

Package ‘fgsea’

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Title Fast Gene Set Enrichment Analysis

Version 1.0.2

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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 (>= 3.3), Rcpp

Imports data.table, BiocParallel, stats, ggplot2 (>= 2.2.0), gridExtra, grid, fastmatch

Suggests testthat, knitr, rmarkdown, reactome.db, AnnotationDbi, parallel

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LazyData true

LinkingTo Rcpp

RoxygenNote 5.0.1

VignetteBuilder knitr

URL <https://github.com/ctlab/fgsea/>

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

NeedsCompilation yes

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calcGseaStat	<i>Calculates GSEA statistics for a given query gene set</i>
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Description

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

Usage

```
calcGseaStat(stats, selectedStats, gseaParam = 1, returnAllExtremes = FALSE,
  returnLeadingEdge = FALSE)
```

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.

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

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

 calcGseaStatCumulative

Calculates GSEA statistic values for all the prefixes of a gene set

Description

Takes $O(k^{\{3/2\}})$ time, where k is a size of 'selectedSize'.

Usage

```
calcGseaStatCumulative(stats, selectedStats, gseaParam)
```

Arguments

stats	Named numeric vector with gene-level statistics sorted in decreasing order (order is not checked)
selectedStats	indexes of selected genes in a 'stats' array
gseaParam	GSEA weight parameter (0 is unweighted, suggested value is 1)

Value

Numeric vector of GSEA statistics for all prefixes of selectedStats.

Examples

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

 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.

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")`

fgsea

*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

```
fgsea(pathways, stats, nperm, minSize = 1, maxSize = Inf, 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 $1/nperm$
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.
nproc	If not equal to zero sets BPPARAM to use nproc workers (default = 0).
gseaParam	GSEA parameter value.
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/GSEAUUserGuideTEXT.htm#_Running_a_Leading.

Examples

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

gmtPathways	Returns a list of pathways from a GMT file.
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Description

Returns a list of pathways from a GMT file.

Usage

```
gmtPathways(gmt.file)
```

Arguments

gmt.file	Path to a GMT file.
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Value

A list of vectors with gene sets.

Examples

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

plotEnrichment	Plots GSEA enrichment plot.
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Description

Plots GSEA enrichment plot.

Usage

```
plotEnrichment(pathway, stats, gseaParam = 1)
```

Arguments

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

Value

ggplot object with the enrichment plot.

Examples

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

## End(Not run)
```

<code>plotGseaTable</code>	<i>Plots table of enrichment graphs using ggplot and gridExtra.</i>
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Description

Plots table of enrichment graphs using ggplot and gridExtra.

Usage

```
plotGseaTable(pathways, stats, fgseaRes, gseaParam = 1, colwidths = c(5, 3,
  0.8, 1.2, 1.2))
```

Arguments

<code>pathways</code>	Pathways to plot table, as in ‘fgsea’ function.
<code>stats</code>	Gene-level stats, as in ‘fgsea’ function.
<code>fgseaRes</code>	Table with fgsea results.
<code>gseaParam</code>	GSEA-like parameter. Adjusts displayed statistic values, values closer to 0 flatten plots. Default = 1, value of 0.5 is a good choice too.
<code>colwidths</code>	Vector of five elements corresponding to column width for grid.arrange.

Value

TableGrob object returned by grid.arrange.

Examples

```
data(examplePathways)
data(exampleRanks)
fgseaRes <- fgsea(examplePathways, exampleRanks, nperm=1000,
                 minSize=15, maxSize=100)
topPathways <- fgseaRes[head(order(pval), n=15)][order(NES), pathway]
## Not run:
plotGseaTable(examplePathways[topPathways], exampleRanks,
              fgseaRes, gseaParam=0.5)

## End(Not run)
```

reactomePathways	<i>Returns a list of Reactome pathways for given Entrez gene IDs</i>
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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))
```

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