

Package ‘clusterProfiler’

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Type Package

Title statistical analysis and visualization of functional profiles
for genes and gene clusters

Version 3.8.1

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Description This package implements methods to analyze and visualize
functional profiles (GO and KEGG) of gene and gene clusters.

Depends R (>= 3.4.0)

Imports AnnotationDbi, DOSE (>= 3.5.1), enrichplot (>= 0.99.7),
ggplot2, GO.db, GOSemSim, magrittr, methods, plyr, qvalue,
rvcheck, stats, tidyr, utils

Suggests AnnotationHub, GSEABase, KEGG.db, knitr, org.Hs.eg.db,
prettydoc, pathview, ReactomePA, testthat

Remotes GuangchuangYu/DOSE, GuangchuangYu/enrichplot

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0

URL <https://guangchuangyu.github.io/software/clusterProfiler>

BugReports <https://github.com/GuangchuangYu/clusterProfiler/issues>

biocViews Annotation, Clustering, GeneSetEnrichment, GO, KEGG,
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Giovanni Dall'Olio [ctb] (formula interface of compareCluster)

R topics documented:

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clusterProfiler-package

statistical analysis and visualization of functional profiles for genes and gene clusters The package implements methods to analyze and visualize functional profiles of gene and gene clusters.

Description

statistical analysis and visualization of functional profiles for genes and gene clusters The package implements methods to analyze and visualize functional profiles of gene and gene clusters.

bitr

*bitr***Description**

Biological Id TRanslator

Usage

```
bitr(geneID, fromType, toType, OrgDb, drop = TRUE)
```

Arguments

| | |
|----------|----------------|
| geneID | input gene id |
| fromType | input id type |
| toType | output id type |
| OrgDb | annotation db |
| drop | drop NA or not |

Value

data.frame

Author(s)

Guangchuang Yu

bitr_kegg

*bitr_kegg***Description**

convert biological ID using KEGG API

Usage

```
bitr_kegg(geneID, fromType, toType, organism, drop = TRUE)
```

Arguments

| | |
|----------|---|
| geneID | input gene id |
| fromType | input id type |
| toType | output id type |
| organism | supported organism, can be search using search_kegg_organism function |
| drop | drop NA or not |

Value

data.frame

Author(s)

Guangchuang Yu

`browseKEGG`*browseKEGG*

Description

open KEGG pathway with web browser

Usage`browseKEGG(x, pathID)`**Arguments**

| | |
|---------------------|---|
| <code>x</code> | an instance of <code>enrichResult</code> or <code>gseaResult</code> |
| <code>pathID</code> | pathway ID |

Value

url

Author(s)

Guangchuang Yu

`buildGOMap`*buildGOMap*

Description

building GO mapping files

Usage`buildGOMap(gomap)`**Arguments**

| | |
|--------------------|---|
| <code>gomap</code> | data.frame with two columns of GO and gene ID |
|--------------------|---|

Details

provided by a data.frame of GO (column 1) and gene (column 2) direct annotation this function will building gene to GO and GO to gene mapping, with directly and indirectly (ancestor GO term) annotation.

Value

data.frame, GO annotation with indirect annotation

Author(s)

Yu Guangchuang

compareCluster *Compare gene clusters functional profile*

Description

Given a list of gene set, this function will compute profiles of each gene cluster.

Usage

```
compareCluster(geneClusters, fun = "enrichGO", data = "", ...)
```

Arguments

| | |
|--------------|---|
| geneClusters | a list of entrez gene id. Alternatively, a formula of type Entrez~group |
| fun | One of "groupGO", "enrichGO", "enrichKEGG", "enrichDO" or "enrichPathway". |
| data | if geneClusters is a formula, the data from which the clusters must be extracted. |
| ... | Other arguments. |

Value

A clusterProfResult instance.

Author(s)

Guangchuang Yu <https://guangchuangyu.github.io>

See Also

[compareClusterResult-class](#), [groupGO](#) [enrichGO](#)

Examples

```
## Not run:
data(gcSample)
xx <- compareCluster(gcSample, fun="enrichKEGG",
                     organism="hsa", pvalueCutoff=0.05)
as.data.frame(xx)
# plot(xx, type="dot", caption="KEGG Enrichment Comparison")

## formula interface
mydf <- data.frame(Entrez=c('1', '100', '1000', '100101467',
                           '100127206', '100128071'),
                  group = c('A', 'A', 'A', 'B', 'B', 'B'),
                  othergroup = c('good', 'good', 'bad', 'bad', 'good', 'bad'))
```

```
xx.formula <- compareCluster(Entrez~group, data=mydf,
                             fun='groupGO', OrgDb='org.Hs.eg.db')
as.data.frame(xx.formula)

## formula interface with more than one grouping variable
xx.formula.twogroups <- compareCluster(Entrez~group+othergroup, data=mydf,
                                       fun='groupGO', OrgDb='org.Hs.eg.db')
as.data.frame(xx.formula.twogroups)

## End(Not run)
```

compareClusterResult-class

Class "compareClusterResult" This class represents the comparison result of gene clusters by GO categories at specific level or GO enrichment analysis.

Description

Class "compareClusterResult" This class represents the comparison result of gene clusters by GO categories at specific level or GO enrichment analysis.

Slots

compareClusterResult cluster comparing result
 geneClusters a list of genes
 fun one of groupGO, enrichGO and enrichKEGG
 .call function call

Author(s)

Guangchuang Yu <https://guangchuangyu.github.io>

See Also

[groupGOResult](#) [enrichResult](#) [compareCluster](#)

DataSet

Datasets gcSample contains a sample of gene clusters.

Description

Datasets gcSample contains a sample of gene clusters.
 Datasets kegg_species contains kegg species information

dotplot,compareClusterResult-method
dotplot

Description

dot plot method

Usage

```
## S4 method for signature 'compareClusterResult'
dotplot(object, x = ~Cluster,
        color = "p.adjust", showCategory = 5, split = NULL, font.size = 12,
        title = "", by = "geneRatio", includeAll = TRUE)
```

Arguments

| | |
|--------------|---------------------------------------|
| object | compareClusterResult object |
| x | x variable |
| color | one of pvalue or p.adjust |
| showCategory | category numbers |
| split | ONTOLOGY or NULL |
| font.size | font size |
| title | figure title |
| by | one of geneRatio, Percentage or count |
| includeAll | logical |

download_KEGG *download_KEGG*

Description

download the latest version of KEGG pathway/module

Usage

```
download_KEGG(species, keggType = "KEGG", keyType = "kegg")
```

Arguments

| | |
|----------|---|
| species | species |
| keggType | one of 'KEGG' or 'MKEGG' |
| keyType | supported keyType, see <code>bitr_kegg</code> |

Value

list

Author(s)

Guangchuang Yu

`dropGO`*dropGO*

Description

drop GO term of specific level or specific terms (mostly too general).

Usage`dropGO(x, level = NULL, term = NULL)`**Arguments**`x` an instance of 'enrichResult' or 'compareClusterResult'`level` GO level`term` GO term**Value**

modified version of x

Author(s)

Guangchuang Yu

`enrichDAVID`*enrichDAVID*

Description

enrichment analysis by DAVID

Usage`enrichDAVID(gene, idType = "ENTREZ_GENE_ID", universe, minGSSize = 10,
maxGSSize = 500, annotation = "GOTERM_BP_FAT", pvalueCutoff = 0.05,
pAdjustMethod = "BH", qvalueCutoff = 0.2, species = NA, david.user)`

Arguments

| | |
|---------------|---|
| gene | input gene |
| idType | id type |
| universe | background genes |
| minGSSize | minimal size of genes annotated for testing |
| maxGSSize | maximal size of genes annotated for testing |
| annotation | dauid annotation |
| pvalueCutoff | pvalueCutoff |
| pAdjustMethod | one of "BH" and "bonferroni" |
| qvalueCutoff | qvalutCutoff |
| species | species |
| dauid.user | dauid user |

Value

A enrichResult instance

Author(s)

Guangchuang Yu

enricher

enricher

Description

A universal enrichment analyzer

Usage

```
enricher(gene, pvalueCutoff = 0.05, pAdjustMethod = "BH", universe,
  minGSSize = 10, maxGSSize = 500, qvalueCutoff = 0.2, TERM2GENE,
  TERM2NAME = NA)
```

Arguments

| | |
|---------------|--|
| gene | a vector of gene id |
| pvalueCutoff | pvalue cutoff |
| pAdjustMethod | one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none" |
| universe | background genes |
| minGSSize | minimal size of genes annotated for testing |
| maxGSSize | maximal size of genes annotated for testing |
| qvalueCutoff | qvalue cutoff |
| TERM2GENE | user input annotation of TERM TO GENE mapping, a data.frame of 2 column with term and gene |
| TERM2NAME | user input of TERM TO NAME mapping, a data.frame of 2 column with term and name |

Value

A enrichResult instance

Author(s)

Guangchuang Yu

enrichGO

GO Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment GO categories after FDR control.

Description

GO Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment GO categories after FDR control.

Usage

```
enrichGO(gene, OrgDb, keyType = "ENTREZID", ont = "MF",
         pvalueCutoff = 0.05, pAdjustMethod = "BH", universe, qvalueCutoff = 0.2,
         minGSSize = 10, maxGSSize = 500, readable = FALSE, pool = FALSE)
```

Arguments

| | |
|---------------|--|
| gene | a vector of entrez gene id. |
| OrgDb | OrgDb |
| keyType | keytype of input gene |
| ont | One of "MF", "BP", and "CC" subontologies. |
| pvalueCutoff | Cutoff value of pvalue. |
| pAdjustMethod | one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none" |
| universe | background genes |
| qvalueCutoff | qvalue cutoff |
| minGSSize | minimal size of genes annotated by Ontology term for testing. |
| maxGSSize | maximal size of genes annotated for testing |
| readable | whether mapping gene ID to gene Name |
| pool | If ont='ALL', whether pool 3 GO sub-ontologies |

Value

An enrichResult instance.

Author(s)

Guangchuang Yu <https://guangchuangyu.github.io>

See Also

[enrichResult-class](#), [compareCluster](#)

Examples

```
## Not run:
  data(geneList, package = "DOSE")
  de <- names(geneList)[1:100]
  yy <- enrichGO(de, 'org.Hs.eg.db', ont="BP", pvalueCutoff=0.01)
  head(yy)

## End(Not run)
```

| | |
|------------|--|
| enrichKEGG | <i>KEGG Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment KEGG categories with FDR control.</i> |
|------------|--|

Description

KEGG Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment KEGG categories with FDR control.

Usage

```
enrichKEGG(gene, organism = "hsa", keyType = "kegg", pvalueCutoff = 0.05,
  pAdjustMethod = "BH", universe, minGSSize = 10, maxGSSize = 500,
  qvalueCutoff = 0.2, use_internal_data = FALSE)
```

Arguments

| | |
|-------------------|--|
| gene | a vector of entrez gene id. |
| organism | supported organism listed in ' http://www.genome.jp/kegg/catalog/org_list.html ' |
| keyType | one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot' |
| pvalueCutoff | Cutoff value of pvalue. |
| pAdjustMethod | one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none" |
| universe | background genes |
| minGSSize | minimal size of genes annotated by Ontology term for testing. |
| maxGSSize | maximal size of genes annotated for testing |
| qvalueCutoff | qvalue cutoff |
| use_internal_data | logical, use KEGG.db or latest online KEGG data |

Value

A enrichResult instance.

Author(s)

Guangchuang Yu <http://ygc.name>

See Also

[enrichResult-class](#), [compareCluster](#)

Examples

```
data(geneList, package='DOSE')
de <- names(geneList)[1:100]
yy <- enrichKEGG(de, pvalueCutoff=0.01)
head(yy)
```

| | |
|-------------|--|
| enrichMKEGG | <i>KEGG Module Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment KEGG Module categories with FDR control.</i> |
|-------------|--|

Description

KEGG Module Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment KEGG Module categories with FDR control.

Usage

```
enrichMKEGG(gene, organism = "hsa", keyType = "kegg", pvalueCutoff = 0.05,
  pAdjustMethod = "BH", universe, minGSSize = 10, maxGSSize = 500,
  qvalueCutoff = 0.2)
```

Arguments

| | |
|---------------|--|
| gene | a vector of entrez gene id. |
| organism | supported organism listed in ' http://www.genome.jp/kegg/catalog/org_list.html ' |
| keyType | one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot' |
| pvalueCutoff | Cutoff value of pvalue. |
| pAdjustMethod | one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none" |
| universe | background genes |
| minGSSize | minimal size of genes annotated by Ontology term for testing. |
| maxGSSize | maximal size of genes annotated for testing |
| qvalueCutoff | qvalue cutoff |

Value

A `enrichResult` instance.

```
fortify.compareClusterResult
      fortify
```

Description

convert compareClusterResult to a data.frame that ready for plot

Usage

```
## S3 method for class 'compareClusterResult'
fortify(model, data, showCategory = 5,
        by = "geneRatio", split = NULL, includeAll = TRUE)
```

Arguments

| | |
|--------------|---------------------------------------|
| model | compareClusterResult object |
| data | not use here |
| showCategory | category numbers |
| by | one of geneRatio, Percentage or count |
| split | ONTOLOGY or NULL |
| includeAll | logical |

Value

data.frame

Author(s)

Guangchuang Yu

```
getGOLevel          get GOIDs at a specific level
```

Description

query GOIDs at a specific level.

Usage

```
getGOLevel(ont, level)
```

Arguments

| | |
|-------|----------|
| ont | Ontology |
| level | GO level |

Value

a vector of GOIDs

Author(s)

Guangchuang Yu <http://guangchuangyu.github.io>

| | |
|---------------|----------------------|
| Gff2GeneTable | <i>Gff2GeneTable</i> |
|---------------|----------------------|

Description

read GFF file and build gene information table

Usage

```
Gff2GeneTable(gffFile, compress = TRUE)
```

Arguments

| | |
|----------|----------------------|
| gffFile | GFF file |
| compress | compress file or not |

Details

given a GFF file, this function extracts information from it and save it in working directory

Value

file save.

Author(s)

Yu Guangchuang

| | |
|--------|---------------|
| go2ont | <i>go2ont</i> |
|--------|---------------|

Description

convert goid to ontology (BP, CC, MF)

Usage

```
go2ont(goid)
```

Arguments

| | |
|------|--------------------|
| goid | a vector of GO IDs |
|------|--------------------|

Value

data.frame

Author(s)

Guangchuang Yu

go2term

go2term

Description

convert goid to descriptive term

Usage

```
go2term(goid)
```

Arguments

goid a vector of GO IDs

Value

data.frame

Author(s)

Guangchuang Yu

gofilter

gofilter

Description

filter GO enriched result at specific level

Usage

```
gofilter(x, level = 4)
```

Arguments

x output from enrichGO or compareCluster
level GO level

Value

updated object

Author(s)

Guangchuang Yu

| | |
|---------|--|
| groupGO | <i>Functional Profile of a gene set at specific GO level. Given a vector of genes, this function will return the GO profile at a specific level.</i> |
|---------|--|

Description

Functional Profile of a gene set at specific GO level. Given a vector of genes, this function will return the GO profile at a specific level.

Usage

```
groupGO(gene, OrgDb, keyType = "ENTREZID", ont = "CC", level = 2,  
        readable = FALSE)
```

Arguments

| | |
|----------|---|
| gene | a vector of entrez gene id. |
| OrgDb | OrgDb |
| keyType | key type of input gene |
| ont | One of "MF", "BP", and "CC" subontologies. |
| level | Specific GO Level. |
| readable | if readable is TRUE, the gene IDs will mapping to gene symbols. |

Value

A groupGOResult instance.

Author(s)

Guangchuang Yu <http://ygc.name>

See Also

[groupGOResult-class](#), [compareCluster](#)

Examples

```
data(gcSample)  
yy <- groupGO(gcSample[[1]], 'org.Hs.eg.db', ont="BP", level=2)  
head(summary(yy))  
#plot(yy)
```

groupGOResult-class *Class "groupGOResult" This class represents the result of functional Profiles of a set of gene at specific GO level.*

Description

Class "groupGOResult" This class represents the result of functional Profiles of a set of gene at specific GO level.

Slots

result GO classification result
 ontology Ontology
 level GO level
 organism one of "human", "mouse" and "yeast"
 gene Gene IDs
 readable logical flag of gene ID in symbol or not.

Author(s)

Guangchuang Yu <https://guangchuangyu.github.io>

See Also

[compareClusterResult](#) [compareCluster](#) [groupGO](#)

GSEA

GSEA

Description

a universal gene set enrichment analysis tools

Usage

```
GSEA(geneList, exponent = 1, nPerm = 1000, minGSSize = 10,
      maxGSSize = 500, pvalueCutoff = 0.05, pAdjustMethod = "BH", TERM2GENE,
      TERM2NAME = NA, verbose = TRUE, seed = FALSE, by = "fgsea")
```

Arguments

| | |
|--------------|---|
| geneList | order ranked geneList |
| exponent | weight of each step |
| nPerm | number of permutations |
| minGSSize | minimal size of each geneSet for analyzing |
| maxGSSize | maximal size of genes annotated for testing |
| pvalueCutoff | pvalue cutoff |

| | |
|---------------|--|
| pAdjustMethod | p value adjustment method |
| TERM2GENE | user input annotation of TERM TO GENE mapping, a data.frame of 2 column with term and gene |
| TERM2NAME | user input of TERM TO NAME mapping, a data.frame of 2 column with term and name |
| verbose | logical |
| seed | logical |
| by | one of 'fgsea' or 'DOSE' |

Value

gseaResult object

Author(s)

Guangchuang Yu

| | |
|-------|--------------|
| gseGO | <i>gseGO</i> |
|-------|--------------|

Description

Gene Set Enrichment Analysis of Gene Ontology

Usage

```
gseGO(geneList, ont = "BP", OrgDb, keyType = "ENTREZID", exponent = 1,
      nPerm = 1000, minGSSize = 10, maxGSSize = 500, pvalueCutoff = 0.05,
      pAdjustMethod = "BH", verbose = TRUE, seed = FALSE, by = "fgsea")
```

Arguments

| | |
|---------------|---|
| geneList | order ranked geneList |
| ont | one of "BP", "MF", "CC" or "GO" |
| OrgDb | OrgDb |
| keyType | keytype of gene |
| exponent | weight of each step |
| nPerm | permutation numbers |
| minGSSize | minimal size of each geneSet for analyzing |
| maxGSSize | maximal size of genes annotated for testing |
| pvalueCutoff | pvalue Cutoff |
| pAdjustMethod | pvalue adjustment method |
| verbose | print message or not |
| seed | logical |
| by | one of 'fgsea' or 'DOSE' |

Value

gseaResult object

Author(s)

Yu Guangchuang

gseKEGG

*gseKEGG***Description**

Gene Set Enrichment Analysis of KEGG

Usage

```
gseKEGG(geneList, organism = "hsa", keyType = "kegg", exponent = 1,
        nPerm = 1000, minGSSize = 10, maxGSSize = 500, pvalueCutoff = 0.05,
        pAdjustMethod = "BH", verbose = TRUE, use_internal_data = FALSE,
        seed = FALSE, by = "fgsea")
```

Arguments

| | |
|-------------------|--|
| geneList | order ranked geneList |
| organism | supported organism listed in ' http://www.genome.jp/kegg/catalog/org_list.html ' |
| keyType | one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot' |
| exponent | weight of each step |
| nPerm | permutation numbers |
| minGSSize | minimal size of each geneSet for analyzing |
| maxGSSize | maximal size of genes annotated for testing |
| pvalueCutoff | pvalue Cutoff |
| pAdjustMethod | pvalue adjustment method |
| verbose | print message or not |
| use_internal_data | logical, use KEGG.db or latest online KEGG data |
| seed | logical |
| by | one of 'fgsea' or 'DOSE' |

Value

gseaResult object

Author(s)

Yu Guangchuang

gseMKEGG

*gseMKEGG***Description**

Gene Set Enrichment Analysis of KEGG Module

Usage

```
gseMKEGG(geneList, organism = "hsa", keyType = "kegg", exponent = 1,
         nPerm = 1000, minGSSize = 10, maxGSSize = 500, pvalueCutoff = 0.05,
         pAdjustMethod = "BH", verbose = TRUE, seed = FALSE, by = "fgsea")
```

Arguments

| | |
|---------------|--|
| geneList | order ranked geneList |
| organism | supported organism listed in ' http://www.genome.jp/kegg/catalog/org_list.html ' |
| keyType | one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot' |
| exponent | weight of each step |
| nPerm | permutation numbers |
| minGSSize | minimal size of each geneSet for analyzing |
| maxGSSize | maximal size of genes annotated for testing |
| pvalueCutoff | pvalue Cutoff |
| pAdjustMethod | pvalue adjustment method |
| verbose | print message or not |
| seed | logical |
| by | one of 'fgsea' or 'DOSE' |

Value

gseaResult object

Author(s)

Yu Guangchuang

| | |
|--------|---------------|
| idType | <i>idType</i> |
|--------|---------------|

Description

list ID types supported by annoDb

Usage

```
idType(OrgDb = "org.Hs.eg.db")
```

Arguments

OrgDb annotation db

Value

character vector

Author(s)

Guangchuang Yu

| | |
|-----------------|------------------------|
| KEGG_path2extid | <i>KEGG_path2extid</i> |
|-----------------|------------------------|

Description

query all genes in a KEGG pathway or module

Usage

```
KEGG_path2extid(keggID, species = sub("\\d+$", "", keggID),
  keggType = "Path", keyType = "kegg")
```

Arguments

keggID KEGG ID, path or module ID
 species species
 keggType one of 'Path' or 'Module'
 keyType KEGG gene type, one of "ncbi-proteinid", "ncbi-geneid", "uniprot", or "kegg"

Value

extid vector

Author(s)

guangchuang yu

| | |
|---------|----------------|
| ko2name | <i>ko2name</i> |
|---------|----------------|

Description

convert ko ID to descriptive name

Usage

```
ko2name(ko)
```

Arguments

ko ko ID

Value

data.frame

Author(s)

guangchuang yu

| | |
|--------------|---------------------|
| merge_result | <i>merge_result</i> |
|--------------|---------------------|

Description

merge a list of enrichResult objects to compareClusterResult

Usage

```
merge_result(enrichResultList)
```

Arguments

enrichResultList
 a list of enrichResult objects

Value

a compareClusterResult instance

Author(s)

Guangchuang Yu

| | |
|-------------|--------------------|
| plotGOgraph | <i>plotGOgraph</i> |
|-------------|--------------------|

Description

plot GO graph

Usage

```
plotGOgraph(x, firstSigNodes = 10, useInfo = "all", sigForAll = TRUE,
            useFullNames = TRUE, ...)
```

Arguments

| | |
|---------------|--|
| x | output of enrichGO or gseGO |
| firstSigNodes | number of significant nodes (rectangle nodes in the graph) |
| useInfo | additional info |
| sigForAll | if TRUE the score/p-value of all nodes in the DAG is shown, otherwise only score will be shown |
| useFullNames | logical |
| ... | additional parameter of showSigOfNodes, please refer to topGO |

Value

GO DAG graph

Author(s)

Guangchuang Yu

See Also

[showSigOfNodes](#)

| | |
|-------------------------|--------------------------------|
| plotting.clusterProfile | <i>plotting-clusterProfile</i> |
|-------------------------|--------------------------------|

Description

Internal plot function for plotting compareClusterResult

Usage

```
plotting.clusterProfile(clProf.reshape.df, x = ~Cluster, type = "dot",
                        colorBy = "p.adjust", by = "geneRatio", title = "", font.size = 12)
```

Arguments

| | |
|--------------------------------|-------------------------------------|
| <code>clProf.reshape.df</code> | data frame of compareCluster result |
| <code>x</code> | x variable |
| <code>type</code> | one of dot and bar |
| <code>colorBy</code> | one of pvalue or p.adjust |
| <code>by</code> | one of percentage and count |
| <code>title</code> | graph title |
| <code>font.size</code> | graph font size |

Value

ggplot object

Author(s)

Guangchuang Yu <https://guangchuangyu.github.io>

read.gmt

read.gmt

Description

parse gmt file to a data.frame

Usage

```
read.gmt(gmtfile)
```

Arguments

| | |
|----------------------|----------|
| <code>gmtfile</code> | gmt file |
|----------------------|----------|

Value

data.frame

Author(s)

Guangchuang Yu

search_kegg_organism *search_kegg_organism*

Description

search kegg organism, listed in http://www.genome.jp/kegg/catalog/org_list.html

Usage

```
search_kegg_organism(str, by = "scientific_name", ignore.case = FALSE)
```

Arguments

| | |
|-------------|---|
| str | string |
| by | one of 'kegg.code', 'scientific_name' and 'common_name' |
| ignore.case | TRUE or FALSE |

Value

data.frame

Author(s)

Guangchuang Yu

simplify *simplify method*

Description

simplify output from enrichGO by removing redundancy of enriched GO terms
simplify output from compareCluster by removing redundancy of enriched GO terms

Usage

```
## S4 method for signature 'enrichResult'
simplify(x, cutoff = 0.7, by = "p.adjust",
         select_fun = min, measure = "Wang", semData = NULL)

## S4 method for signature 'compareClusterResult'
simplify(x, cutoff = 0.7, by = "p.adjust",
         select_fun = min, measure = "Wang", semData = NULL)
```

Arguments

| | |
|------------|--|
| x | output of enrichGO |
| cutoff | similarity cutoff |
| by | feature to select representative term, selected by 'select_fun' function |
| select_fun | function to select feature passed by 'by' parameter |
| measure | method to measure similarity |
| semData | GOSemSimDATA object |

Value

updated enrichResult object
 updated compareClusterResult object

Author(s)

Guangchuang Yu
 Guangchuang Yu

References

issue #28 <https://github.com/GuangchuangYu/clusterProfiler/issues/28>

| | |
|-------------|--------------------|
| uniprot_get | <i>uniprot_get</i> |
|-------------|--------------------|

Description

retrieves annotation data from uniprot

Usage

```
uniprot_get(taxID)
```

Arguments

taxID taxonomy ID

Value

gene table data frame

Author(s)

guangchuang yu

| | |
|----------|---|
| viewKEGG | <i>viewKEGG function is for visualize KEGG pathways works with enrichResult object to visualize enriched KEGG pathway</i> |
|----------|---|

Description

viewKEGG function is for visualize KEGG pathways works with enrichResult object to visualize enriched KEGG pathway

Usage

```
viewKEGG(obj, pathwayID, foldChange, color.low = "green",
  color.high = "red", kegg.native = TRUE, out.suffix = "clusterProfiler")
```

Arguments

| | |
|-------------|--------------------------------|
| obj | enrichResult object |
| pathwayID | pathway ID or index |
| foldChange | fold change values |
| color.low | color of low foldChange genes |
| color.high | color of high foldChange genes |
| kegg.native | logical |
| out.suffix | suffix of output file |

References

Luo et al. (2013) Pathview: an R/Bioconductor package for pathway-based data integration and visualization. *Bioinformatics* (Oxford, England), 29:14 1830–1831, 2013. ISSN 1367-4803 <http://bioinformatics.oxfordjournals.org/content/abstract/29/14/1830.abstract> PMID: 23740750

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