, and axis values
`isInteractive`	Boolean, determine whether the plot is interactive

Value

A ggplot object

Examples

```
ranked <- rankGenes(toy_expr_se)
scoredf <- simpleScore(ranked, upSet = toy_gs_up, downSet = toy_gs_dn)
plotDispersion(scoredf)
plotDispersion(scoredf, isInteractive = TRUE)
```

`plotNull` *Plot the empirically estimated null distribution and associated p-values*

Description

This function takes the results from function `generateNull()` and plots the density curves of permuted scores for the provided samples via `sampleNames` parameter. It can plot null distribution(s) for a single sample or multiple samples.

Usage

```
plotNull(
  permuteResult,
  scoredf,
  pvals,
  sampleNames = NULL,
  cutoff = 0.01,
  textSize = 2,
  labelSize = 5
)
```

Arguments

`permuteResult`	A matrix, null distributions for each sample generated using the `generateNull()` function
`scoredf`	A dataframe, singscores generated using the `simpleScore()` function
`pvals`	A vector, estimated p-values using the `getPvals()` function `permuteResult`,`scoredf` and `pvals` are the results for the same samples.
`sampleNames`	A character vector, sample IDs for which null distributions will be plotted
`cutoff`	numeric, the cutoff value for determining significance
`textSize`	numeric, size of axes labels, axes values and title
`labelSize`	numeric, size of label texts

Value

a ggplot object

Author(s)

Ruqian Lyu

Examples

```
ranked <- rankGenes(toy_expr_se)
scoredf <- simpleScore(ranked, upSet = toy_gs_up, downSet = toy_gs_dn)
# find out what backends can be registered on your machine
BiocParallel::registered()
# the first one is the default backend, and it can be changed explicitly.
permuteResult = generateNull(upSet = toy_gs_up, downSet = toy_gs_dn, ranked,
B =10, seed = 1,useBPPARAM = NULL)
# call the permutation function to generate the empirical scores
#for B times.
pvals <- getPvals(permuteResult,scoredf)
# plot for all samples
plotNull(permuteResult,scoredf,pvals,sampleNames = names(pvals))
#plot for the first sample
plotNull(permuteResult,scoredf,pvals,sampleNames = names(pvals)[1])
```

---

plotRankDensity *Plot the densities of ranks for one sample*

Description

This function takes a single-column data frame, which is a single-column subset of the ranked matrix data generated using `rankGenes()` function, and the gene sets of interest as inputs. It plots the density of ranks for genes in the gene set and overlays a barcode plot of these ranks. Ranks are normalized by dividing them by the maximum rank. Densities are estimated using KDE.

Usage

```
plotRankDensity(
  rankData,
  upSet,
  downSet = NULL,
  isInteractive = FALSE,
  textSize = 1.5
)

## S4 method for signature 'ANY,vector,missing'
plotRankDensity(
  rankData,
  upSet,
  downSet = NULL,
  isInteractive = FALSE,
  textSize = 1.5
)

## S4 method for signature 'ANY,GeneSet,missing'
plotRankDensity(
  rankData,
```

```
  upSet,
  downSet = NULL,
  isInteractive = FALSE,
  textSize = 1.5
)

## S4 method for signature 'ANY,vector,vector'
plotRankDensity(
  rankData,
  upSet,
  downSet = NULL,
  isInteractive = FALSE,
  textSize = 1.5
)

## S4 method for signature 'ANY,GeneSet,GeneSet'
plotRankDensity(
  rankData,
  upSet,
  downSet = NULL,
  isInteractive = FALSE,
  textSize = 1.5
)
```

Arguments

rankData	one column of the ranked gene expression matrix obtained from the rankGenes() function, use drop = FALSE when subsetting the ranked gene expression matrix, see examples.
upSet	GeneSet object or a vector of gene Ids, up-regulated gene set
downSet	GeneSet object or a vector of gene Ids, down-regulated gene set
isInteractive	Boolean, determine whether the returned plot is interactive
textSize	numberic, set the size of text on the plot

Value

A ggplot object (or a plotly object) with a rank density plot overlayed with a barcode plot

Examples

```
ranked <- rankGenes(toy_expr_se)
plotRankDensity(ranked[,2,drop = FALSE], upSet = toy_gs_up)
```

plotRankDensity_intl *Plot the densities of ranks for one sample*

Description

This function takes a single column data frame, which is a subset of the ranked data obtained from rankGenes()function and gene sets, and it returns plots visualising the density and the rugs of the ran ks.

Usage

```
plotRankDensity_intl(
  rankData,
  upSet,
  downSet = NULL,
  isInteractive = FALSE,
  textSize = 1.2
)
```

Arguments

rankData	one column of the ranked gene expression matrix obtained from the rankGenes() function, use drop = FALSE when subsetting the ranked gene expression matrix, see examples.
upSet	GeneSet object, up regulated gene set
downSet	GeneSet object, down regulated gene set
isInteractive	Boolean, determin whether the returned plot is interactive
textSize	numeric, set the size of text on the plot

Value

A ggplot object (optionally interactive) demonstrating the rank density along with rug plot

See Also

"GeneSet"

`plotScoreLandscape` *Plot landscape of two gene signatures scores*

Description

This function takes two data frames which are outputs from the simpleScore() function and plots the relationship between the two gene set scores for samples in the gene expression matrix.Scoredf1 and Scoredf2 are two scoring results of the same set of samples against two different gene signatures. If you wish to use the plotting function but with some customized inputs (instead of outputs from the `simpleScore` function), you need to make sure the formats are the same To be specific, you need to have column names "TotalScore" "TotalDispersion" "UpScore" "UpDispersion" "DownScore" "DownDispersion" and rows names as samples.

Usage

```
plotScoreLandscape(
  scoredf1,
  scoredf2,
  scorenames = c(),
  textSize = 1.2,
  isInteractive = FALSE,
  hexMin = 100
)
```

Arguments

`scoredf1`	data.frame, result of the simpleScore() function which scores the gene expression matrix against a gene set of interest
`scoredf2`	data.frame, result of the simpleScore() function which scores the gene expression matrix against another gene set of interest
`scorenames`	character vector of length 2, names for the two scored gene set/signatures stored in scoredf1 and scoredf2
`textSize`	numeric, set the text size for the plot, default as 1.5
`isInteractive`	boolean, whether the plot is interactive default as FALSE
`hexMin`	integer, the threshold which decides whether hex bin plot or scatter plot is displayed, default as 100

Value

A ggplot object, a scatter plot, demonstrating the relationship between scores from two signatures on the same set of samples.

Examples

```
ranked <- rankGenes(toy_expr_se)
scoredf <- simpleScore(ranked, upSet = toy_gs_up, downSet = toy_gs_dn)
scoredf2 <- simpleScore(ranked, upSet = toy_gs_up)
plotScoreLandscape(scoredf, scoredf2)
```

`projectScoreLandscape` *Project data on the landscape plot obtained from* `plotScoreLandscape()`

Description

This function takes the output (ggplot object) of the function `plotScoreLandscape()` and a new dataset. It projects the new data points onto the landscape plot and returns a new ggplot object with projected data points.

Usage

```
projectScoreLandscape(
  plotObj = NULL,
  scoredf1,
  scoredf2,
  annot = NULL,
  annot_name = NULL,
  subSamples = NULL,
  sampleLabels = NULL,
  isInteractive = FALSE
)
```

Arguments

`plotObj`	a ggplot object, resulted from `plotScoreLandscape()`
`scoredf1`	data.frame, result of the simpleScore() function which scores the gene expression matrix against a gene set of interest
`scoredf2`	data.frame, result of the simpleScore() function which scores the gene expression matrix against another gene set of interest. Scores in scoredf1 and scoredf2 consist of the new data points that will be projected on the `plotObj` landscape plot.
`annot`	any numeric, character or factor annotation provided by the user that needs to be plot. Alternatively, this can be a character specifying the column of scoredf1 holding the annotation. Annotations must be ordered in the same way as the scores
`annot_name`	character, legend title for the annotation
`subSamples`	vector of character or indices for subsetting the scoredfs, default as NULL and all samples in scoredfs will be plotted. The subsetted samples are projected onto the landscape plot of `plotObj`.

sampleLabels	vector of character, sample names to display, ordered in the same way as samples are ordered in the 'scoredfs' data.frames and with labels for all samples. Samples whose labels should not be displayed should be left as empty strings or NAs. Default as NULL which means the projected points are not labelled.
isInteractive	boolean, whether the plot is interactive default as FALSE

Value

New data points on the already plotted ggplot object from plotScoreLanscape()

See Also

plotScoreLandscape() @examples ranked <- rankGenes(toy_expr_se) scoredf1 <- simpleScore(ranked, upSet = toy_gs_up, downSet = toy_gs_dn) scoredf2 <- simpleScore(ranked, upSet = toy_gs_up) psl <- plotScoreLandscape(scoredf1, scoredf2) projectScoreLandscape(psl,scoredf1, scoredf2)

---

rankGenes *Rank genes by the gene expression intensities*

Description

The rankGenes function is a generic function that can deal with mutilple types of inputs. Given a matrix of gene expression that has samples in columns, genes in rows, and values being gene expression intensity,rankGenes ranks gene expression intensities in each sample.

It can also work with S4 objects that have gene expression matrix as a component (i.e ExpressionSet, DGEList,SummarizedExperiment). It calls the rank function in the base package which ranks the gene expression matrix by its absolute expression level. If the input is S4 object of DGEList, ExpressionSet, or SummarizedExperiment, it will extract the gene expression matrix from the object and rank the genes. The default 'tiesMethod' is set to 'min'.

Usage

```
rankGenes(expreMatrix, tiesMethod = "min", stableGenes = NULL)

## S4 method for signature 'matrix'
rankGenes(expreMatrix, tiesMethod = "min", stableGenes = NULL)

## S4 method for signature 'data.frame'
rankGenes(expreMatrix, tiesMethod = "min", stableGenes = NULL)

## S4 method for signature 'DGEList'
rankGenes(expreMatrix, tiesMethod = "min", stableGenes = NULL)

## S4 method for signature 'ExpressionSet'
rankGenes(expreMatrix, tiesMethod = "min", stableGenes = NULL)

## S4 method for signature 'SummarizedExperiment'
rankGenes(expreMatrix, tiesMethod = "min", stableGenes = NULL)
```

Arguments

expreMatrix	matrix, data.frame, ExpressionSet, DGEList or SummarizedExperiment storing gene expression measurements
tiesMethod	character, indicating what method to use when dealing with ties
stableGenes	character, containing a list of stable genes to be used to rank genes using expression of stable genes. This is required when using the stable genes dependent version of singscore (see details in simpleScore). Stable genes for solid cancers (carcinomas) and blood transcriptomes can be obtained using the getStableGenes function

Value

The ranked gene expression matrix that has samples in columns and genes in rows. Unit normalised ranks are returned if data is ranked using stable genes

See Also

getStableGenes, simpleScore, rank, "ExpressionSet", "SummarizedExperiment", "DGEList"

Examples

```
rankGenes(toy_expr_se) # toy_expr_se is a gene expression dataset

# ExpressionSet object
emat <- SummarizedExperiment::assay(toy_expr_se)
e <- Biobase::ExpressionSet(assayData = as.matrix(emat))
rankGenes(e)

#scoring using the stable version of singscore
rankGenes(e, stableGenes = c('2', '20', '25'))

## Not run:
#for real cancer or blood datasets, use getStableGenes()
rankGenes(cancer_expr, stableGenes = getStableGenes(5))
rankGenes(blood_expr, stableGenes = getStableGenes(5, type = 'blood'))

## End(Not run)
```

---

scoredf_ccle_epi *Pre-computed scores of the CCLE dataset against an epithelial gene signature*

Description

This data.frame stores pre-computed scores of the CCLE dataset Barretina et al calculated using the simpleScore() function against the epithelial gene signature from Tan, Tuan Zea et al. The data.frame has scores for 55 samples. Please refer to the vignettes for instructions on how to obtain the full datasets.

Usage

```
scoredf_ccle_epi
```

Format

An object of class `data.frame` with 55 rows and 2 columns.

References

Barretina, Jordi, Giordano Caponigro, Nicolas Stransky, Kavitha Venkatesan, Adam A Margolin, Sungjoon Kim, Christopher J Wilson, et al. 2012. "The Cancer Cell Line Encyclopedia Enables Predictive Modelling of Anticancer Drug Sensitivity." Nature 483 (7391): 603–7.

Tan, Tuan Zea, Qing Hao Miow, Yoshio Miki, Tetsuo Noda, Seiichi Mori, Ruby Yun-Ju Huang, and Jean Paul Thiery. 2014–10AD. "Epithelial-Mesenchymal Transition Spectrum Quantification and Its Efficacy in Deciphering Survival and Drug Responses of Cancer Patients." EMBO Molecular Medicine 6 (10). Oxford, UK: BlackWell Publishing Ltd: 1279–93. doi:10.15252/emmm.201404208.

See Also

scoredf_ccle_mes

`scoredf_ccle_mes` *Pre-computed scores of the CCLE dataset against a mesenchymal gene signature*

Description

This data.frame stores pre-computed scores of the CCLE dataset Barretina et al calculated using the `simpleScore()` function against the mesenchymal gene signature from Tan, Tuan Zea et al. The data.frame has scores for 55 samples. Please refer to the vignettes for instructions on how to obtain the full datasets.

Usage

```
scoredf_ccle_mes
```

Format

An object of class `data.frame` with 55 rows and 2 columns.

References

Barretina, Jordi, Giordano Caponigro, Nicolas Stransky, Kavitha Venkatesan, Adam A Margolin, Sungjoon Kim, Christopher J Wilson, et al. 2012. "The Cancer Cell Line Encyclopedia Enables Predictive Modelling of Anticancer Drug Sensitivity." Nature 483 (7391): 603–7.

Tan, Tuan Zea, Qing Hao Miow, Yoshio Miki, Tetsuo Noda, Seiichi Mori, Ruby Yun-Ju Huang, and Jean Paul Thiery. 2014–10AD. "Epithelial-Mesenchymal Transition Spectrum Quantification and Its Efficacy in Deciphering Survival and Drug Responses of Cancer Patients." EMBO Molecular Medicine 6 (10). Oxford, UK: BlackWell Publishing Ltd: 1279–93 doi:10.15252/emmm.201404208.

See Also

scoredf_ccle_epi

`scoredf_tcga_epi` *Pre-computed scores of the TCGA breast cancer gene expression matrix against an epithelial signature*

Description

This data.frame stores pre-computed scores of the TCGA dataset calculated using the `simpleScore()` function against the epithelial gene signature from Tan, Tuan Zea et al. Please refer to the vignettes for instructions on how to obtain the full datasets.

Usage

```
scoredf_tcga_epi
```

Format

An object of class `data.frame` with 1119 rows and 2 columns.

References

Tan, Tuan Zea, Qing Hao Miow, Yoshio Miki, Tetsuo Noda, Seiichi Mori, Ruby Yun-Ju Huang, and Jean Paul Thiery. 2014–10AD. "Epithelial-Mesenchymal Transition Spectrum Quantification and Its Efficacy in Deciphering Survival and Drug Responses of Cancer Patients." EMBO Molecular Medicine 6 (10). Oxford, UK: BlackWell Publishing Ltd: 1279–93 doi:10.15252/emmm.201404208.

See Also

scoredf_tcga_mes

`scoredf_tcga_mes` *Pre-computed scores of the TCGA breast cancer gene expression matrix against a mesenchymal signature*

Description

This data.frame stores pre-computed scores of the TCGA dataset calculated using the `simpleScore()` function against the mesenchymal gene signature from Tan, Tuan Zea et al. Please refer to the vignettes for instructions on how to obtain the full datasets.

Usage

```
scoredf_tcga_mes
```

Format

An object of class `data.frame` with 1119 rows and 2 columns.

References

Tan, Tuan Zea, Qing Hao Miow, Yoshio Miki, Tetsuo Noda, Seiichi Mori, Ruby Yun-Ju Huang, and Jean Paul Thiery. 2014–10AD. "Epithelial-Mesenchymal Transition Spectrum Quantification and Its Efficacy in Deciphering Survival and Drug Responses of Cancer Patients." EMBO Molecular Medicine 6 (10). Oxford, UK: BlackWell Publishing Ltd: 1279–93 doi:10.15252/emmm.201404208.

See Also

scoredf_tcga_epi

`simpleScore` *single-sample gene-set scoring method*

Description

This function computes 'singscores' using an **unmodified** ranked gene expression matrix obtained from the `rankGenes()` function and a gene set or a pair of up-regulated and down-regulated gene sets. It returns a data.frame of scores and dispersions for each sample. The gene sets can be in vector format or as GeneSet objects (from GSEABase packages). If samples need to be scored against a single gene set, the `upSet` argument should be used to pass the gene set while the `downSet` argument is set to `NULL`. This setting is ideal for gene sets representing gene ontologies where the nature of the genes is unknown (up- or down-regulated).

Usage

```
simpleScore(
  rankData,
  upSet,
  downSet = NULL,
  subSamples = NULL,
  centerScore = TRUE,
  dispersionFun = mad,
  knownDirection = TRUE
)

## S4 method for signature 'matrix,vector,missing'
simpleScore(
  rankData,
  upSet,
  downSet = NULL,
  subSamples = NULL,
  centerScore = TRUE,
  dispersionFun = mad,
```

```
  knownDirection = TRUE
)

## S4 method for signature 'matrix,GeneSet,missing'
simpleScore(
  rankData,
  upSet,
  downSet = NULL,
  subSamples = NULL,
  centerScore = TRUE,
  dispersionFun = mad,
  knownDirection = TRUE
)

## S4 method for signature 'matrix,vector,vector'
simpleScore(
  rankData,
  upSet,
  downSet = NULL,
  subSamples = NULL,
  centerScore = TRUE,
  dispersionFun = mad,
  knownDirection = TRUE
)

## S4 method for signature 'matrix,GeneSet,GeneSet'
simpleScore(
  rankData,
  upSet,
  downSet = NULL,
  subSamples = NULL,
  centerScore = TRUE,
  dispersionFun = mad,
  knownDirection = TRUE
)
```

Arguments

rankData	A matrix object, ranked gene expression matrix data generated using the rankGenes() function (make sure this matrix is not modified, see details)
upSet	A GeneSet object or character vector of gene IDs of up-regulated gene set or a gene set where the nature of genes is not known
downSet	A GeneSet object or character vector of gene IDs of down-regulated gene set or NULL where only a single gene set is provided
subSamples	A vector of sample labels/indices that will be used to subset the rankData matrix. All samples will be scored if not provided
centerScore	A Boolean, specifying whether scores should be centered around 0, default as TRUE. Note: scores never centered if knownDirection = FALSE

`dispersionFun` A function, dispersion function with default being `mad`

`knownDirection` A boolean, determining whether the gene set should be considered to be directional or not. A gene set is directional if the type of genes in it are known i.e. up- or down-regulated. This should be set to TRUE if the gene set is composed of both up- AND down-regulated genes. Defaults to TRUE. This parameter becomes irrelevant when both upSet(Colc) and downSet(Colc) are provided.

Details

Signature scores can be computed using transcriptome-wide measurements or using a smaller set of measuremnts. If ranks are computed using the default invocation of `rankgenes`, the former method is applied where the rank of each gene in the signature is computed relative to all other genes in the dataset. Accuracy of this approximation of the relative expression of a gene will be improved if all or most transctripts are measured in the experiment. This was the approach proposed in the original manucript of singscore (Foroutan M, Bhuva DD, et al 2018).

If instead a selected panel of genes is measured (such as from nanostring or RT-qPCR), a different rank approximation methods using a small set of stable genes can be used. This approach only requires measurements of genes in the signature and a small set of stable genes. This approach of scoring can be invoked by producing a rank matrix by passing in the `stableGenes` argument of `rankGenes`. Stable genes in solid cancers and in blood can be retrieved using `getStableGenes`. Upon providing a set of stable genes, `rankGenes` automatically ranks all genes relative to these stable genes. When `simpleScore` is provided with a rank matrix constructed using stable genes, it automatically computes scores using a new approach. Details of the set of stable genes, the new rank estimation approach and the new scoring approach will soon be published (manuscript in preparation).

Value

A data.frame consists of singscores and dispersions for all samples

References

Foroutan, M., Bhuva, D. D., Lyu, R., Horan, K., Cursons, J., & Davis, M. J. (2018). Single sample scoring of molecular phenotypes. BMC bioinformatics, 19(1), 1-10.

See Also

`rankGenes`, `getStableGenes`, `rank`, `"GeneSet"`

Examples

```
ranked <- rankGenes(toy_expr_se)
scoredf <- simpleScore(ranked, upSet = toy_gs_up, downSet = toy_gs_dn)
# toy_gs_up is a GeneSet object, alternatively a vector of gene ids may also
# be supplied.
```

singscore *singscore: A package for deriving gene-set scores at a single sample level*

Description

The package provides functions for calculating gene-set enrichment scores at a single-sample level using gene expression data. It includes functions to perform hypothesis testing and provides visualisations to enable diagnosis of scores and gene sets along with visualisations to enable exploration of results.

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See Also

Useful links:

- https://davislaboratory.github.io/singscore
- Report bugs at https://github.com/DavisLaboratory/singscore/issues

tgfb_expr_10_se *An example gene expression dataset*

Description

A microarray gene expression dataset that was originally obtained from the integrated TGFb-EMT data published by (Foroutan et al, 2017). (ComBat corrected values). `tgfb_expr_10` is a subset of the integrated TGFb-EMT data consisting of 10 samples (4 TGFb treated and 6 controls) each with expression values for 11900 genes.

Usage

```
tgfb_expr_10_se
```

Format

A SummarizedExperiment object

Source

Foroutan et al,2017

References

Foroutan, Momeneh, Joseph Cursons, Soroor Hediyeh-Zadeh, Erik W Thompson, and Melissa J Davis. 2017. "A Transcriptional Program for Detecting Tgfbeta-Induced Emt in Cancer." Molecular Cancer Research. American Association for Cancer Research. doi:10.1158/1541-7786.MCR-16-0313.

`tgfb_gs_dn` *Gene set of down-regulated genes for the TGFb-induced EMT gene signature*

Description

A GeneSet object that contains the down-regulated genes of the TGFb-induced EMT gene signature that was derived by (Foroutan et al,2017), using two meta-analysis techniques. The gene signature contains an up-regulated gene set (up-set) and a down-regulated gene set (down-set). Please refer to the vignettes for the steps to acquire the exact data object.

Usage

```
tgfb_gs_dn
```

Format

A GeneSet object

Source

Foroutan et al,2017

References

Foroutan, Momeneh, Joseph Cursons, Soroor Hediyeh-Zadeh, Erik W Thompson, and Melissa J Davis. 2017. "A Transcriptional Program for Detecting Tgfbeta-Induced Emt in Cancer." Molecular Cancer Research. American Association for Cancer Research. doi:10.1158/1541-7786.MCR-16-0313.

See Also

"GeneSet",tgfb_gs_up

tgfb_gs_up *Gene set of up-regulated genes for the TGFb-induced EMT gene signature*

Description

A GeneSet object that contains the up-regulated genes of the TGFb-induced EMT gene signature that was derived by (Foroutan et al.,2017), using two meta-analysis techniques. The gene signature contains an up-regulated gene set (up-set) and a down-regulated gene set (down-set). Please refer to the vignettes for the steps to acquire the exact data object.

Usage

```
tgfb_gs_up
```

Format

A GeneSet object

Source

Foroutan et al,2017

References

Foroutan, Momeneh, Joseph Cursons, Soroor Hediyeh-Zadeh, Erik W Thompson, and Melissa J Davis. 2017. "A Transcriptional Program for Detecting Tgfbeta-Induced Emt in Cancer." Molecular Cancer Research. American Association for Cancer Research. doi:10.1158/1541-7786.MCR-16-0313.

See Also

"GeneSet",tgfb_gs_dn

---

toy_expr_se *A toy gene expression dataset of two samples*

Description

A toy dataset consisting of 2 samples with the expression values of 20 genes. The data was created by sampling 2 samples and 20 genes from the dataset by Foroutan et al, 2017.

Usage

```
toy_expr_se
```

Format

A SummarizedExperiment of 2 samples each with 20 genes

D_Ctrl_R1 a control sample

D_TGFb_R1 a TGFb-treated sample

Source

Foroutan et al.,2017

References

Foroutan, Momeneh, Joseph Cursons, Soroor Hediyeh-Zadeh, Erik W Thompson, and Melissa J Davis. 2017. "A Transcriptional Program for Detecting Tgfbeta-Induced Emt in Cancer." Molecular Cancer Research. American Association for Cancer Research. doi:10.1158/1541-7786.MCR-16-0313.

`toy_gs_dn` *A gene set object of down-regulated genes for the toy dataset*

Description

A GeneSet object with 5 genes randomly selected from the toy dataset. These genes are independent of those in toy_gs_up

Usage

```
toy_gs_dn
```

Format

A GSEABase::GeneSet object with 5 genes

See Also

"GeneSet",toy_expr_se,toy_gs_up

toy_gs_up *A gene set object of up-regulated genes for the toy dataset*

Description

A GeneSet object with 5 genes randomly selected from the toy dataset. These genes are independent of those in toy_gs_dn

Usage

```
toy_gs_up
```

Format

A GeneSet object with 5 genes

See Also

"GeneSet",toy_expr_se,toy_gs_dn

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