Package ‘fgsea’

April 3, 2024

Title Fast Gene Set Enrichment Analysis

Version 1.28.0

Description The package implements an algorithm for fast gene set enrichment analysis. Using the fast algorithm allows to make more permutations and get more fine grained p-values, which allows to use accurate standard approaches to multiple hypothesis correction.

biocViews GeneExpression, DifferentialExpression, GeneSetEnrichment, Pathways

SystemRequirements C++11

Depends R (>= 4.1)

Imports Rcpp, data.table, BiocParallel, stats, ggplot2 (>= 2.2.0), cowplot, grid, fastmatch, Matrix, scales, utils

Suggests testthat, knitr, rmarkdown, reactome.db, AnnotationDbi, parallel, org.Mm.eg.db, limma, GEOquery, msigdb, aggregation, Seurat

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BugReports https://github.com/ctlab/fgsea/issues

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calcGseaStat

Calculates GSEA statistics for a given query gene set

Description

Takes $O(k \log k)$ time, where $k$ is a size of `selectedSize`.

Usage

calcGseaStat(
  stats,
  selectedStats,
  gseaParam = 1,
  returnAllExtremes = FALSE,
  returnLeadingEdge = FALSE,
  scoreType = c("std", "pos", "neg")
)

Arguments

stats
  Named numeric vector with gene-level statistics sorted in decreasing order (order is not checked).

selectedStats
  Indexes of selected genes in the `stats` array.

gseaParam
  GSEA weight parameter (0 is unweighted, suggested value is 1).

returnAllExtremes
  If TRUE return not only the most extreme point, but all of them. Can be used for enrichment plot

returnLeadingEdge
  If TRUE return also leading edge genes.

scoreType
  This parameter defines the GSEA score type. Possible options are ("std", "pos", "neg")

Value

Value of GSEA statistic if both returnAllExtremes and returnLeadingEdge are FALSE. Otherwise returns list with the following elements:

- res – value of GSEA statistic
- tops – vector of top peak values of cumulative enrichment statistic for each gene;
- bottoms – vector of bottom peak values of cumulative enrichment statistic for each gene;
- leadingGene – vector with indexes of leading edge genes that drive the enrichment, see http://software.broadinstitute.org/gsea/doc/GSEAUserGuideTEXT.htm#_Running_a_Leading.
Examples

```r
data(exampleRanks)
data(examplePathways)
ranks <- sort(exampleRanks, decreasing=TRUE)
es <- calcGseaStat(ranks, na.omit(match(examplePathways[[1]], names(ranks))))
```

---

calcGseaStatBatchCpp  *Calculates GSEA statistic values for all gene sets in ‘selectedStats’ list.*

---

Description

Takes \( O(n + mK\log K) \) time, where \( n \) is the number of genes, \( m \) is the number of gene sets, and \( k \) is the mean gene set size.

Usage

```r
calcGseaStatBatchCpp(stats, selectedGenes, geneRanks)
```

Arguments

- **stats**  
  Numeric vector of gene-level statistics sorted in decreasing order
- **selectedGenes**  
  List of integer vector with integer gene IDs (from 1 to n)
- **geneRanks**  
  Integer vector of gene ranks

Value

Numeric vector of GSEA statistics of the same length as ‘selectedGenes’ list

---

collapsePathways  *Collapse list of enriched pathways to independent ones.*

---

Description

Collapse list of enriched pathways to independent ones.

Usage

```r
collapsePathways(
  fgseaRes,
  pathways,
  stats,
  pval.threshold = 0.05,
  nperm = 10/pval.threshold,
  gseaParam = 1
)
```
collapsePathwaysGeseca

Arguments

fgseaRes Table with results of running fgsea(), should be filtered by p-value, for example by selecting ones with padj < 0.01.
pathways List of pathways, should contain all the pathways present in ‘fgseaRes’.
stats Gene-level statistic values used for ranking, the same as in ‘fgsea()’.
pval.threshold Two pathways are considered dependent when p-value of enrichment of one pathways on background of another is greater then ‘pval.threshold’.
nperm Number of permutations to test for independence, should be several times greater than ‘1/pval.threshold’. Default value: ‘10/pval.threshold’.
gseaParam GSEA parameter, same as for ‘fgsea()’

Value

Named list with two elements: ‘mainPathways’ containing IDs of pathways not reducable to each other, and ‘parentPathways’ with vector describing for all the pathways to which ones they can be reduced. For pathways from ‘mainPathways’ vector ‘parentPathways’ contains ‘NA’ values.

Examples

data(examplePathways)
data(exampleRanks)
fgseaRes <- fgsea(examplePathways, exampleRanks, nperm=10000, maxSize=500)
collapsedPathways <- collapsePathways(fgseaRes[order(pval)][padj < 0.01], examplePathways, exampleRanks)
mainPathways <- fgseaRes[pathway %in% collapsedPathways$mainPathways][
  order(-NES), pathway]

Description

Collapse list of enriched pathways to independent ones (GESECA version, highly experimental).

Usage

collapsePathwaysGeseca(
  gesecaRes, pathways, E,
  center = TRUE,
  scale = FALSE,
  eps = min(c(1e-50, gesecaRes$pval)),
  checkDepth = 10,
Arguments

gesecaRes  Table with results of running geseca(), should be filtered by p-value, for example by selecting ones with padj < 0.01.
pathways    List of pathways, should contain all the pathways present in ‘gesecaRes’.
E            expression matrix, the same as in ‘geseca()’.
center      a logical value indicating whether the gene expression should be centered to have zero mean before the analysis takes place. The default is TRUE. The value is passed to scale.
scale       a logical value indicating whether the gene expression should be scaled to have unit variance before the analysis takes place. The default is FALSE. The value is passed to scale.
eps          eps parameter for internal gesecaMultilevel runs. Default: min(c(1e-50, gesecaRes$pval))
checkDepth  how much pathways to check against
nproc        If not equal to zero sets BPPARAM to use nproc workers (default = 0).
BPPARAM     Parallelization parameter used in bplapply.

Description

Collapse list of enriched pathways to independent ones. Version for ORA hypergeometric test.

Usage

collapsePathwaysORA(foraRes, pathways, genes, universe, pval.threshold = 0.05)

Arguments

foraRes  Table with results of running fgsea(), should be filtered by p-value, for example by selecting ones with padj < 0.01.
pathways    List of pathways, should contain all the pathways present in ‘fgseaRes’.
genes      Set of query genes, same as in ‘fora()’
universe    A universe from which ‘genes’ were selected, same as in ‘fora()’
pval.threshold Two pathways are considered dependent when p-value of enrichment of one pathways on background of another is greater then ‘pval.threshold’.
exampleExpressionMatrix

**Value**

Named list with two elements: ‘mainPathways’ containing IDs of pathways not reducable to each other, and ‘parentPathways’ with vector describing for all the pathways to which ones they can be reduced. For pathways from ‘mainPathways’ vector ‘parentPathways’ contains ‘NA’ values.

**Examples**

```r
data(examplePathways)
data(exampleRanks)
foraRes <- fora(examplePathways, genes=tail(names(exampleRanks), 200), universe=names(exampleRanks))
collapsedPathways <- collapsePathwaysORA(foraRes[order(pval)][padj < 0.01],
  examplePathways,
  genes=tail(names(exampleRanks), 200),
  universe=names(exampleRanks))

mainPathways <- foraRes[pathway %in% collapsedPathways$mainPathways][
  order(pval), pathway]
```

---

exampleExpressionMatrix

_example of expression values obtained for GSE14308._

**Description**

Expression data was obtained by preprocessing the GSE14308 dataset. For the matrix of gene expression value, the following steps were performed:

- expression values were log2-scaled
- quantile-type normalization was performed between arrays
- rows were collapsed by ‘ENTREZID’
- rows were sorted in descending order by mean expression value per gene
- finally, top-10_000 genes were taken

The exact script is available as `system.file("gen_gse14308_expression_matrix.R", package="fgsea")`

---

examplePathways

_example list of mouse Reactome pathways._

**Description**

The list was obtained by selecting all the pathways from ‘reactome.db’ package that contain mouse genes. The exact script is available as `system.file("gen.reactome.pathways.R", package="fgsea")`
### exampleRanks

*Example vector of gene-level statistics obtained for Th1 polarization.*

### fgsea

*Wrapper to run methods for preranked gene set enrichment analysis.*

#### Description

The data were obtained by doing differential expression between Naive and Th1-activated states for GEO dataset GSE14308. The exact script is available as `system.file("gen_gene_ranks.R", package="fgsea")`

#### Usage

```r
fgsea(
  pathways,
  stats,
  minSize = 1,
  maxSize = length(stats) - 1,
  gseaParam = 1,
  ...
)
```

#### Arguments

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pathways</td>
<td>List of gene sets to check.</td>
</tr>
<tr>
<td>stats</td>
<td>Named vector of gene-level stats. Names should be the same as in 'pathways'</td>
</tr>
<tr>
<td>minSize</td>
<td>Minimal size of a gene set to test. All pathways below the threshold are excluded.</td>
</tr>
<tr>
<td>maxSize</td>
<td>Maximal size of a gene set to test. All pathways above the threshold are excluded.</td>
</tr>
<tr>
<td>gseaParam</td>
<td>GSEA parameter value, all gene-level stats are raised to the power of 'gseaParam'</td>
</tr>
<tr>
<td>...</td>
<td>optional arguments for functions <code>fgseaSimple</code>, <code>fgseaMultilevel</code></td>
</tr>
</tbody>
</table>

#### Value

A table with GSEA results. Each row corresponds to a tested pathway.
Examples

data(examplePathways)
data(exampleRanks)
fgseaRes <- fgsea(examplePathways, exampleRanks, maxSize=500)
# Testing only one pathway is implemented in a more efficient manner
fgseaRes1 <- fgsea(examplePathways[1], exampleRanks)

fgseaLabel

Runs label-permuring gene set enrichment analysis.

Description

Runs label-permuring gene set enrichment analysis.

Usage

fgseaLabel(
    pathways,
    mat,
    labels,
    nperm,
    minSize = 1,
    maxSize = nrow(mat) - 1,
    nproc = 0,
    gseaParam = 1,
    BPPARAM = NULL
)

Arguments

pathways  List of gene sets to check.
mat       Gene expression matrix. Row name should be the same as in ‘pathways’
labels    Numeric vector of labels for the correlation score of the same length as the
          number of columns in ‘mat’
nperm     Number of permutations to do. Minimal possible nominal p-value is about
          1/nperm
minSize   Minimal size of a gene set to test. All pathways below the threshold are ex-
          cluded.
maxSize   Maximal size of a gene set to test. All pathways above the threshold are ex-
          cluded.
nproc     If not equal to zero sets BPPARAM to use nproc workers (default = 0).
gseaParam GSEA parameter value, all gene-level stats are raised to the power of ‘gsea-
          Param’ before calculation of GSEA enrichment scores.
BPPARAM   Parallelization parameter used in bplapply. Can be used to specify cluster to
          run. If not initialized explicitly or by setting ‘nproc’ default value ‘bpparam()’
          is used.
Value

A table with GSEA results. Each row corresponds to a tested pathway. The columns are the following:

- **pathway** – name of the pathway as in 'names(pathway)';
- **pval** – an enrichment p-value;
- **padj** – a BH-adjusted p-value;
- **ES** – enrichment score, same as in Broad GSEA implementation;
- **NES** – enrichment score normalized to mean enrichment of random samples of the same size;
- **nMoreExtreme** – a number of times a random gene set had a more extreme enrichment score value;
- **size** – size of the pathway after removing genes not present in 'names(stats)'.
- **leadingEdge** – vector with indexes of leading edge genes that drive the enrichment, see http://software.broadinstitute.org/gsea/doc/GSEAUserGuideTEXT.htm#_Running_a_Leading.

Examples

```r
library(limma)
library(GEOquery)
es <- getGEO("GSE19429", AnnotGPL = TRUE)[[1]]
exprs(es) <- normalizeBetweenArrays(log2(exprs(es)+1), method="quantile")
es <- es[!grepl("///", fData(es)$`Gene ID`), ]
es <- es[fData(es)$`Gene ID` != "", ]
es <- es[order(apply(exprs(es), 1, mean), decreasing=TRUE), ]
es <- es[!duplicated(fData(es)$`Gene ID`), ]
rownames(es) <- fData(es)$`Gene ID`

pathways <- reactomePathways(rownames(es))
mat <- exprs(es)
labels <- as.numeric(as.factor(gsub(".*", "", es$title)))
fgseaRes <- fgseaLabel(pathways, mat, labels, nperm = 1000, minSize = 15, maxSize = 500)
```

---

**fgseaMultilevel**

Runs preranked gene set enrichment analysis.

**Description**

This feature is based on the adaptive multilevel splitting Monte Carlo approach. This allows us to exceed the results of simple sampling and calculate arbitrarily small P-values.
Usage

```r
gseaMultilevel(
    pathways, 
    stats, 
    sampleSize = 101, 
    minSize = 1, 
    maxSize = length(stats) - 1, 
    eps = 1e-50, 
    scoreType = c("std", "pos", "neg"), 
    nproc = 0, 
    gseaParam = 1, 
    BPPARAM = NULL, 
    nPermSimple = 1000, 
    absEps = NULL
)
```

Arguments

- **pathways**: List of gene sets to check.
- **stats**: Named vector of gene-level stats. Names should be the same as in 'pathways'
- **sampleSize**: The size of a random set of genes which in turn has size = pathwaySize
- **minSize**: Minimal size of a gene set to test. All pathways below the threshold are excluded.
- **maxSize**: Maximal size of a gene set to test. All pathways above the threshold are excluded.
- **eps**: This parameter sets the boundary for calculating the p value.
- **scoreType**: This parameter defines the GSEA score type. Possible options are ("std", "pos", "neg"). By default ("std") the enrichment score is computed as in the original GSEA. The "pos" and "neg" score types are intended to be used for one-tailed tests (i.e. when one is interested only in positive ("pos") or negative ("neg") enrichment).
- **nproc**: If not equal to zero sets BPPARAM to use nproc workers (default = 0).
- **gseaParam**: GSEA parameter value, all gene-level stats are raised to the power of 'gseaParam' before calculation of GSEA enrichment scores.
- **BPPARAM**: Parallelization parameter used in bplapply. Can be used to specify cluster to run. If not initialized explicitly or by setting 'nproc' default value 'bpparam()' is used.
- **nPermSimple**: Number of permutations in the simple fgsea implementation for preliminary estimation of P-values.
- **absEps**: deprecated, use 'eps' parameter instead

Value

A table with GSEA results. Each row corresponds to a tested pathway. The columns are the following
fgseaSimple

- pathway – name of the pathway as in ‘names(pathway)’;
- pval – an enrichment p-value;
- padj – a BH-adjusted p-value;
- log2err – the expected error for the standard deviation of the P-value logarithm.
- ES – enrichment score, same as in Broad GSEA implementation;
- NES – enrichment score normalized to mean enrichment of random samples of the same size;
- size – size of the pathway after removing genes not present in ‘names(stats)’.
- leadingEdge – vector with indexes of leading edge genes that drive the enrichment, see http://software.broadinstitute.org/gsea/doc/GSEAUserGuideTEXT.htm#_Running_a_Leading.

Examples

data(examplePathways)
data(exampleRanks)
fgseaMultilevelRes <- fgseaMultilevel(examplePathways, exampleRanks, maxSize=500)

fgseaSimple

Runs preranked gene set enrichment analysis.

Description

The function takes about $O(nk^{3/2})$ time, where $n$ is number of permutations and $k$ is a maximal size of the pathways. That means that setting ‘maxSize’ parameter with a value of ~500 is strongly recommended.

Usage

fgseaSimple(
  pathways, 
  stats, 
  nperm, 
  minSize = 1, 
  maxSize = length(stats) - 1, 
  scoreType = c("std", "pos", "neg"), 
  nproc = 0, 
  gseaParam = 1, 
  BPPARAM = NULL
)

Arguments

- pathways List of gene sets to check.
- stats Named vector of gene-level stats. Names should be the same as in 'pathways'
- nperm Number of permutations to do. Minimal possible nominal p-value is about 1/nperm
**fgseaSimple**

- **minSize**: Minimal size of a gene set to test. All pathways below the threshold are excluded.
- **maxSize**: Maximal size of a gene set to test. All pathways above the threshold are excluded.
- **scoreType**: This parameter defines the GSEA score type. Possible options are ("std", "pos", "neg"). By default ("std") the enrichment score is computed as in the original GSEA. The "pos" and "neg" score types are intended to be used for one-tailed tests (i.e. when one is interested only in positive ("pos") or negative ("neg") enrichment).
- **nproc**: If not equal to zero sets BPPARAM to use nproc workers (default = 0).
- **gseaParam**: GSEA parameter value, all gene-level stats are raised to the power of ‘gseaParam’ before calculation of GSEA enrichment scores.
- **BPPARAM**: Parallelization parameter used in bplapply. Can be used to specify cluster to run. If not initialized explicitly or by setting ‘nproc’ default value ‘bpparam()’ is used.

**Value**

A table with GSEA results. Each row corresponds to a tested pathway. The columns are the following:

- pathway – name of the pathway as in ‘names(pathway)’;
- pval – an enrichment p-value;
- padj – a BH-adjusted p-value;
- ES – enrichment score, same as in Broad GSEA implementation;
- NES – enrichment score normalized to mean enrichment of random samples of the same size;
- nMoreExtreme – a number of times a random gene set had a more extreme enrichment score value;
- size – size of the pathway after removing genes not present in ‘names(stats)’.

**Examples**

data(examplePathways)
data(exampleRanks)
fgseaRes <- fgseaSimple(examplePathways, exampleRanks, nperm=10000, maxSize=500)
# Testing only one pathway is implemented in a more efficient manner
fgseaRes1 <- fgseaSimple(examplePathways[1], exampleRanks, nperm=10000)
fgseaSimpleImpl

Runs preranked gene set enrichment analysis for preprocessed input data.

Description

Runs preranked gene set enrichment analysis for preprocessed input data.

Usage

fgseaSimpleImpl(
  pathwayScores,
  pathwaysSizes,
  pathwaysFiltered,
  leadingEdges,
  permPerProc,
  seeds,
  toKeepLength,
  stats,
  BPPARAM,
  scoreType
)

Arguments

  pathwayScores  Vector with enrichment scores for the 'pathways'.
  pathwaysSizes  Vector of pathways sizes.
  pathwaysFiltered  Filtered pathways.
  leadingEdges  Leading edge genes.
  permPerProc  Parallelization parameter for permutations.
  seeds  Seed vector
  toKeepLength  Number of 'pathways' that meet the condition for 'minSize' and 'maxSize'.
  stats  Named vector of gene-level stats. Names should be the same as in 'pathways'
  BPPARAM  Parallelization parameter used in bplapply.
  scoreType  This parameter defines the GSEA score type. Possible options are ('std', 'pos', 'neg') Can be used to specify cluster to run. If not initialized explicitly or by setting 'nproc' default value 'bpparam()' is used.

Value

A table with GSEA results. Each row corresponds to a tested pathway. The columns are the following:

  • pathway – name of the pathway as in 'names(pathway)';
fora

• pval – an enrichment p-value;
• padj – a BH-adjusted p-value;
• ES – enrichment score, same as in Broad GSEA implementation;
• NES – enrichment score normalized to mean enrichment of random samples of the same size;
• nMoreExtreme’ – a number of times a random gene set had a more extreme enrichment score value;
• size – size of the pathway after removing genes not present in 'names(stats)';
• leadingEdge – vector with indexes of leading edge genes that drive the enrichment, see http://software.broadinstitute.org/gsea/doc/GSEAUserGuideTEXT.htm#_Running_a_Leading.

### Description
Simple overrepresentation analysis based on hypergeometric test

### Usage
```r
fora(pathways, genes, universe, minSize = 1, maxSize = length(universe) - 1)
```

### Arguments
- **pathways**
  List of gene sets to check.
- **genes**
  Set of query genes
- **universe**
  A universe from which 'genes' were selected
- **minSize**
  Minimal size of a gene set to test. All pathways below the threshold are excluded.
- **maxSize**
  Maximal size of a gene set to test. All pathways above the threshold are excluded.

### Value
A table with ORA results. Each row corresponds to a tested pathway. The columns are the following:

- **pathway** – name of the pathway as in 'names(pathway)';
- **pval** – an enrichment p-value from hypergeometric test;
- **padj** – a BH-adjusted p-value;
- **overlap** – size of the overlap;
- **size** – size of the gene set;
- **leadingEdge** – vector with overlapping genes.
Examples

data(examplePathways)
data(exampleRanks)
foraRes <- fora(examplePathways, genes=tail(names(exampleRanks), 200), universe=names(exampleRanks))

geseca  Runs multilevel Monte-Carlo variant for performing gene sets co-regulation analysis

Description

This function is based on the adaptive multilevel splitting Monte Carlo approach and allows to estimate arbitrarily small P-values for the task of analyzing variance along a set of genes.

Usage

geseca(
  pathways,
  E,
  minSize = 1,
  maxSize = nrow(E) - 1,
  center = TRUE,
  scale = FALSE,
  sampleSize = 101,
  eps = 1e-50,
  nproc = 0,
  BPPARAM = NULL,
  nPermSimple = 1000
)

Arguments

dpathways  List of gene sets to check.

dE  expression matrix, rows corresponds to genes, columns corresponds to samples.

dminSize  Minimal size of a gene set to test. All pathways below the threshold are excluded.

dmaxSize  Maximal size of a gene set to test. All pathways above the threshold are excluded.

dcenter  a logical value indicating whether the gene expression should be centered to have zero mean before the analysis takes place. The default is TRUE. The value is passed to scale.

dscale  a logical value indicating whether the gene expression should be scaled to have unit variance before the analysis takes place. The default is FALSE. The value is passed to scale.

dsampleSize  sample size for conditional sampling.
gesecaSimple

eps
nproc
BPPARAM
nPermSimple

This parameter sets the boundary for calculating P-values.
If not equal to zero sets BPPARAM to use nproc workers (default = 0).
Parallelization parameter used in bplapply.
Number of permutations in the simple geseca implementation for preliminary estimation of P-values.

Value

A table with GESECA results. Each row corresponds to a tested pathway. The columns are the following

- pathway – name of the pathway as in 'names(pathways)';
- pctVar – percent of explained variance along gene set;
- pval – P-value that corresponds to the gene set score;
- padj – a BH-adjusted p-value;
- size – size of the pathway after removing genes not present in 'rownames(E)'.

Examples

data("exampleExpressionMatrix")
data("examplePathways")
gr <- geseca(examplePathways, exampleExpressionMatrix, minSize=15, maxSize=500)

gesecaSimple

Runs simple variant for performing gene sets co-regulation analysis

Description

This function is based on the rude Monte Carlo sampling approach and P-value calculation accuracy is limited to ‘1 / nperm’ value.

Usage

gesecaSimple(
  pathways,
  E,
  minSize = 1,
  maxSize = nrow(E) - 1,
  center = TRUE,
  scale = FALSE,
  nperm = 1000,
  nproc = 0,
  BPPARAM = NULL
)
Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pathways</td>
<td>List of gene sets to check.</td>
</tr>
<tr>
<td>E</td>
<td>Expression matrix, rows corresponds to genes, columns corresponds to samples.</td>
</tr>
<tr>
<td>minSize</td>
<td>Minimal size of a gene set to test. All pathways below the threshold are excluded.</td>
</tr>
<tr>
<td>maxSize</td>
<td>Maximal size of a gene set to test. All pathways above the threshold are excluded.</td>
</tr>
<tr>
<td>center</td>
<td>a logical value indicating whether the gene expression should be centered to have zero mean before the analysis takes place. The default is TRUE. The value is passed to scale.</td>
</tr>
<tr>
<td>scale</td>
<td>a logical value indicating whether the gene expression should be scaled to have unit variance before the analysis takes place. The default is FALSE. The value is passed to scale.</td>
</tr>
<tr>
<td>nperm</td>
<td>Number of permutations to do. Minimal possible nominal p-value is about 1/nperm</td>
</tr>
<tr>
<td>nproc</td>
<td>If not equal to zero sets BPPARAM to use nproc workers (default = 0).</td>
</tr>
<tr>
<td>BPPARAM</td>
<td>Parallelization parameter used in bplapply.</td>
</tr>
</tbody>
</table>

Value

A table with GESECA results. Each row corresponds to a tested pathway. The columns are the following

- pathway – name of the pathway as in 'names(pathways)';
- pctVar – percent of explained variance along gene set;
- pval – P-value that corresponds to the gene set score;
- padj – a BH-adjusted p-value;
- size – size of the pathway after removing genes not present in 'rownames(E)'.

Examples

```r
data("exampleExpressionMatrix")
data("examplePathways")
gesecaRes <- gesecaSimple(examplePathways, exampleExpressionMatrix, minSize=15, maxSize=500)
```

---

**Description**

Returns a list of pathways from a GMT file.

**Usage**

```r
gmtPathways(gmt.file)```
mapIdsList

Arguments

gmt.file Path to a GMT file.

Value

A list of vectors with gene sets.

Examples

```r
pathways <- gmtPathways(system.file("extdata", "mouse.reactome.gmt", package="fgsea"))
```

---

**mapIdsList**

Efficiently converts collection of pathways using `AnnotationDbi::mapIds` function. Parameters are the same as for `mapIds` except for keys, which is assumed to be a list of vectors.

---

Description

Efficiently converts collection of pathways using `AnnotationDbi::mapIds` function. Parameters are the same as for `mapIds` except for keys, which is assumed to be a list of vectors.

Usage

```r
mapIdsList(x, keys, column, keytype, ...)
```

Arguments

- `x` the AnnotationDb object. But in practice this will mean an object derived from an AnnotationDb object such as a OrgDb or ChipDb object.
- `keys` a list of vectors with gene ids
- `column` the column to search on
- `keytype` the keytype that matches the keys used
- `...` other parameters passed to `AnnotationDbi::mapIds`

See Also

`AnnotationDbi::mapIds`

Examples

```r
library(org.Mm.eg.db)
data(exampleRanks)
fgseaRes <- fgsea(examplePathways, exampleRanks, maxSize=500, eps=1e-4)
fgseaRes[, leadingEdge := mapIdsList(org.Mm.eg.db, keys=leadingEdge, column="SYMBOL", keytype="ENTREZID")]
```
### multilevelError

Calculates the expected error for the standard deviation of the P-value logarithm.

**Description**

Calculates the expected error for the standard deviation of the P-value logarithm.

**Usage**

```
multilevelError(pval, sampleSize)
```

**Arguments**

- `pval` : P-value
- `sampleSize` : equivalent to `sampleSize` in `fgseaMultilevel`

**Value**

The value of the expected error

**Examples**

```
expectedError <- multilevelError(pval=1e-10, sampleSize=1001)
```

### multilevelImpl

Calculates P-values for preprocessed data.

**Description**

Calculates P-values for preprocessed data.

**Usage**

```
multilevelImpl(
    multilevelPathwaysList, 
    stats, 
    sampleSize, 
    seed, 
    eps, 
    sign = FALSE, 
    BPPARAM = NULL
)
```
plotCoregulationProfile

Arguments

- multilevelPathwaysList: List of pathways for which P-values will be calculated.
- stats: Named vector of gene-level stats. Names should be the same as in 'pathways'
- sampleSize: The size of a random set of genes which in turn has size = pathwaySize
- seed: 'seed' parameter from 'fgseaMultilevel'
- eps: This parameter sets the boundary for calculating the p value.
- sign: This option will be used in future implementations.
- BPPARAM: Parallelization parameter used in bplapply. Can be used to specify cluster to run. If not initialized explicitly or by setting 'nproc' default value 'bpparam()' is used.

Value

List of P-values.

plotCoregulationProfile

Plots expression profile of a gene set

Description

Plots expression profile of a gene set

Usage

plotCoregulationProfile(
  pathway,
  E,
  center = TRUE,
  scale = FALSE,
  titles = colnames(E),
  conditions = NULL
)

Arguments

- pathway: Gene set to plot.
- E: matrix with gene expression values
- center: a logical value indicating whether the gene expression should be centered to have zero mean before the analysis takes place. The default is TRUE. The value is passed to scale.
- scale: a logical value indicating whether the gene expression should be scaled to have unit variance before the analysis takes place. The default is FALSE. The value is passed to scale.
plotCoregulationProfileReduction

Sample titles to use for labels
conditions sample grouping to use for coloring

Value

ggplot object with the coregulation profile plot

Description

Plot a spatial expression profile of a gene set

Usage

plotCoregulationProfileReduction(
  pathway,
  object,
  title = NULL,
  assay = DefaultAssay(object),
  reduction = NULL,
  colors = c("darkblue", "lightgrey", "darkred"),
  guide = "colourbar",
  ...
)

Arguments

pathway Gene set to plot or a list of gene sets (see details below)
object Seurat object
title plot title
assay assay to use for obtaining scaled data, preferably with
reduction reduction to use for plotting (one of the ‘Seurat::Reductions(object)’)
colors vector of three colors to use in the color scheme
guide option for ‘ggplot2::scale_color_gradientn’ to control for presence of the color
legend the same universe of genes in the scaled data
...
additional arguments for Seurat::FeaturePlot

Value

ggplot object (or a list of objects) with the coregulation profile plot

When the input is a list of pathways, pathway names are used for titles. A list of ggplot objects is returned in that case.
plotCoregulationProfileSpatial

Plot a spatial expression profile of a gene set

Description

Plot a spatial expression profile of a gene set

Usage

plotCoregulationProfileSpatial(
  pathway,
  object,
  title = NULL,
  assay = DefaultAssay(object),
  colors = c("darkblue", "lightgrey", "darkred"),
  guide = "colourbar"
)

Arguments

pathway Gene set to plot or a list of gene sets (see details below)
object Seurat object
title plot title
assay assay to use for obtaining scaled data, preferably with the same universe of genes in the scaled data
colors vector of three colors to use in the color scheme
guide option for 'ggplot2::scale_color_gradientn' to control for presence of the color legend the same universe of genes in the scaled data

Value

ggplot object (or a list of objects) with the coregulation profile plot

When the input is a list of pathways, pathway names are used for titles. A list of ggplot objects a returned in that case.
plotEnrichment

Plots GSEA enrichment plot. For more flexibility use ‘plotEnrichmentData’ function.

Description

Plots GSEA enrichment plot. For more flexibility use ‘plotEnrichmentData’ function.

Usage

plotEnrichment(pathway, stats, gseaParam = 1, ticksSize = 0.2)

Arguments

pathway Gene set to plot.
stats Gene-level statistics.
gseaParam GSEA parameter.
ticksSize width of vertical line corresponding to a gene (default: 0.2)

Value

ggplot object with the enrichment plot.

Examples

data(examplePathways)
data(exampleRanks)
## Not run:
plotEnrichment(examplePathways["5991130_Programmed_Cell_Death"],
               exampleRanks)
## End(Not run)

plotEnrichmentData

Returns data required for doing an enrichment plot.

Description

Returns data required for doing an enrichment plot.

Usage

plotEnrichmentData(pathway, stats, gseaParam = 1)
plotEnrichmentData

Arguments

pathway Gene set to plot.
stats Gene-level statistics.
gseaParam GSEA parameter.

Value

returns list with the following data: * 'curve' - data.table with the coordinates of the enrichment curve; * 'ticks' - data.table with statistic entries for each pathway gene, adjusted with gseaParam; * 'stats' - data.table with statistic values for all of the genes, adjusted with gseaParam; * 'posES', 'negES', 'spreadES' - values of the positive enrichment score, negative enrichment score, and difference between them; * 'maxAbsStat' - maximal absolute value of statistic entries, adjusted with gseaParam

Examples

```r
library(ggplot2)
data(examplePathways)
data(exampleRanks)
pd <- plotEnrichmentData(
  pathway = examplePathways[["5991130_Programmed_Cell_Death"]],
  stats = exampleRanks
)

with(pd, ggplot(data=curve) +
  geom_line(aes(x=rank, y=ES), color="green") +
  geom_ribbon(data=stats,
    mapping=aes(x=rank, ymin=0,
      ymax=stat/maxAbsStat*(spreadES/4)),
    fill="grey") +
  geom_segment(data=ticks,
    mapping=aes(x=rank, y=-spreadES/16,
      xend=rank, yend=spreadES/16),
    size=0.2) +
  geom_hline(yintercept=posES, colour="red", linetype="dashed") +
  geom_hline(yintercept=negES, colour="red", linetype="dashed") +
  geom_hline(yintercept=0, colour="black") +
  theme(
    panel.background = element_blank(),
    panel.grid.major=element_line(color="grey92")
  ) +
  labs(x="rank", y="enrichment score")
)```

plotGesecaTable

Plots table of gene set profiles.

Description

Plots table of gene set profiles.

Usage

```r
plotGesecaTable(
  gesecaRes,
  pathways,
  E,
  center = TRUE,
  scale = FALSE,
  colwidths = c(5, 3, 0.8, 1.2, 1.2),
  titles = colnames(E),
  colors = c("blue", "white", "red"),
  pathwayLabelStyle = NULL,
  headerLabelStyle = NULL,
  valueStyle = NULL,
  axisLabelStyle = NULL,
  axisLabelHeightScale = NULL
)
```

Arguments

- `gesecaRes` Table with geseca results.
- `pathways` Pathways to plot table, as in `geseca` function.
- `E` gene expression matrix, as in `geseca` function.
- `center` a logical value indicating whether the gene expression should be centered to have zero mean before the analysis takes place. The default is TRUE. The value is passed to `scale`.
- `scale` a logical value indicating whether the gene expression should be scaled to have unit variance before the analysis takes place. The default is FALSE. The value is passed to `scale`.
- `colwidths` Vector of five elements corresponding to column width for grid.arrange. Can be both units and simple numeric vector, in latter case it defines proportions, not actual sizes. If column width is set to zero, the column is not drawn.
- `titles` sample titles to use an axis labels. Default to `colnames(E)`
- `colors` vector of three colors to use in the color scheme
- `pathwayLabelStyle` list with style parameter adjustments for pathway labels. For example, `list(size=10, color="red")` set the font size to 10 and color to red. See `cowplot::draw_text` for possible options.
headerLabelStyle

similar to `pathwayLabelStyle` but for the table header.

valueStyle

similar to `pathwayLabelStyle` but for pctVar and p-value columns.

axisLabelStyle

list with style parameter adjustments for sample labels. See `ggplot2::element_text` for possible options.

axisLabelHeightScale

height of the row with axis labels compared to other rows. When set to `NULL` the value is determined automatically.

Value

`ggplot` object with gene set profile plots

### Description

Plots table of enrichment graphs using `ggplot` and `gridExtra`.

### Usage

```r
plotGseaTable(
  pathways,
  stats,
  fgseaRes,
  gseaParam = 1,
  colwidths = c(5, 3, 0.8, 1.2, 1.2),
  pathwayLabelStyle = NULL,
  headerLabelStyle = NULL,
  valueStyle = NULL,
  axisLabelStyle = NULL,
  render = NULL
)
```

### Arguments

- **pathways**: Pathways to plot table, as in `fgsea` function.
- **stats**: Gene-level stats, as in `fgsea` function.
- **fgseaRes**: Table with fgsea results.
- **gseaParam**: GSEA-like parameter. Adjusts displayed statistic values, values closer to 0 flatten plots. Default = 1, value of 0.5 is a good choice too.
- **colwidths**: Vector of five elements corresponding to column width for `grid.arrange`. Can be both units and simple numeric vector, in latter case it defines proportions, not actual sizes. If column width is set to zero, the column is not drawn.
reactomePathways

pathwayLabelStyle
   list with style parameter adjustments for pathway labels. For example, `list(size=10, color="red")` set the font size to 10 and color to red. See `cowplot::draw_text` for possible options.

headerLabelStyle
   similar to `pathwayLabelStyle` but for the table header.

valueStyle
   similar to `pathwayLabelStyle` but for NES and p-value columns.

axisLabelStyle
   list with style parameter adjustments for stats axis labels. See `ggplot2::element_text` for possible options.

render
   (deprecated)

Value
   ggplot object with enrichment barcode plots

Examples
   data(examplePathways)
   data(exampleRanks)
   fgseaRes <- fgsea(examplePathways, exampleRanks, minSize=15, maxSize=500)
   topPathways <- fgseaRes[head(order(pval), n=15)][order(NES), pathway]
   plotGseaTable(examplePathways[topPathways], exampleRanks, fgseaRes, gseaParam=0.5)

reactomePathways  Returns a list of Reactome pathways for given Entrez gene IDs

Description
   Returns a list of Reactome pathways for given Entrez gene IDs

Usage
   reactomePathways(genes)

Arguments
   genes  Entrez IDs of query genes.

Value
   A list of vectors with gene sets.

Examples
   data(exampleRanks)
   pathways <- reactomePathways(names(exampleRanks))
writeGmtPathways  Write collection of pathways (list of vectors) to a gmt file

Description
Write collection of pathways (list of vectors) to a gmt file

Usage
writeGmtPathways(pathways, gmt.file)

Arguments
pathways  a named list of vectors with gene ids
gmt.file  name of the output file

Examples
data(examplePathways)
writeGmtPathways(examplePathways, tempfile("examplePathways", fileext=".gmt"))
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