

Package ‘genekitr’

July 19, 2022

Type Package

Title Gene Analysis Toolkit in R

Version 1.0.3

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URL <https://www.genekitr.fun/>

BugReports <https://github.com/GangLiLab/genekitr/issues>

Description An analysis toolkit focused on genes. It mainly includes five features (search, convert, analysis, plot, and export). The user just needs to input feature id ('entrez', 'symbol', 'ensembl' or 'uniprot') to retrieve feature information and PubMed records, to convert id types, to easily do enrichment analysis and draw publication-level plots of GO, KEGG and GSEA, to plot group interaction and export results as sheets in one excel file to easily share and communicate with others.

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Encoding UTF-8

LazyData true

Depends R (>= 3.6)

Imports clusterProfiler, dplyr, DOSE, europepmc, fst, geneset, ggplot2, ggraph, igraph, magrittr, openxlsx, stringr, stringi, tidyrr, VennDiagram, rlang

Suggests AnnotationDbi, BiocManager, cowplot, ComplexUpset, data.table, forcats, fgsea, futile.logger, ggplotify, ggsci, ggupset, ggrepel, ggridges, ggnewscale, GOplot, GOsemSim, labeling, msigdb, pheatmap, tm, treemap, RColorBrewer, rappdirs, RCurl, reshape2, rio, rrvgo, scales, stats, testthat (>= 3.0.0), tibble, wordcloud, knitr, rmarkdown

RoxygenNote 7.2.0

NeedsCompilation no

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Repository CRAN

Date/Publication 2022-07-19 02:40:02 UTC

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as.enrichdat	<i>Modify dataframe for enrichment plot</i>
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Description

To make sure colname contains Description, Count, FoldEnrich/GeneRatio, pvalue/qvalue/p.adjust

Usage

```
as.enrichdat(enrich_df)
```

Arguments

enrich_df Enrichment analysis ‘data.frame’ result.

Value

‘data.frame’

Datasets	<i>Datasets geneList entrez gene list with decreasing fold change value</i>
----------	-----------------------------------------------------------------------------

Description

Datasets geneList entrez gene list with decreasing fold change value

Datasets Differential expression analysis result of GSE42872

Datasets msig_species contains msigdb species information

Datasets msig_category contains msigdb category information

Datasets biocOrg_name contains organism name of bioconductor

Datasets keggOrg_name contains organism name of KEGG https://www.genome.jp/kegg/catalog/org_list.html

Datasets ensOrg_name contains organism name of ensembl

Datasets hsapiens_probe_platform contains human probe platforms

expoSheet	<i>Export list of datasets into different Excel sheets</i>
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Description

Export list of datasets into different Excel sheets

Usage

```
expoSheet(
  data_list,
  data_name,
  filename = NULL,
  dir = tempdir(),
  overwrite = TRUE
)
```

Arguments

data_list	List of datasets.
data_name	Character of data names.
filename	A character string naming an xlsx file.
dir	A character string naming output directory.
overwrite	If TRUE, overwrite any existing file.

Value

An Excel file.

Examples

```
## Not run:
library(openxlsx)
expoSheet(
  data_list = list(mtcars, ToothGrowth),
  data_name = c("mtcars", "tooth"),
  filename = "test.xlsx", dir = tempdir()
)

## End(Not run)
```

genGSEA

Gene Set Enrichment Analysis (FCS method)

Description

Gene Set Enrichment Analysis (FCS method)

Usage

```
genGSEA(
  genelist,
  geneset,
  padj_method = "BH",
  p_cutoff = 0.05,
  q_cutoff = 0.05,
  min_gset_size = 10,
  max_gset_size = 500,
  set_seed = FALSE
)
```

Arguments

genelist	Order ranked genelist in decreasing order, gene can be entrez, ensembl or symbol.
geneset	Gene set is a two-column data.frame with term id and gene id. Please use package ‘geneset’ to select available gene set or make new one.
padj_method	One of "BH", "BY", "bonferroni", "fdr", "hochberg", "holm", "hommel", "none"
p_cutoff	Numeric of cutoff for both unadjusted and adjusted pvalue, default is 0.05.
q_cutoff	Numeric of cutoff for qvalue, default is 0.05.
min_gset_size	Numeric of minimal size of each geneset for analyzing, default is 10.
max_gset_size	Numeric of maximal size of each geneset for analyzing, default is 500.
set_seed	GSEA permutations are performed using random reordering, which causes slightly difference results after every time running. If user want to get same result every time for same input, please set ‘set_seed = TRUE’ or ‘set.seed()’ prior to running.

Value

A 'data.frame'.

Examples

```
## Not run:  
# only gene ids  
data(geneList, package = "genekitr")  
gs <- geneset::getGO(org = "human", ont = "mf")  
gse <- genGSEA(genelist = geneList, geneset = gs)  
  
## End(Not run)
```

genInfo

Get gene related information

Description

Get gene related information

Usage

```
genInfo(id = NULL, org = "hs", unique = FALSE, keepNA = TRUE)
```

Arguments

id	Gene id (symbol, ensembl or entrez id) or uniprot id. If this argument is NULL, return all gene info.
org	Latin organism shortname from 'ensOrg_name'. Default is human.
unique	Logical, if one-to-many mapping occurs, only keep one record with fewest NA. Default is FALSE.
keepNA	If some id has no match at all, keep it or not. Default is TRUE.

Value

A 'data.frame'.

Examples

```
# example1: input list with fake id and one-to-many mapping id  
x <- genInfo(id = c(  
  "MCM10", "CDC20", "S100A9", "MMP1", "BCC7",  
  "FAKEID", "TP53", "HBD", "NUDT10"  
)  
)  
  
# example2: statistics of human gene biotypes
```

```
genInfo(org = "hs") %>%
  {
    table(.$gene_biotype)
  }
```

genORA

Gene Over-Representation enrichment Analysis (ORA method)

Description

Gene Over-Representation enrichment Analysis (ORA method)

Usage

```
genORA(
  id,
  geneset,
  group_list = NULL,
  padj_method = "BH",
  p_cutoff = 0.05,
  q_cutoff = 0.15,
  min_gset_size = 10,
  max_gset_size = 500,
  universe
)
```

Arguments

id	A vector of gene id which can be entrezid, ensembl, symbol or uniprot.
geneset	Gene set is a two-column data.frame with term id and gene id. Please use package 'geneset' to select available gene set or make new one.
group_list	A list of gene group information, default is NULL.
padj_method	One of "BH", "BY", "bonferroni", "fdr", "hochberg", "holm", "hommel", "none"
p_cutoff	Numeric of cutoff for both unadjusted and adjusted pvalue, default is 0.05.
q_cutoff	Numeric of cutoff for qvalue, default is 0.15.
min_gset_size	Numeric of minimal size of each geneset for analyzing, default is 10.
max_gset_size	Numeric of maximal size of each geneset for analyzing, default is 500.
universe	Character of background genes. If missing, all genes in geneset will be used as background.

Value

A 'data.frame'.

Examples

```
## Not run:
# only gene ids
data(geneList, package = "genekitr")
id <- names(geneList)[abs(geneList) > 1]
gs <- geneset::getGO(org = "human", ont = "mf")
ora <- genORA(id, geneset = gs)

# gene id with groups
id <- c(head(names(geneList), 100), tail(names(geneList), 100))
group <- list(
  group1 = c(rep("up", 100), rep("down", 100)),
  group2 = c(rep("A", 130), rep("B", 70))
)
gora <- genORA(id, geneset = gs, group_list = group)

## End(Not run)
```

getPubmed

Get pubmed paper records by searching abstract

Description

Get pubmed paper records by searching abstract

Usage

```
getPubmed(term, add_term = NULL, num = 100)
```

Arguments

term	query terms e.g. gene id, GO/KEGG pathway
add_term	other searching terms Default is NULL
num	limit the number of records . Default is 100.

Value

A list of 'tibble' for pubmed records

Examples

```
term <- c("Tp53", "Brca1", "Tet2")
add_term <- c("stem cell", "mouse")
l <- getPubmed(term, add_term, num = 30)
# very easy to output
expoSheet(l, data_name = term, filename = "test.xlsx", dir = tempdir())
```

importCP	<i>Import clusterProfiler result</i>
----------	--------------------------------------

Description

Import clusterProfiler result

Usage

```
importCP(object, type = c("go", "gsea", "other"))
```

Arguments

object	clusterProfiler object.
type	object type from "go", "gsea" and "other". "other" includes ORA (over-representation analysis) of KEGG, DOSE,...

Value

‘data.frame‘

importPanther	<i>Import Panther web result</i>
---------------	----------------------------------

Description

Import Panther web result

Usage

```
importPanther(panther_file)
```

Arguments

panther_file	Panther result file.
--------------	----------------------

Value

‘data.frame‘

Description

Plot for GO and KEGG enrichment analysis

Usage

```
plotEnrich(
  enrich_df,
  fold_change = NULL,
  plot_type = c("bar", "wego", "dot", "bubble", "lollipop", "geneheat", "genechord",
    "network", "gomap", "goheat", "gotangram", "wordcloud", "upset"),
  term_metric = c("FoldEnrich", "GeneRatio", "Count", "RichFactor"),
  stats_metric = c("p.adjust", "pvalue", "qvalue"),
  sim_method = c("Resnik", "Lin", "Rel", "Jiang", "Wang", "JC"),
  up_color = "#E31A1C",
  down_color = "#1F78B4",
  show_gene = "all",
  xlim_left = 0,
  xlim_right = NA,
  wrap_length = NULL,
  org = NULL,
  ont = NULL,
  scale_ratio,
  layout,
  n_term,
  ...
)
```

Arguments

enrich_df	Enrichment analysis 'data.frame' result.
fold_change	Fold change or logFC values with gene IDs as names. Used in "heat" and "chord" plot.
plot_type	Choose from "bar", "wego", "bubble", "dot", "lollipop", "geneheat", "genechord", "network", "gomap", "goheat", "gotangram", "wordcloud", "upset".
term_metric	Pathway term metric from one of 'GeneRatio', 'Count', 'FoldEnrich' and 'RichFactor'.
stats_metric	Statistic metric from one of "pvalue", "p.adjust", "qvalue".
sim_method	Method of calculating the similarity between nodes, one of one of "Resnik", "Lin", "Rel", "Jiang", "Wang" or "JC" (Jaccard's similarity index). Only "JC" supports KEGG data. Used in "map", "goheat", "gotangram", "wordcloud".
up_color	Color of higher statistical power (e.g. Pvalue 0.01) or higher logFC, default is "red".

down_color	Color of lower statistical power (e.g. Pvalue 1) or lower logFC, default is "blue".
show_gene	Select genes to show. Default is "all". Used in "heat" and "chord" plot.
xlim_left	X-axis left limit, default is 0.
xlim_right	X-axis right limit, default is NA.
wrap_length	Numeric, wrap text if longer than this length. Default is NULL.
org	Organism name from 'biocOrg_name'.
ont	One of "BP", "MF", and "CC".
scale_ratio	Numeric, scale of node and line size.
layout	Graph layout in "map" plot, e.g, "circle", "dh", "drl", "fr", "graphopt", "grid", "lgl", "kk", "mds", "nicely" (default), "randomly", "star".
n_term	Number of terms (used in WEGO plot)
...	other arguments from 'plot_theme' function

Value

A ggplot object

Examples

```
## Not run:
## example data
library(ggplot2)
library(igraph)
library(ggraph)
data(geneList, package = "genekitr")
id <- names(geneList)[abs(geneList) > 1.5]
logfc <- geneList[id]

gs <- geneset::getGO(org = "human", ont = "bp")
ego <- genORA(id, geneset = gs)
ego <- ego[1:10, ]
all_ego <- genGO(id,
  org = "human", ont = "all", pvalueCutoff = 0.01,
  qvalueCutoff = 0.01
)

## example plots
plotEnrich(ego, plot_type = "dot")

plotEnrich(ego, plot_type = "bubble", scale_ratio = 0.4)

plotEnrich(ego, plot_type = "bar")

plotEnrich(all_ego, plot_type = "wego")

plotEnrich(ego,
  plot_type = "lollipop",
  down_color = "#325CAC", up_color = "#E69056",
```

```

    wrap_length = 25, scale_ratio = 0.4
  )

plotEnrich(ego, plot_type = "geneheat")

show_gene <- c("BRCA2", "CDK1", "JUN", "MCM8", "TIPIN")
plotEnrich(ego, plot_type = "geneheat", show_gene = show_gene)
plotEnrich(ego, fold_change = logfc, plot_type = "geneheat", show_gene = show_gene)

plotEnrich(ego, fold_change = logfc, plot_type = "genechord", show_gene = show_gene)

plotEnrich(ego, plot_type = "network", scale_ratio = 0.5)

plotEnrich(ego, plot_type = "gomap", wrap_length = 25)

plotEnrich(ego, plot_type = "goheat", sim_method = "Rel")

plotEnrich(ego, plot_type = "gotangram", sim_method = "Rel")

plotEnrich(ego, plot_type = "wordcloud")

plotEnrich(ego, plot_type = "upset", main_text_size = 15, legend_text_size = 8)

## End(Not run)

```

plotEnrichAdv	<i>Advanced Plot for GO and KEGG enrichment analysis Both up and down regulated pathways could be plotted in one figure as two-side barplot</i>
---------------	-------------------------------------------------------------------------------------------------------------------------------------------------

Description

Advanced Plot for GO and KEGG enrichment analysis Both up and down regulated pathways could be plotted in one figure as two-side barplot

Usage

```

plotEnrichAdv(
  up_enrich_df,
  down_enrich_df,
  plot_type = c("one", "two"),
  term_metric = c("FoldEnrich", "GeneRatio", "Count", "RichFactor"),
  stats_metric = c("p.adjust", "pvalue", "qvalue"),
  wrap_length = NULL,
  xlim_left = NULL,
  xlim_right = NULL,
  color,
  ...
)

```

Arguments

up_enrich_df	Enrichment analysis 'data.frame' for up-regulated genes.
down_enrich_df	Enrichment analysis 'data.frame' for down-regulated genes.
plot_type	Choose from "one" and "two". "One" represents both up and down pathways are plotted together; "two" represents up and down are plotted seperately.
term_metric	Pathway term metric from one of 'GeneRatio', 'Count', 'FoldEnrich' and 'Rich-Factor'.
stats_metric	Statistic metric from one of "pvalue", "p.adjust", "qvalue".
wrap_length	Numeric, wrap text if longer than this length. Default is NULL.
xlim_left	X-axis left limit
xlim_right	X-axis right limit
color	Plot colors.
...	other arguments from 'plot_theme' function

Value

A ggplot object

plotGSEA

GSEA plot

Description

GSEA plot

Usage

```
plotGSEA(
  gsea_list,
  plot_type = c("volcano", "classic", "fgsea", "ridge", "bar"),
  stats_metric = c("p.adjust", "pvalue", "qvalue"),
  show_pathway = NULL,
  show_gene = NULL,
  colour = NULL,
  wrap_length = NULL,
  ...
)
```

Arguments

gsea_list	GSEA result from 'genGSEA' function
plot_type	GSEA plot type, one of 'volcano', 'classic', 'fgsea', 'ridge' or 'bar'.
stats_metric	Statistic metric from one of "pvalue", "p.adjust", "qvalue".
show_pathway	Select plotting pathways by number (will choose top N pathways) or pathway name (choose from ID column).
show_gene	Select genes to show. Default is "all". Used in "classic" plot.
colour	Colour vector. Deafault is NULL. Used in volcano, ridge and bar plot.
wrap_length	Numeric, wrap text if longer than this length. Default is NULL.
...	other arguments transfer to 'plot_theme' function

Value

A ggplot object

Examples

```
## Not run:
library(ggplot2)
## get GSEA result
data(geneList, package = "genekitr")
gs <- geneset::getMsigdb(org = "human", category = "H")
gse <- genGSEA(genelist = geneList, geneset = gs)

## volcano plot
# get top3 of up and down pathways
plotGSEA(gse, plot_type = "volcano", show_pathway = 3)
# choose pathway by character
pathways <- c('HALLMARK_KRAS_SIGNALING_UP', 'HALLMARK_P53_PATHWAY', 'HALLMARK_GLYCOLYSIS')
plotGSEA(gse, plot_type = "volcano", show_pathway = pathways)

## classic pathway plot
genes <- c('ENG', 'TP53', 'MET')
plotGSEA(gse, plot_type = "classic", show_pathway = pathways, show_gene = genes)

## fgsea table plot
plotGSEA(gse, plot_type = "fgsea", show_pathway = 3)

## ridgeplot
plotGSEA(gse,
  plot_type = "ridge",
  show_pathway = 10, stats_metric = "p.adjust"
)

## two-side barplot
plotGSEA(gse,
  plot_type = "bar", main_text_size = 8,
  colour = c("navyblue", "orange")
)
```

```
## End(Not run)
```

plotVenn	<i>Venn plot for groups of genes</i>
----------	--------------------------------------

Description

If gene group over 4, plot will be visualized using UpSet plot.

Usage

```
plotVenn(venn_list, use_venn = TRUE, color = NULL, alpha_degree = 0.3, ...)
```

Arguments

venn_list	A list of gene id.
use_venn	Logical, use venn to plot, default is 'TRUE', the other option is upsetplot for large list.
color	Colors for gene lists, default is NULL.
alpha_degree	Alpha transparency of each circle's area, default is 0.3.
...	other arguments transfer to 'plot_theme' function

Value

A ggplot object

Examples

```
library(ggplot2)
set1 <- paste0(rep("gene", 30), sample(1:1000, 30))
set2 <- paste0(rep("gene", 40), sample(1:1000, 40))
set3 <- paste0(rep("gene", 50), sample(1:1000, 50))
set4 <- paste0(rep("gene", 60), sample(1:1000, 60))
set5 <- paste0(rep("gene", 70), sample(1:1000, 70))
sm_gene_list <- list(gset1 = set1, gset2 = set2, gset3 = set3)
la_gene_list <- list(
  gset1 = set1, gset2 = set2, gset3 = set3,
  gset4 = set4, gset5 = set5
)
plotVenn(sm_gene_list,
  use_venn = TRUE,
  color = ggsci::pal_lancet()(3),
  alpha_degree = 1,
  main_text_size = 1.5,
  border_thick = 0
)
```

```

plotVenn(la_gene_list,
  use_venn = FALSE,
  main_text_size = 15,
  legend_text_size = 8,
  legend_position = 'left'
)

```

plotVolcano

Volcano plot for differential expression analysis

Description

Volcano plot for differential expression analysis

Usage

```

plotVolcano(
  deg_df,
  stat_metric = c("p.adjust", "pvalue"),
  stat_cutoff = 0.05,
  logFC_cutoff = 1,
  up_color = "red",
  down_color = "blue",
  show_gene = NULL,
  dot_size = 1.75,
  ...
)

```

Arguments

deg_df	DEG dataframe with gene id, logFC and stat(e.g. pvalue/qvalue).
stat_metric	Statistic metric from "pvalue" or "p.adjust".
stat_cutoff	Statistic cutoff, default is 0.05.
logFC_cutoff	Log2 fold change cutoff, default is 1 which is actually 2 fold change.
up_color	Color of up-regulated genes, default is "red".
down_color	Color of down-regulated genes, default is "blue".
show_gene	Select genes to show, default is no genes to show.
dot_size	Volcano dot size, default is 1.75.
...	other arguments from 'plot_theme' function

Value

A ggplot object

Examples

```
## Not run:
library(ggplot2)
data(deg, package = "genekitr")
plotVolcano(deg, "p.adjust", remove_legend = T, dot_size = 3)

# show some genes
plotVolcano(deg, "p.adjust",
  remove_legend = T,
  show_gene = c("CD36", "DUSP6", "IER3", "CDH7")
)

## End(Not run)
```

plot_theme

Themes for all plots

Description

Change ggplot text, font, legend and border

Usage

```
plot_theme(
  main_text_size = 8,
  legend_text_size = 6,
  font_type = "sans",
  border_thick = 1.5,
  remove_grid = TRUE,
  remove_border = FALSE,
  remove_main_text = FALSE,
  remove_legend_text = FALSE,
  remove_legend = FALSE
)
```

Arguments

`main_text_size` Numeric, main text size

`legend_text_size` Numeric, legend text size

`font_type` Character, specify the plot text font family, default is "sans".

`border_thick` Numeric, border thickness, default is 1. If set 0, remove both border and ticks.

`remove_grid` Logical, remove background grid lines, default is FALSE.

`remove_border` Logical, remove border line, default is FALSE.


```

remove_main_text
    Logical, remove all axis text, default is FALSE.
remove_legend_text
    Logical, remove all legend text, default is FALSE.
remove_legend
    Logical, remove entire legend, default is FALSE.

```

Value

ggplot theme

Examples

```

library(ggplot2)
ggplot(mtcars, aes(x = wt, y = mpg)) +
  geom_point() +
  plot_theme(font_type = "Times", border_thick = 2)

```

simGO	<i>Simplifity GO enrichment result</i>
-------	----------------------------------------

Description

Simplifity GO enrichment result

Usage

```

simGO(
  enrich_df,
  sim_method = c("Resnik", "Lin", "Rel", "Jiang", "Wang"),
  org = NULL,
  ont = NULL
)

```

Arguments

enrich_df	GO enrichment analysis of 'genORA()' result.
sim_method	Method of calculating the similarity between nodes, one of one of "Resnik", "Lin", "Rel", "Jiang", "Wang" methods.
org	Organism name from 'biocOrg_name'.
ont	One of "bp", "mf", and "cc".

Value

A 'data.frame' contains simplified GO terms.

transId	<i>Transform gene id among symbol, entrezid, ensembl and uniprot.</i>
---------	-----------------------------------------------------------------------

Description

Transform gene id among symbol, entrezid, ensembl and uniprot.

Usage

```
transId(id, transTo, org = "hs", unique = FALSE, keepNA = FALSE)
```

Arguments

id	Gene ids.
transTo	Transform to what type. User could select one or more from "symbol", "entrez", "ensembl" or "uniprot."
org	Latin organism shortname from 'ensOrg_name'. Default is human.
unique	Logical, if one-to-many mapping occurs, only keep one record with fewest NA. Default is FALSE.
keepNA	If some id has no match at all, keep it or not. Default is FALSE.

Value

data frame, first column is input id and others are converted id.

Examples

```
## Not run:
# example1:
transId(
  id = c("Cyp2c23", "Fhit", "Gal3st2b", "Trp53", "Tp53"),
  transTo = "ensembl", org = "mouse", keepNA = FALSE
)

## example2: input id with one-to-many mapping and fake one
transId(
  id = c("MMD2", "HBD", "RNR1", "TEC", "BCC7", "FAKEID", "TP53"),
  transTo = c("entrez", "ensembl"), keepNA = TRUE
)

# example3: auto-recognize ensembl version number
transId("ENSG00000141510.11", "symbol")

## End(Not run)
```

transProbe	<i>Transform probe id to symbol, entrezid, ensembl or uniprot.</i>
------------	--------------------------------------------------------------------

Description

Transform probe id to symbol, entrezid, ensembl or uniprot.

Usage

```
transProbe(id, transTo, org = "human", platform = NULL)
```

Arguments

id	probe ids.
transTo	Transform to what type. User could select one or more from "symbol", "entrez", "ensembl" or "uniprot."
org	'human'.
platform	Probe platform. If NULL, program will detect automatically.

Value

data frame, first column is probe id and others are converted id.

Examples

```
## Not run:  
data(deg, package = "genekitr")  
id <- deg$probe_id  
transProbe(id, transTo = "symbol")  
  
## End(Not run)
```

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