

Package: gsEasy (via r-universe)

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Type Package

Title Gene Set Enrichment Analysis in R

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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](https://doi.org/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 7.2.1

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Repository <https://daniel-jg.r-universe.dev>

RemoteUrl <https://github.com/cran/gsEasy>

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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.

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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.

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

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