Package 'gsEasy'

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Type Package

Title Gene Set Enrichment Analysis in R

Version 1.4

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Description R-interface to C++ implementation of the rank/score permutation based GSEA test (Subramanian et al 2005 <doi:10.1073/pnas.0506580102>).

License GPL (>= 2)

Imports Rcpp (>= 0.11.2), ontologyIndex (>= 2.0)

LinkingTo Rcpp

Depends R (>= 3.0.0)

Suggests markdown, knitr

VignetteBuilder knitr

RoxygenNote 6.0.1

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R topics documented:

gsEasy-package *Gene Set Enrichment Analysis in R*

Description

R-interface to C++ implementation of the rank/score based GSEA test described by Subramanian et al 2005.

Details

Package:	gsEasy
Type:	Package
Version:	1.0
Date:	2016-01-11
License:	GPL >= 2

Author(s)

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References

Subramanian, A, Tamayo, P, Mootha, VK, Mukherjee, S, Ebert, BL, Gillette, MA, Paulovich, A, Pomeroy, SL, Golub, TR, Lander, ES, Mesirov, JP (2005). Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. Proc. Natl. Acad. Sci. U.S.A., 102, 43:15545-50, doi: 10.1073/pnas.0506580102.

Ashburner et al. Gene ontology: tool for the unification of biology (2000) Nat Genet 25(1):25-9

get_GO_gene_sets *Create list of gene sets defined by GO term annotation*

Description

Note, this function takes several minutes to execute.

Usage

```
get_GO_gene_sets(GO_annotation_file,
  GO_file = "http://purl.obolibrary.org/obo/go.obo", min_genes = 15,
  max_genes = 500, verbose = TRUE)
```

Arguments

GO_annotation_file	File path of annotation file, which should contain a column of genes and a column of terms. Can be downloaded from at http://geneontology.org/gene-associations/gene_association.goa_human.gz.
GO_file	File path of gene ontology.
min_genes	Minimum number of genes in gene sets.
max_genes	Maximum number of genes in gene sets.
verbose	Print progress.

Value

List of character vectors of term IDs.

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get_ontological_gene_sets

Create list of gene sets defined by ontological annotation

Description

Create list of gene sets defined by ontological annotation

Usage

```
get_ontological_gene_sets(ontology, gene, term, min_genes = 1,
  max_genes = 500)
```

Arguments

ontology	ontology_index object.
gene	Character vector of genes.
term	Character vector of term IDs annotated to corresponding genes.
min_genes	Minimum number of genes in gene sets.
max_genes	Maximum number of genes in gene sets.

Value

List of character vectors of term IDs.

GO_gene_sets *GO term gene sets*

Description

List of gene sets annotated by each GO term

Format

List of character vectors of genes per GO term, and named by term ID.

Details

Based on gene-GO term annotations downloaded from `geneontology.org`. Only contains gene sets for terms with up to 500 genes.

gset *Gene set enrichment test*

Description

Gene set enrichment test

Usage

```
gset(S, N = NULL, r = NULL, p = 1, min_its = 200, max_its = 1e+05,
  significance_threshold = 0.05, log_dismiss = -10, raw_score = FALSE)
```

Arguments

`S`	Ranks of gene set
`N`	Integer value. Only required if `r` is not specified.
`r`	Rank/correlation scores. If `S` is `character`, then `r` must be named by gene or be a character vector of the gene names in rank order (necessarily containing `S`).
`p`	Weighting of ranking/correlations, see Subramanian et. al 2005.
`min_its`	Minimum number of null permutations to compare.
`max_its`	Maximum number of null permutations to compare.
`significance_threshold`	Maximum p-value of significant result.
`log_dismiss`	Threshold log probability of returning a significant result, below which function returns current p-value.
`raw_score`	Logical value determining whether to return the raw value of the gene set enrichment score.

Value

Numeric value - p-value of enrichment.

Examples

```
gset(S=1:5 * 2, N=1000)
gset(S=letters[1:3], r=letters)
```

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