Package ‘liger’
January 25, 2021

Type Package
Title Lightweight Iterative Geneset Enrichment
Version 2.0.1
Description Gene Set Enrichment Analysis (GSEA) is a computational method that determines whether an a priori defined set of genes shows statistically significant, concordant differences between two biological states. The original algorithm is detailed in Subramanian et al. with ‘Java’ implementations available through the Broad Institute (Subramanian et al. 2005 <doi:10.1073/pnas.0506580102>). The ‘liger’ package provides a lightweight R implementation of this enrichment test on a list of values (Fan et al., 2017 <doi:10.5281/zenodo.887386>). Given a list of values, such as p-values or log-fold changes derived from differential expression analysis or other analyses comparing biological states, this package enables you to test a priori defined set of genes for enrichment to enable interpretability of highly significant or high fold-change genes.

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LazyData TRUE
Depends R (>= 2.10)
Imports graphics, stats, Rcpp, matrixStats, parallel
LinkingTo Rcpp, RcppArmadillo
Suggests knitr, rmarkdown, testthat
VignetteBuilder knitr

URL https://github.com/JEFworks/liger

BugReports https://github.com/JEFworks/liger/issues

RoxygenNote 7.1.0

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NeedsCompilation yes
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Repository CRAN

Date/Publication 2021-01-25 05:50:09 UTC
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bulk.gsea

**Bulk gene set enrichment analysis**

**Description**

Bulk gene set enrichment analysis

**Usage**

bulk.gsea(
  values,
  set.list,
  power = 1,
  rank = FALSE,
  weight = rep(1, length(values)),
  n.rand = 10000,
  mc.cores = 1,
  quantile.threshold = min(100/n.rand, 0.1),
  return.details = FALSE,
  skip.qval.estimation = FALSE
)

**Arguments**

- **values**: vector of values with associated gene names; values must be named, according to names appearing in set.list elements
- **set.list**: list of gene sets
- **power**: an exponent to control the weight of the step (default: 1)
- **rank**: whether to use ranks as opposed to values (default: FALSE)
- **weight**: additional weights associated with each value (default: rep(1,length(values)))
- **n.rand**: number of random permutations used to assess significance (default: 1e4)
- **mc.cores**: number of cores for parallel processing (default: 1)
- **quantile.threshold**: threshold used (default: min(100/n.rand,0.1))
- **return.details**: whether to return extended details (default: FALSE)
- **skip.qval.estimation**: whether to skip q-value estimation for multiple testing (default: FALSE)
gsea

Gene set enrichment analysis

description

Gene set enrichment analysis

usage

gsea( 
values, 
geneset, 
power = 1, 
rank = FALSE, 
weight = rep(1, length(values)), 
n.rand = 10000, 
plot = TRUE, 
main = "", 
return.details = FALSE, 
quantile.threshold = min(100/n.rand, 0.1), 
random.seed = 1, 
mc.cores = 1 
)

arguments

values vector of values with associated gene names; values must be named, according
to names appearing in set elements

geneset vector of genes in the gene set

power an exponent to control the weight of the step (default: 1)

rank whether to use ranks as opposed to values (default: FALSE)

weight additional weights associated with each value (default: rep(1,length(values)))

n.rand number of random permutations used to assess significance (default: 1e4)

plot whether to plot (default: TRUE)
iterative.bulk.gsea

Iterative bulk gene set enrichment analysis

Description

Iterative bulk gene set enrichment analysis

Usage

iterative.bulk.gsea(
  ..., 
  set.list, 
  threshold.eval = 10, 
  n.rand = c(100, 1000, 10000), 
  verbose = TRUE 
)

Arguments

... arguments to be passed to bulk.gsea
set.list list of gene sets
threshold.eval threshold for applying additional permutations (default: 10)
n.rand list of number of random permutations used to assess significance (default: c(1e2, 1e3, 1e4))
verbose whether to use high verbosity level (default: TRUE)
Examples

data("org.Hs.GO2Symbol.list")
universe <- unique(unlist(org.Hs.GO2Symbol.list))  # get universe
gs <- org.Hs.GO2Symbol.list[[1]]  # get a gene set
vals <- rnorm(length(universe), 0, 10)  # simulate values
names(vals) <- universe
vals[gs] <- rnorm(length(gs), 100, 10)
gs.list <- org.Hs.GO2Symbol.list # get gene sets
# reduce n.rand for speed
iterative.bulk.gsea(values = vals, set.list = gs.list[1:3], mc.cores = 1, n.rand=100)

Description

This package contains permutation-based gene set enrichment functionalities in R

| org.Hs.GO2Symbol.list | Human Gene Ontology to HUGO Symbol list |

Usage

org.Hs.GO2Symbol.list

Format

List with each entry as a Gene Ontology gene set

Source

http://geneontology.org/docs/download-ontology/
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