Package 'ReporterScore'

March 29, 2024

Type Package

Title Generalized Reporter Score-Based Enrichment Analysis for Omics Data

Version 0.1.4

Description Inspired by the classic 'RSA', we developed the improved 'Generalized Reporter Score-based Analysis (GRSA)' method, implemented in the R package 'ReporterScore', along with comprehensive visualization methods and pathway databases. 'GRSA' is a threshold-free method that works well with all types of biomedical features, such as genes, chemical compounds, and microbial species. Importantly, the 'GRSA' supports multi-group and longitudinal experimental designs, because of the included multi-group-compatible statistical methods.

License GPL-3

Encoding UTF-8

RoxygenNote 7.2.3

Imports magrittr, dplyr, stats, ggplot2 (>= 3.2.0), pcutils (>= 0.2.5), utils, scales, ggnewscale, ggrepel, reshape2, stringr, foreach

Suggests knitr, rmarkdown, plyr, e1071, factoextra, snow, doSNOW, pheatmap, readr, R.utils, KEGGREST, clusterProfiler, enrichplot, pathview, GSA, vegan, MetaNet, igraph, ggraph, PADOG, safe, rSEA, GSVA

Depends R (>= 4.2.0)

VignetteBuilder knitr

BugReports https://github.com/Asa12138/ReporterScore/issues

URL https://github.com/Asa12138/ReporterScore

NeedsCompilation no

Author Chen Peng [aut, cre] (<https://orcid.org/0000-0002-9449-7606>)

Maintainer Chen Peng <pengchen2001@zju.edu.cn>

Repository CRAN

Date/Publication 2024-03-29 16:30:09 UTC

R topics documented:

`cm_test_k` *Test the proper clusters k for c_means*

Description

Test the proper clusters k for c_means

C-means cluster

Usage

```
cm_test_k(otu_group, filter_var, fast = TRUE)

c_means(otu_group, k_num, filter_var)
```

Arguments

`otu_group`	standardize data
`filter_var`	filter the highest var
`fast`	whether do the gap_stat?
`k_num`	cluster number

Value

ggplot

ggplot

See Also

Other C_means: `RSA_by_cm()`

Examples

```
if (requireNamespace("e1071") && requireNamespace("factoextra")) {
  data(otutab, package = "pcutils")
  pcutils::hebing(otutab, metadata$Group) -> otu_group
  cm_test_k(otu_group, filter_var = 0.7)
  cm_res <- c_means(otu_group, k_num = 3, filter_var = 0.7)
  plot(cm_res, 0.8)
```

```
}
```

`Compound_htable` *Compound htable from 'KEGG'*

Description

Compound htable from 'KEGG'

See Also

Other data: `CPDlist`, `GOlist`, `KO_htable`, `KOlist`, `Module_htable`, `Pathway_htable`, `hsa_kegg_pathway`, `mmu_kegg_pathway`

`CPDlist` *The CPDlist used for enrichment.*

Description

an list contains two data.frame named pathway and module.

Format

four columns in each data.frame.

id "map0010" or "M00001"

K_num contians how many Compounds in this pathway or module

KOs Compounds name

Description the description of this pathway or module

See Also

Other data: `Compound_htable`, `GOlist`, `KO_htable`, `KOlist`, `Module_htable`, `Pathway_htable`, `hsa_kegg_pathway`, `mmu_kegg_pathway`

custom_modulelist *Build a custom modulelist*

Description

Build a custom modulelist

Transform a modulelist to a list

Usage

```
custom_modulelist(pathway2ko, pathway2desc = NULL, verbose = TRUE)

transform_modulelist(mymodulelist, mode = 1)
```

Arguments

pathway2ko	user input annotation of Pathway to KO mapping, a data.frame of 2 column with pathway and ko.
pathway2desc	user input of Pathway TO Description mapping, a data.frame of 2 column with pathway and description.
verbose	verbose
mymodulelist	mymodulelist
mode	1~2

Value

a custom modulelist

modulelist

See Also

Other modulelist: custom_modulelist_from_org(), get_features()

Other modulelist: custom_modulelist_from_org(), get_features()

Examples

```
mydat <- data.frame(pathway = paste0("PATHWAY", rep(seq_len(2), each = 5)), ko = paste0("K", 1:10))
mymodulelist <- custom_modulelist(mydat)
print(mymodulelist)
transform_modulelist(mymodulelist)
```

custom_modulelist_from_org *Custom modulelist from a specific organism*

Description

Custom modulelist from a specific organism

Usage

```
custom_modulelist_from_org(
  org = "hsa",
  feature = "ko",
  gene = "symbol",
  verbose = TRUE
)
```

Arguments

org	kegg organism, listed in https://www.genome.jp/kegg/catalog/org_list.html, default, "hsa"
feature	one of "ko", "gene", "compound"
gene	one of "symbol","id"
verbose	logical

Value

modulelist

See Also

Other modulelist: custom_modulelist(), get_features()

Examples

```
hsa_pathway <- custom_modulelist_from_org(org = "hsa", feature = "gene")
```

gene2ko *Transfer gene symbol table to KO table*

Description

You can use ‘clusterProfiler::bitr()‘ to transfer your table from other gene_id to gene_symbol.

Usage

```
gene2ko(genedf, org = "hsa")
```

Arguments

genedf	,rowname is gene symbol (e.g. PFKM), colnames is samples
org	kegg organism, listed in 'https://www.genome.jp/kegg/catalog/org_list.html', default, 'hsa'

Value

kodf

Examples

```
data("genedf")
KOdf <- gene2ko(genedf, org = "hsa")
```

genedf *human gene table*

Description

human gene table

See Also

Other test_data: KO_abundance, reporter_score_res

get_features *get features in a modulelist*

Description

get features in a modulelist

Usage

```
get_features(map_id = "map00010", ko_stat = NULL, modulelist = NULL)
```

Arguments

map_id	map_id in modulelist
ko_stat	NULL or ko_stat result from pvalue2zs
modulelist	NULL or customized modulelist dataframe, must contain 'id','K_num','KOs','Description' columns. Take the 'KOlist' as example, use custom_modulelist.

Value

KOids, or data.frame with these KOids.

See Also

Other modulelist: custom_modulelist_from_org(), custom_modulelist()

Examples

```
get_features(map_id = "map00010")
```

get_reporter_score *Calculate reporter score*

Description

Calculate reporter score

Usage

```
get_reporter_score(
  ko_stat,
  type = c("pathway", "module")[1],
  feature = "ko",
  threads = 1,
  modulelist = NULL,
  perm = 4999,
  verbose = TRUE,
  p.adjust.method2 = "BH",
  min_exist_KO = 3,
  max_exist_KO = 600
)
```

Arguments

ko_stat	ko_stat result from pvalue2zs
type	'pathway' or 'module' for default KOlist for microbiome, 'CC', 'MF', 'BP', 'ALL' for default GOlist for homo sapiens. And org in listed in 'https://www.genome.jp/kegg/catalog/org_ such as 'hsa' (if your kodf is come from a specific organism, you should specify type here).
feature	one of 'ko', 'gene', 'compound'
threads	default 1
modulelist	NULL or customized modulelist dataframe, must contain 'id','K_num','KOs','Description' columns. Take the 'KOlist' as example, use custom_modulelist.
perm	permutation number, default: 4999.
verbose	logical
p.adjust.method2	p.adjust.method for the correction of ReporterScore, see p.adjust
min_exist_KO	min exist KO number in a pathway (default, 3, when a pathway contains KOs less than 3, there will be no RS)
max_exist_KO	max exist KO number in a pathway (default, 600, when a pathway contains KOs more than 600, there will be no RS)

Value

reporter_res data.frame

See Also

Other GRSA: ko.test(), pvalue2zs(), reporter_score()

Examples

```
data("KO_abundance_test")
ko_pvalue <- ko.test(KO_abundance, "Group", metadata)
ko_stat <- pvalue2zs(ko_pvalue, mode = "directed")
reporter_s1 <- get_reporter_score(ko_stat, perm = 499)
```

GOlist *The GOlist used for enrichment.*

Description

an list contains three data.frame named BP, CC, MF.

Format

four columns in each data.frame.

id "map0010" or "M00001"

K_num contians how many Genes in this GO term

KOs Genes name

Description the description of this GO term

See Also

Other data: CPDlist, Compound_htable, KO_htable, KOlist, Module_htable, Pathway_htable, hsa_kegg_pathway, mmu_kegg_pathway

---

hsa_kegg_pathway *pathway information for "hsa"*

Description

pathway information for "hsa"

See Also

Other data: CPDlist, Compound_htable, GOlist, KO_htable, KOlist, Module_htable, Pathway_htable, mmu_kegg_pathway

ko.test *Differential analysis or Correlation analysis for KO-abundance table*

Description

Differential analysis or Correlation analysis for KO-abundance table

Usage

```
ko.test(
  kodf,
  group,
  metadata = NULL,
  method = "wilcox.test",
  pattern = NULL,
  p.adjust.method1 = "none",
  threads = 1,
  verbose = TRUE
)
```

Arguments

kodf	KO_abundance table, rowname is ko id (e.g. K00001),colnames is samples.
group	The comparison groups (at least two categories) in your data, one column name of metadata when metadata exist or a vector whose length equal to columns number of kodf. And you can use factor levels to change order.
metadata	sample information data.frame contains group
method	the type of test. Default is 'wilcox.test'. Allowed values include: • t.test (parametric) and wilcox.test (non-parametric). Perform comparison between two groups of samples. If the grouping variable contains more than two levels, then a pairwise comparison is performed. • anova (parametric) and kruskal.test (non-parametric). Perform one-way ANOVA test comparing multiple groups. • 'pearson', 'kendall', or 'spearman' (correlation), see cor.
pattern	a named vector matching the group, e.g. c('G1'=1,'G2'=3,'G3'=2), use the correlation analysis with specific pattern to calculate p-value.
p.adjust.method1	p.adjust.method for 'ko.test', see p.adjust
threads	default 1
verbose	logical

Value

ko_pvalue data.frame

See Also

Other GRSA: get_reporter_score(), pvalue2zs(), reporter_score()

Examples

```
data("KO_abundance_test")
ko_pvalue <- ko.test(KO_abundance, "Group", metadata)
```

KOlist *The KOlist used for enrichment.*

Description

an list contains two data.frame named pathway and module.

Format

four columns in each data.frame.

id "map0010" or "M00001"

K_num contians how many KOs in this pathway or module

KOs KOs name

Description the description of this pathway or module

See Also

Other data: CPDlist, Compound_htable, GOlist, KO_htable, Module_htable, Pathway_htable, hsa_kegg_pathway, mmu_kegg_pathway

---

KO_abundance *The KOs abundance table and group table.*

Description

The KOs abundance table and group table.

The KOs abundance table and group table.

See Also

Other test_data: genedf, reporter_score_res

KO_enrich *Perform enrichment analysis*

Description

This function performs KO enrichment analysis using the ‘clusterProfiler‘ package.

Usage

```
KO_enrich(
  ko_stat,
  padj_threshold = 0.05,
  logFC_threshold = NULL,
  add_mini = NULL,
  p.adjust.method = "BH",
  type = c("pathway", "module")[1],
  feature = "ko",
  modulelist = NULL,
  verbose = TRUE
)

as.enrich_res(gsea_res)
```

Arguments

ko_stat	ko_stat dataframe from ko.test.
padj_threshold	p.adjust threshold to determine whether a feature significant or not. p.adjust < padj_threshold, default: 0.05
logFC_threshold	logFC threshold to determine whether a feature significant or not. abs(logFC)>logFC_threshold, default: NULL
add_mini	add_mini when calculate the logFC. e.g (10+0.1)/(0+0.1), default 0.05*min(avg_abundance)
p.adjust.method	The method used for p-value adjustment (default: "BH").
type	"pathway" or "module" for default KOlist_file.
feature	one of "ko", "gene", "compound"
modulelist	NULL or customized modulelist dataframe, must contain "id","K_num","KOs","Description" columns. Take the ‘KOlist‘ as example, use custom_modulelist.
verbose	logical
gsea_res	gsea_res from KO_gsea

Value

A data frame containing the enrichment results.

enrich_res object

See Also

Other common_enrich: KO_fisher(), KO_gsa(), KO_gsea(), KO_gsva(), KO_padog(), KO_safe(), KO_sea(), plot_enrich_res()

Examples

```
## use `enricher` from the `clusterProfiler` package.
if (requireNamespace("clusterProfiler")) {
  data("reporter_score_res")
  enrich_res <- KO_enrich(reporter_score_res)
  plot(enrich_res)
}
```

KO_fisher *Perform fisher's exact enrichment analysis*

Description

Perform fisher's exact enrichment analysis

Usage

```
KO_fisher(
  ko_stat,
  padj_threshold = 0.05,
  logFC_threshold = NULL,
  add_mini = NULL,
  p.adjust.method = "BH",
  type = c("pathway", "module")[1],
  feature = "ko",
  modulelist = NULL,
  verbose = TRUE
)
```

Arguments

ko_stat	ko_stat dataframe from ko.test.
padj_threshold	p.adjust threshold to determine whether a feature significant or not. p.adjust < padj_threshold, default: 0.05
logFC_threshold	logFC threshold to determine whether a feature significant or not. abs(logFC)>logFC_threshold, default: NULL
add_mini	add_mini when calculate the logFC. e.g (10+0.1)/(0+0.1), default 0.05*min(avg_abundance)
p.adjust.method	The method used for p-value adjustment (default: "BH").
type	"pathway" or "module" for default KOlist_file.

feature	one of "ko", "gene", "compound"
modulelist	NULL or customized modulelist dataframe, must contain "id","K_num","KOs","Description" columns. Take the 'KOlist' as example, use custom_modulelist.
verbose	logical

Value

data.frame

See Also

Other common_enrich: KO_enrich(), KO_gsa(), KO_gsea(), KO_gsva(), KO_padog(), KO_safe(), KO_sea(), plot_enrich_res()

Examples

```
## use `fisher.test` from the `stats` package.
data("reporter_score_res")
fisher_res <- KO_fisher(reporter_score_res)
```

KO_gsa *Perform gene set analysis*

Description

Perform gene set analysis

Usage

```
KO_gsa(
  reporter_res,
  method = "Two class unpaired",
  p.adjust.method = "BH",
  verbose = TRUE,
  perm = 1000,
  ...
)
```

Arguments

reporter_res	reporter_res
method	Problem type: "quantitative" for a continuous parameter; "Two class unpaired" ; "Survival" for censored survival outcome; "Multiclass" : more than 2 groups, coded 1,2,3...; "Two class paired" for paired outcomes, coded -1,1 (first pair), -2,2 (second pair), etc
p.adjust.method	"BH"

verbose	TRUE
perm	1000
...	additional parameters to GSA

Value

enrich_res object

See Also

Other common_enrich: KO_enrich(), KO_fisher(), KO_gsea(), KO_gsva(), KO_padog(), KO_safe(), KO_sea(), plot_enrich_res()

Examples

```
## use `GSA` from the `GSA` package.
if (requireNamespace("GSA")) {
  data("reporter_score_res")
  gsa_res <- KO_gsa(reporter_score_res, p.adjust.method = "none", perm = 200)
  plot(gsa_res)
}
```

KO_gsea *Perform gene set enrichment analysis*

Description

Perform gene set enrichment analysis

Usage

```
KO_gsea(
  ko_stat,
  weight = "logFC",
  add_mini = NULL,
  p.adjust.method = "BH",
  type = c("pathway", "module")[1],
  feature = "ko",
  modulelist = NULL,
  verbose = TRUE
)
```

Arguments

ko_stat	ko_stat dataframe from ko.test.
weight	the metric used for ranking, default: logFC
add_mini	add_mini when calculate the logFC. e.g (10+0.1)/(0+0.1), default 0.05*min(avg_abundance)
p.adjust.method	The method used for p-value adjustment (default: "BH").
type	"pathway" or "module" for default KOlist_file.
feature	one of "ko", "gene", "compound"
modulelist	NULL or customized modulelist dataframe, must contain "id","K_num","KOs","Description" columns. Take the 'KOlist' as example, use custom_modulelist.
verbose	logical

Value

DOSE object

See Also

Other common_enrich: KO_enrich(), KO_fisher(), KO_gsa(), KO_gsva(), KO_padog(), KO_safe(), KO_sea(), plot_enrich_res()

Examples

```
message("The following example require some time to run:")

## use `GSEA` from the `clusterProfiler` package.
if (requireNamespace("clusterProfiler")) {
  data("reporter_score_res")
  gsea_res <- KO_gsea(reporter_score_res, p.adjust.method = "none")
  enrichplot::gseaplot(gsea_res, geneSetID = data.frame(gsea_res)$ID[1])
  gsea_res_df <- as.enrich_res(gsea_res)
  plot(gsea_res_df)
}
```

KO_gsva *Perform Gene Set Variation Analysis*

Description

Perform Gene Set Variation Analysis

Usage

```
KO_gsva(
  reporter_res,
  verbose = TRUE,
  method = "wilcox.test",
  p.adjust.method = "BH",
  ...
)
```

Arguments

reporter_res	reporter_res
verbose	verbose
method	see ko.test
p.adjust.method	p.adjust.method
...	additional parameters to gsva

Value

enrich_res

See Also

Other common_enrich: KO_enrich(), KO_fisher(), KO_gsa(), KO_gsea(), KO_padog(), KO_safe(), KO_sea(), plot_enrich_res()

Examples

```
## use `gsva` from the `GSVA` package.
if (requireNamespace("GSVA")) {
  data("reporter_score_res")
  gsva_res <- KO_gsva(reporter_score_res, p.adjust.method = "none")
}
```

KO_htable *KO htable from 'KEGG'*

Description

KO htable from 'KEGG'

See Also

Other data: CPDlist, Compound_htable, GOlist, KOlist, Module_htable, Pathway_htable, hsa_kegg_pathway, mmu_kegg_pathway

KO_padog *Perform Pathway Analysis with Down-weighting of Overlapping Genes (PADOG)*

Description

Perform Pathway Analysis with Down-weighting of Overlapping Genes (PADOG)

Usage

```
KO_padog(
  reporter_res,
  verbose = TRUE,
  perm = 1000,
  p.adjust.method = "BH",
  ...
)
```

Arguments

reporter_res	The input reporter result.
verbose	If TRUE, print verbose messages. Default is TRUE.
perm	The number of permutations. Default is 1000.
p.adjust.method	Method for p-value adjustment. Default is "BH".
...	Additional parameters to be passed to padog function.

Value

A data frame containing PADOG results for KO enrichment.

A data frame with columns "ID," "Description," "K_num," "Exist_K_num," "p.value," and "p.adjust."

See Also

Other common_enrich: KO_enrich(), KO_fisher(), KO_gsa(), KO_gsea(), KO_gsva(), KO_safe(), KO_sea(), plot_enrich_res()

Examples

```
## use `PADOG` from the `PADOG` package.
if (requireNamespace("PADOG")) {
  data("reporter_score_res")
  padog_res <- KO_padog(reporter_score_res,
    verbose = TRUE,
    perm = 200, p.adjust.method = "none"
  )
```

```
}
```

KO_safe *Perform Significance Analysis of Function and Expression*

Description

Perform Significance Analysis of Function and Expression

Usage

```
KO_safe(
  reporter_res,
  verbose = TRUE,
  perm = 1000,
  C.matrix = NULL,
  p.adjust.method = "BH",
  ...
)
```

Arguments

reporter_res	The input reporter result.
verbose	If TRUE, print verbose messages. Default is TRUE.
perm	The number of permutations. Default is 1000.
C.matrix	The contrast matrix. Default is NULL, and it will be generated from the module list.
p.adjust.method	Method for p-value adjustment. Default is "BH".
...	Additional parameters to be passed to safe function.

Value

A data frame containing SAFE results for KO enrichment.

See Also

Other common_enrich: KO_enrich(), KO_fisher(), KO_gsa(), KO_gsea(), KO_gsva(), KO_padog(), KO_sea(), plot_enrich_res()

Examples

```
## use `safe` from the `safe` package.
if (requireNamespace("safe")) {
  data("reporter_score_res")
  safe_res <- KO_safe(reporter_score_res,
    verbose = TRUE,
    perm = 200, p.adjust.method = "none"
  )
}
```

KO_sea *Perform Simultaneous Enrichment Analysis*

Description

Perform Simultaneous Enrichment Analysis

Usage

```
KO_sea(reporter_res, verbose = TRUE, ...)
```

Arguments

reporter_res	The input reporter result.
verbose	If TRUE, print verbose messages. Default is TRUE.
...	Additional parameters to be passed to SEA function.

Value

enrich_res

See Also

Other common_enrich: KO_enrich(), KO_fisher(), KO_gsa(), KO_gsea(), KO_gsva(), KO_padog(), KO_safe(), plot_enrich_res()

Examples

```
## use `SEA` from the `rSEA` package.
if (requireNamespace("rSEA")) {
  data("reporter_score_res")
  sea_res <- KO_sea(reporter_score_res, verbose = TRUE)
}
```

load_CARDinfo *Load the CARDinfo (from CARD database)*

Description

Load the CARDinfo (from CARD database)

Usage

```
load_CARDinfo(verbose = TRUE)
```

Arguments

verbose	logical

Value

CARDinfo

load_GOlist *Load the GOlist (from 'GO' database)*

Description

Load the GOlist (from 'GO' database)

Load the GOinfo (from GO)

Usage

```
load_GOlist(verbose = TRUE)

load_GOinfo(verbose = TRUE)
```

Arguments

verbose	logical

Value

GOlist

GOinfo

load_htable *Load the specific table (from 'KEGG')*

Description

Load the specific table (from 'KEGG')

Load the KOlist (from 'KEGG')

Load the CPDlist (from 'KEGG')

Load the KO description (from 'KEGG')

Load the KO_htable (from 'KEGG')

Load the Pathway_htable (from 'KEGG')

Load the Module_htable (from 'KEGG')

Load the Compound_htable (from 'KEGG')

Load the pathway information for an organism (from 'KEGG')

Usage

```
load_htable(type, verbose = TRUE)

load_KOlist(verbose = TRUE)

load_CPDlist(verbose = TRUE)

load_KO_desc(verbose = TRUE)

load_KO_htable(verbose = TRUE)

load_Pathway_htable(verbose = TRUE)

load_Module_htable(verbose = TRUE)

load_Compound_htable(verbose = TRUE)

load_org_pathway(org = "hsa", verbose = TRUE)
```

Arguments

type	"ko", "module", "pathway", "compound" ...
verbose	logical
org	kegg organism, listed in https://www.genome.jp/kegg/catalog/org_list.html, default, "hsa"

Value

KO_htable

KOlist

CPDlist

KO description

KO_htable

Pathway_htable

Module_htable

Compound_htable

KOlist

Examples

```
Pathway_htable <- load_htable("pathway")
head(Pathway_htable)
```

`mmu_kegg_pathway` *pathway information for "mmu"*

Description

pathway information for "mmu"

See Also

Other data: `CPDlist`, `Compound_htable`, `GOlist`, `KO_htable`, `KOlist`, `Module_htable`, `Pathway_htable`, `hsa_kegg_pathway`

`modify_description` *Modify the pathway description before plotting*

Description

Modify the pathway description before plotting

Usage

```
modify_description(
  reporter_res,
  pattern = " - Homo sapiens (human)",
  replacement = ""
)
```

Arguments

reporter_res	reporter_res
pattern	str, like " - Homo sapiens (human)"
replacement	str, like ""

Value

reporter_res

Examples

```
data("reporter_score_res")
modify_description(reporter_score_res, pattern = " - Homo sapiens (human)")
```

Module_htable *Module htable from 'KEGG'*

Description

Module htable from 'KEGG'

See Also

Other data: CPDlist, Compound_htable, GOlist, KO_htable, KOlist, Pathway_htable, hsa_kegg_pathway, mmu_kegg_pathway

---

Pathway_htable *Pathway htable from 'KEGG'*

Description

Pathway htable from 'KEGG'

See Also

Other data: CPDlist, Compound_htable, GOlist, KO_htable, KOlist, Module_htable, hsa_kegg_pathway, mmu_kegg_pathway

plot.cm_res *Plot c_means result*

Description

Plot c_means result

Usage

```
## S3 method for class 'cm_res'
plot(
  x,
  filter_membership,
  mode = 1,
  show.clust.cent = TRUE,
  show_num = TRUE,
  ...
)
```

Arguments

x	a cm_res object
filter_membership	filter membership
mode	1~2
show.clust.cent	show cluster center?
show_num	show number of each cluster?
...	additional

Value

ggplot

plot_enrich_res *Plot enrich_res*

Description

Plot enrich_res

Plot enrich_res

Usage

```
plot_enrich_res(
  enrich_res,
  mode = 1,
  padj_threshold = 0.05,
  show_ID = FALSE,
  Pathway_description = TRUE,
  facet_level = FALSE,
  facet_anno = NULL,
  str_width = 50,
  facet_str_width = 15,
  ...
)

## S3 method for class 'enrich_res'
plot(
  x,
  mode = 1,
  padj_threshold = 0.05,
  show_ID = FALSE,
  Pathway_description = TRUE,
  facet_level = FALSE,
  facet_anno = NULL,
  str_width = 50,
  facet_str_width = 15,
  ...
)
```

Arguments

enrich_res	enrich_res object
mode	plot style: 1~2
padj_threshold	p.adjust threshold
show_ID	show pathway id
Pathway_description	show KO description rather than KO id.
facet_level	facet plot if the type is "pathway" or "module"
facet_anno	annotation table for facet, two columns, first is level summary, second is pathway id.
str_width	default: 50
facet_str_width	str width for facet label
...	add
x	enrich_res object

Value

ggplot

ggplot

See Also

Other common_enrich: KO_enrich(), KO_fisher(), KO_gsa(), KO_gsea(), KO_gsva(), KO_padog(), KO_safe(), KO_sea()

`plot_features_box` *Plot features boxplot*

Description

Plot features boxplot

Usage

```
plot_features_box(
  kodf,
  group = NULL,
  metadata = NULL,
  map_id = "map00780",
  select_ko = NULL,
  only_sig = FALSE,
  box_param = NULL,
  modulelist = NULL,
  KO_description = FALSE,
  str_width = 50
)
```

Arguments

kodf	KO_abundance table, rowname is ko id (e.g. K00001),colnames is samples. or result of 'get_reporter_score'
group	The compare group (two category) in your data, one column name of metadata when metadata exist or a vector whose length equal to columns number of kodf.
metadata	metadata
map_id	the pathway or module id
select_ko	select which ko
only_sig	only show the significant features
box_param	parameters pass to group_box
modulelist	NULL or customized modulelist dataframe, must contain "id","K_num","KOs","Description" columns. Take the 'KOlist' as example, use custom_modulelist.
KO_description	show KO description rather than KO id.
str_width	str_width to wrap

Value

ggplot

Examples

```
data("reporter_score_res")
plot_features_box(reporter_score_res,
  select_ko = c("K00059", "K00208", "K00647", "K00652", "K00833", "K01012"),
  box_param = list(p_value1 = FALSE, trend_line = TRUE)
)
plot_features_box(reporter_score_res,
  select_ko = "K00059", KO_description = TRUE,
  box_param = list(p_value1 = FALSE, trend_line = TRUE)
)
```

---

plot_features_distribution

plot the Z-score of features distribution

Description

plot the Z-score of features distribution

Usage

```
plot_features_distribution(
  reporter_res,
  map_id,
  text_size = 4,
  text_position = NULL,
  rug_length = 0.04
)
```

Arguments

reporter_res	result of 'reporter_score'
map_id	the pathway or module id
text_size	text_size=4
text_position	text_position, e.g. c(x=3,y=0.4)
rug_length	rug_length=0.04

Value

ggplot

Examples

```
data("reporter_score_res")
plot_features_distribution(reporter_score_res, map_id = c("map05230", "map03010"))
```

`plot_features_heatmap` *Plot features heatmap*

Description

Plot features heatmap

Usage

```
plot_features_heatmap(
  kodf,
  group = NULL,
  metadata = NULL,
  map_id = "map00780",
  select_ko = NULL,
  only_sig = FALSE,
  columns = NULL,
  modulelist = NULL,
  KO_description = FALSE,
  str_width = 50,
  heatmap_param = list()
)
```

Arguments

`kodf`	KO_abundance table, rowname is ko id (e.g. K00001),colnames is samples. or result of 'get_reporter_score'
`group`	The compare group (two category) in your data, one column name of metadata when metadata exist or a vector whose length equal to columns number of kodf.
`metadata`	metadata
`map_id`	the pathway or module id
`select_ko`	select which ko
`only_sig`	only show the significant KOs
`columns`	change columns
`modulelist`	NULL or customized modulelist dataframe, must contain "id","K_num","KOs","Description" columns. Take the 'KOlist' as example, use `custom_modulelist`.
`KO_description`	show KO description rather than KO id.
`str_width`	str_width to wrap
`heatmap_param`	parameters pass to `pheatmap`

Value

ggplot

Examples

```
if (requireNamespace("pheatmap")) {
  data("reporter_score_res")
  plot_features_heatmap(reporter_score_res, map_id = "map00780")
}
```

`plot_features_in_pathway` *Plot features trend in one pathway or module*

Description

Plot features trend in one pathway or module

Usage

```
plot_features_in_pathway(
  ko_stat,
  map_id = "map00780",
  modulelist = NULL,
  select_ko = NULL,
  box_color = reporter_color,
  show_number = TRUE,
  scale = FALSE,
  feature_type = "KOs",
 line_color = c(Depleted = "seagreen", Enriched = "orange", None = "grey", Significant =
    "red2")
)
```

Arguments

`ko_stat`	ko_stat result from `pvalue2zs` or result of ‘get_reporter_score‘
`map_id`	the pathway or module id
`modulelist`	NULL or customized modulelist dataframe, must contain "id","K_num","KOs","Description" columns. Take the ‘KOlist‘ as example, use `custom_modulelist`.
`select_ko`	select which ko
`box_color`	box and point color, default: c("#e31a1c","#1f78b4")
`show_number`	show the numbers.
`scale`	scale the data by row.
`feature_type`	show in the title ,default: KOs
`line_color`	line color, default: c("Depleted"="seagreen","Enriched"="orange","None"="grey")

Value

ggplot

Examples

```
data("reporter_score_res")
plot_features_in_pathway(ko_stat = reporter_score_res, map_id = "map00860")
```

`plot_features_network` *Plot features network*

Description

Plot features network

Usage

```
plot_features_network(
  ko_stat,
  map_id = "map00780",
  near_pathway = FALSE,
  modulelist = NULL,
 kos_color = c(Depleted = "seagreen", Enriched = "orange", None = "grey", Significant =
    "red2", Pathway = "#80b1d3"),
  pathway_label = TRUE,
  kos_label = TRUE,
  mark_module = FALSE,
  mark_color = NULL,
  return_net = FALSE,
  ...
)
```

Arguments

`ko_stat`	ko_stat result from `pvalue2zs` or result of 'get_reporter_score'
`map_id`	the pathway or module id
`near_pathway`	show the near_pathway if any features exist.
`modulelist`	NULL or customized modulelist dataframe, must contain "id","K_num","KOs","Description" columns. Take the 'KOlist' as example, use `custom_modulelist`.
`kos_color`	default, c("Depleted"="seagreen","Enriched"="orange","None"="grey","Significant"="red2")
`pathway_label`	show pathway_label?
`kos_label`	show kos_label?
`mark_module`	mark the modules?

mark_color	mark colors, default, c("Depleted"="seagreen","Enriched"="orange","None"="grey","Significant"="red2
return_net	return the network
...	additional arguments for c_net_plot

Value

network plot

Examples

```
if (requireNamespace("MetaNet")) {
  data("reporter_score_res")
  plot_features_network(reporter_score_res, map_id = "map05230")
  plot_features_network(reporter_score_res, map_id = "map00780", near_pathway = TRUE)
}
```

---

plot_htable *Plot htable levels*

Description

Plot htable levels

Usage

```
plot_htable(type = "ko", select = NULL, htable = NULL)
```

Arguments

type	"ko", "module", "pathway", "compound"
select	select ids
htable	custom a htable

Value

ggplot

Examples

```
data("KO_abundance_test")
plot_htable(select = rownames(KO_abundance))
```

plot_KEGG_map *plot_KEGG_map*

Description

plot_KEGG_map

Usage

```
plot_KEGG_map(
  ko_stat,
  map_id = "map00780",
  modulelist = NULL,
  type = "pathway",
  feature = "ko",
  color_var = "Z_score",
  save_dir,
  color = c("seagreen", "grey", "orange")
)
```

Arguments

ko_stat	ko_stat result from pvalue2zs or result of ‘get_reporter_score‘
map_id	the pathway or module id
modulelist	NULL or customized modulelist dataframe, must contain "id","K_num","KOs","Description" columns. Take the ‘KOlist‘ as example, use custom_modulelist.
type	"pathway" or "module" for default KOlist for microbiome, "CC", "MF", "BP", "ALL" for default GOlist for homo sapiens. And org in listed in ’https://www.genome.jp/kegg/catalog/org such as "hsa" (if your kodf is come from a specific organism, you should specify type here).
feature	one of "ko", "gene", "compound"
color_var	use which variable to color
save_dir	where to save the png files
color	color

Value

png files

References

https://zhuanlan.zhihu.com/p/357687076

Examples

```
message("The following example will download some files, run yourself:")

if (requireNamespace("pathview")) {
  output_dir <- tempdir()
  data("reporter_score_res")
  plot_KEGG_map(reporter_score_res$ko_stat,
    map_id = "map00780", type = "pathway",
    feature = "ko", color_var = "Z_score", save_dir = output_dir
  )
}
```

`plot_report` *Plot the reporter_res*

Description

Plot the reporter_res

Usage

```
plot_report(
  reporter_res,
  rs_threshold = 1.64,
  mode = 1,
  y_text_size = 13,
  str_width = 100,
  show_ID = FALSE,
  Pathway_description = TRUE,
  facet_level = FALSE,
  facet_anno = NULL,
  facet_str_width = 15
)
```

Arguments

`reporter_res`	result of ‘get_reporter_score‘ or ‘reporter_score‘
`rs_threshold`	plot threshold vector, default:1.64
`mode`	1~2 plot style.
`y_text_size`	y_text_size
`str_width`	str_width to wrap
`show_ID`	show pathway id
`Pathway_description`	show KO description rather than KO id.

facet_level	facet plot if the type is "pathway" or "module"
facet_anno	annotation table for facet, two columns, first is level summary, second is pathway id.
facet_str_width	str width for facet label

Value

ggplot

Examples

```
data("reporter_score_res")
plot_report(reporter_score_res, rs_threshold = c(2.5, -2.5), y_text_size = 10, str_width = 40)
```

---

plot_report_circle_packing

Plot the reporter_res as circle_packing

Description

Plot the reporter_res as circle_packing

Usage

```
plot_report_circle_packing(
  reporter_res,
  rs_threshold = 1.64,
  mode = 2,
  facet_anno = NULL,
  show_ID = FALSE,
  Pathway_description = TRUE,
  str_width = 10,
  show_level_name = "all",
  show_tip_label = TRUE
)
```

Arguments

reporter_res	result of 'get_reporter_score'
rs_threshold	plot threshold vector, default:1.64
mode	1~2 plot style.
facet_anno	annotation table for facet, more two columns, last is pathway name, last second is pathway id.
show_ID	show pathway id

Pathway_description
: show KO description rather than KO id.

str_width
: str_width to wrap

show_level_name
: show the level name?

show_tip_label
: show the tip label?

Value

ggplot

Examples

```
data("reporter_score_res")
if (requireNamespace("igraph") && requireNamespace("ggraph")) {
  plot_report_circle_packing(reporter_score_res, rs_threshold = c(2, -2), str_width = 40)
}
```

---

plot_significance *Plot the significance of pathway*

Description

Plot the significance of pathway

Usage

```
plot_significance(reporter_res, map_id)
```

Arguments

reporter_res
: result of ‘get_reporter_score‘ or ‘reporter_score‘

map_id
: the pathway or module id

Value

ggplot

Examples

```
data("reporter_score_res")
plot_significance(reporter_score_res, map_id = c("map05230", "map03010"))
```

print.reporter_score *Print reporter_score*

Description

Print reporter_score

Usage

```
## S3 method for class 'reporter_score'
print(x, ...)
```

Arguments

x	reporter_score
...	add

Value

No value

print.rs_by_cm *Print rs_by_cm*

Description

Print rs_by_cm

Usage

```
## S3 method for class 'rs_by_cm'
print(x, ...)
```

Arguments

x	rs_by_cm
...	add

Value

No value

pvalue2zs *Transfer p-value of KOs to Z-score*

Description

Transfer p-value of KOs to Z-score

Usage

```
pvalue2zs(
  ko_pvalue,
  mode = c("directed", "mixed")[1],
  p.adjust.method1 = "none"
)
```

Arguments

ko_pvalue	data.frame from ko.test
mode	'mixed' or 'directed' (default, only for two groups differential analysis or multi-groups correlation analysis.), see details in pvalue2zs.
p.adjust.method1	p.adjust.method for 'ko.test', see p.adjust

Details

'**mixed**' mode is the original reporter-score method from Patil, K. R. et al. PNAS 2005. In this mode, the reporter score is **undirected**, and the larger the reporter score, the more significant the enrichment, but it cannot indicate the up-and-down regulation information of the pathway! (Liu, L. et al. iMeta 2023.)

steps:

1. Use the Wilcoxon rank sum test to obtain the P value of the significance of each KO difference between the two groups (ie P_{koi}, i represents a certain KO);

2. Using an inverse normal distribution, convert the P value of each KO into a Z value (Z_{koi}), the formula:

$Z_{koi} = \theta^{-1}(1 - P_{koi})$

3. 'Upgrade' KO to pathway: Z_{koi}, calculate the Z value of the pathway, the formula:

$Z_{pathway} = \frac{1}{\sqrt{k}} \sum Z_{koi}$

where k means A total of k KOs were annotated to the corresponding pathway;

4. Evaluate the degree of significance: permutation (permutation) 1000 times, get the random distribution of $Z_{pathway}$, the formula:

$Z_{adjustedpathway} = (Z_{pathway} - \mu_k)/\sigma_k$

μ_k is The mean of the random distribution, σ_k is the standard deviation of the random distribution.

Instead, '**directed**' mode is a derived version of 'mixed', referenced from https://github.com/wangpeng407/ReporterSc

This approach is based on the same assumption of many differential analysis methods: the expression of most genes has no significant change.

steps:

1. Use the Wilcoxon rank sum test to obtain the P value of the significance of each KO difference between the two groups (ie P_{koi}, i represents a certain KO), and then divide the P value by 2, that is, the range of (0,1] becomes (0,0.5], $P_{koi} = P_{koi}/2$;

2. Using an inverse normal distribution, convert the P value of each KO into a Z value (Z_{koi}), the formula:

$Z_{koi} = \theta^{-1}(1 - P_{koi})$

since the above P value is less than 0.5, all Z values will be greater than 0;

3. Considering whether each KO is up-regulated or down-regulated, calculate $diff\_KO$,

$Z_{koi} = -Z_{koi} \quad (diff\_KO < 0)$,

so Z_{koi} is greater than 0 Up-regulation, Z_{koi} less than 0 is down-regulation;

4. 'Upgrade' KO to pathway: Z_{koi}, calculate the Z value of the pathway, the formula:

$Z_{pathway} = \frac{1}{\sqrt{k}} \sum Z_{koi}$

where k means A total of k KOs were annotated to the corresponding pathway;

5. Evaluate the degree of significance: permutation (permutation) 1000 times, get the random distribution of $Z_{pathway}$, the formula:

$Z_{adjustedpathway} = (Z_{pathway} - \mu_k)/\sigma_k$

μ_k is The mean of the random distribution, σ_k is the standard deviation of the random distribution.

The finally obtained $Z_{adjustedpathway}$ is the Reporter score value enriched for each pathway. In this mode, the Reporter score is directed, and a larger positive value represents a significant up-regulation enrichment, and a smaller negative values represent significant down-regulation enrichment.

However, the disadvantage of this mode is that when a pathway contains about the same number of significantly up-regulates KOs and significantly down-regulates KOs, the final absolute value of Reporter score may approach 0, becoming a pathway that has not been significantly enriched.

Value

ko_stat data.frame

References

1. Patil, K. R. & Nielsen, J. Uncovering transcriptional regulation of metabolism by using metabolic network topology. Proc Natl Acad Sci U S A 102, 2685–2689 (2005). 2. Liu, L., Zhu, R. & Wu, D. Misuse of reporter score in microbial enrichment analysis. iMeta n/a, e95. 3. https://github.com/wangpeng407/Reporte

See Also

Other GRSA: get_reporter_score(), ko.test(), reporter_score()

Examples

```
data("KO_abundance_test")
ko_pvalue <- ko.test(KO_abundance, "Group", metadata)
ko_stat <- pvalue2zs(ko_pvalue, mode = "directed")
```

`reporter_score` *One step to get the reporter score of your KO abundance table.*

Description

One step to get the reporter score of your KO abundance table.

Usage

```
reporter_score(
  kodf,
  group,
  metadata = NULL,
  method = "wilcox.test",
  pattern = NULL,
  p.adjust.method1 = "none",
  mode = c("directed", "mixed")[1],
  verbose = TRUE,
  feature = "ko",
  type = c("pathway", "module")[1],
  p.adjust.method2 = "BH",
  modulelist = NULL,
  threads = 1,
  perm = 4999,
  min_exist_KO = 3,
  max_exist_KO = 600
)
```

Arguments

`kodf`	KO_abundance table, rowname is ko id (e.g. K00001),colnames is samples.
`group`	The comparison groups (at least two categories) in your data, one column name of metadata when metadata exist or a vector whose length equal to columns number of kodf. And you can use factor levels to change order.
`metadata`	sample information data.frame contains group
`method`	the type of test. Default is 'wilcox.test'. Allowed values include: • `t.test` (parametric) and `wilcox.test` (non-parametric). Perform comparison between two groups of samples. If the grouping variable contains more than two levels, then a pairwise comparison is performed.

- anova (parametric) and kruskal.test (non-parametric). Perform one-way ANOVA test comparing multiple groups.
- 'pearson', 'kendall', or 'spearman' (correlation), see cor.

pattern — a named vector matching the group, e.g. c('G1'=1,'G2'=3,'G3'=2), use the correlation analysis with specific pattern to calculate p-value.

p.adjust.method1 — p.adjust.method for 'ko.test', see p.adjust

mode — 'mixed' or 'directed' (default, only for two groups differential analysis or multi-groups correlation analysis.), see details in pvalue2zs.

verbose — logical

feature — one of 'ko', 'gene', 'compound'

type — 'pathway' or 'module' for default KOlist for microbiome, 'CC', 'MF', 'BP', 'ALL' for default GOlist for homo sapiens. And org in listed in 'https://www.genome.jp/kegg/catalog/org_ such as 'hsa' (if your kodf is come from a specific organism, you should specify type here).

p.adjust.method2 — p.adjust.method for the correction of ReporterScore, see p.adjust

modulelist — NULL or customized modulelist dataframe, must contain 'id','K_num','KOs','Description' columns. Take the 'KOlist' as example, use custom_modulelist.

threads — default 1

perm — permutation number, default: 4999.

min_exist_KO — min exist KO number in a pathway (default, 3, when a pathway contains KOs less than 3, there will be no RS)

max_exist_KO — max exist KO number in a pathway (default, 600, when a pathway contains KOs more than 600, there will be no RS)

Value

reporter_score object:

kodf — your input KO_abundance table

ko_stat — ko statistics result contains p.value and z_score

reporter_s — the reporter score in each pathway

modulelist — default KOlist or customized modulelist dataframe

group — The comparison groups in your data

metadata — sample information dataframe contains group

for the 'reporter_s' in result, whose columns represent:

ID — pathway id

Description — pathway description

K_num — total number of KOs/genes in the pathway

Exist_K_num — number of KOs/genes in your inputdata that exist in the pathway

Significant_K_num	number of kos/genes in your inputdata that are significant in the pathway
Z_score	$Z_{pathway} = \frac{1}{\sqrt{k}} \sum Z_{koi}$
BG_Mean	Background mean, μ_k
BG_Sd	Background standard deviation, σ_k
ReporterScore	ReporterScore of the pathway, $ReporterScore = (Z_{pathway} - \mu_k)/\sigma_k$
p.value	p.value of the ReporterScore
p.adjust	adjusted p.value by p.adjust.method2

See Also

Other GRSA: get_reporter_score(), ko.test(), pvalue2zs()

Examples

```
message("The following example require some time to run:")

data("KO_abundance_test")
reporter_score_res <- reporter_score(KO_abundance, "Group", metadata,
  mode = "directed", perm = 499
)
head(reporter_score_res$reporter_s)
reporter_score_res2 <- reporter_score(KO_abundance, "Group2", metadata,
  mode = "mixed",
  method = "kruskal.test", p.adjust.method1 = "none", perm = 499
)
reporter_score_res3 <- reporter_score(KO_abundance, "Group2", metadata,
  mode = "directed",
  method = "pearson", pattern = c("G1" = 1, "G2" = 3, "G3" = 2), perm = 499
)
```

---

reporter_score_res *'reporter_score()' result from KO_abundance_test*

Description

'reporter_score()' result from KO_abundance_test

'reporter_score()' result from KO_abundance_test

Format

a list contain 7 elements.

kodf your input KO_abundance table

ko_stat ko statistics result contains p.value and z_score

reporter_s the reporter score in each pathway

modulelist default KOlist or customized modulelist dataframe

group The compare group (two category) in your data

metadata sample information dataframe contains group

See Also

Other test_data: KO_abundance, genedf

RSA_by_cm *Reporter score analysis after C-means clustering*

Description

Reporter score analysis after C-means clustering

Extract one cluster from rs_by_cm object

Plot c_means result

Usage

```
RSA_by_cm(
  kodf,
  group,
  metadata = NULL,
  k_num = NULL,
  filter_var = 0.7,
  verbose = TRUE,
  method = "pearson",
  ...
)

extract_cluster(rsa_cm_res, cluster = 1)

plot_c_means(
  rsa_cm_res,
  filter_membership,
  mode = 1,
  show.clust.cent = TRUE,
  show_num = TRUE,
  ...
)
```

Arguments

kodf	KO_abundance table, rowname is ko id (e.g. K00001),colnames is samples.
group	The comparison groups (at least two categories) in your data, one column name of metadata when metadata exist or a vector whose length equal to columns number of kodf. And you can use factor levels to change order.
metadata	sample information data.frame contains group
k_num	if NULL, perform the cm_test_k, else an integer
filter_var	see c_means
verbose	verbose
method	method from reporter_score
...	additional
rsa_cm_res	a cm_res object
cluster	integer
filter_membership	filter membership 0~1.
mode	1~2
show.clust.cent	show cluster center?
show_num	show number of each cluster?

Value

rs_by_cm

reporter_score object

ggplot

See Also

Other C_means: cm_test_k()

Examples

```
message("The following example require some time to run:")

if (requireNamespace("e1071") && requireNamespace("factoextra")) {
  data("KO_abundance_test")
  rsa_cm_res <- RSA_by_cm(KO_abundance, "Group2", metadata,
    k_num = 3,
    filter_var = 0.7, method = "pearson", perm = 199
  )
  extract_cluster(rsa_cm_res, cluster = 1)
}
```

update_CARDinfo *update CARDinfo from (from 'CARD' database)*

Description

update CARDinfo from (from 'CARD' database)

Usage

```
update_CARDinfo(download_dir = NULL, card_data = NULL)
```

Arguments

download_dir	download_dir
card_data	card_data from https://card.mcmaster.ca/download/0/broadstreet-v3.2.8.tar.bz2

Value

No value

update_GOlist *Update the GO2gene files (from 'GO' database)*

Description

Download links: http://geneontology.org/docs/download-ontology/ https://asa12138.github.io/FileList/GO

Usage

```
update_GOlist(download_dir = NULL, GO_file = NULL)

update_GOinfo(download_dir = NULL, obo_file = NULL)
```

Arguments

download_dir	download_dir
GO_file	GO_file
obo_file	obo_file from http://current.geneontology.org/ontology/go.obo

Value

No value

update_KEGG *Update files from 'KEGG'*

Description

Download links:

https://rest.kegg.jp/list/pathway https://rest.kegg.jp/link/pathway/ko https://rest.kegg.jp/link/pat
https://rest.kegg.jp/list/module https://rest.kegg.jp/link/module/ko https://rest.kegg.jp/link/module

Usage

```
update_KEGG(download_dir)

update_KO_file(download_dir, RDSfile = NULL)

update_htable(type, keg_file = NULL, download = FALSE, download_dir = NULL)

update_org_pathway(
  org = "hsa",
  RDS_file = NULL,
  download = TRUE,
  download_dir = NULL
)
```

Arguments

download_dir	where to save the .keg file?
RDSfile	saved KO_files.RDS file
type	"ko", "module", "pathway", "compound" ...
keg_file	path of a .keg file, such as ko00001.keg from https://www.genome.jp/kegg-bin/download_htext?htext=ko00001&format=htext.
download	save the .keg file?
org	kegg organism, listed in https://www.genome.jp/kegg/catalog/org_list.html, default, "hsa"
RDS_file	path of a org.RDS file if you saved before.

Value

No value

up_level_KO *Upgrade the KO level*

Description

Upgrade the KO level

Usage

```
up_level_KO(
  KO_abundance,
  level = "pathway",
  show_name = FALSE,
  modulelist = NULL,
  verbose = TRUE
)
```

Arguments

KO_abundance	KO_abundance
level	one of 'pathway', 'module', 'level1', 'level2', 'level3', 'module1', 'module2', 'module3'.
show_name	logical
modulelist	NULL or customized modulelist dataframe, must contain 'id','K_num','KOs','Description' columns. Take the 'KOlist' as example, use custom_modulelist.
verbose	logical

Value

data.frame

Examples

```
data("KO_abundance_test")
KO_level1 <- up_level_KO(KO_abundance, level = "level1", show_name = TRUE)
```

Index