

# 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

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bulk.gsea	<i>Bulk gene set enrichment analysis</i>
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### 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)

**Examples**

```

data("org.Hs.G02Symbol.list")
universe <- unique(unlist(org.Hs.G02Symbol.list)) # get universe
gs <- org.Hs.G02Symbol.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.G02Symbol.list # get gene sets
# reduce n.rand for speed
bulk.gsea(values = vals, set.list = gs.list[1:3], mc.cores = 1, n.rand=100)

```

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)

```

main          plot title (default: "")
return.details whether to return extended details (default: FALSE)
quantile.threshold
                threshold used (default: min(100/n.rand,0.1))
random.seed   random seed (default: 1)
mc.cores      number of cores for parallel processing (default: 1)

```

### Examples

```

data("org.Hs.G02Symbol.list")
universe <- unique(unlist(org.Hs.G02Symbol.list)) # get universe
gs <- org.Hs.G02Symbol.list[[1]] # get a gene set
# fake dummy example where everything in gene set is perfectly enriched
vals <- rnorm(length(universe), 0, 10)
names(vals) <- universe
vals[gs] <- rnorm(length(gs), 100, 10)
# test obviously enriched set, reduce n.rand for speed
gsea(values=vals, geneset=gs, mc.cores=1, n.rand=100, main="G0:Random")

```

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iterative.bulk.gsea    *Iterative bulk gene set enrichment analysis*

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### 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.G02Symbol.list")
universe <- unique(unlist(org.Hs.G02Symbol.list)) # get universe
gs <- org.Hs.G02Symbol.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.G02Symbol.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)
```

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liger

*liger*

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**Description**

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

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org.Hs.G02Symbol.list *Human Gene Ontology to HUGO Symbol list*

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**Description**

Human Gene Ontology to HUGO Symbol list

**Usage**

```
org.Hs.G02Symbol.list
```

**Format**

List with each entry as a Gene Ontology gene set

**Source**

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

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## \* datasets

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