Package 'BioEnricher'

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Type Package

Title Integrate analysis and visualization for bioinformatic enrichment analyzer

Version 0.1.0

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Description The primary strength of BioEnricher lies in addressing two issues: firstly,
it facilitates the seamless integration for enrichment analysis, encompassing diverse
functionalities such as GO, KEGG, WikiPathways, Reactome, MsigDB, Disease Ontology,
Cancer Gene Network, DisGeNET, CellMarker, and CMAP (drugs); secondly, it encapsulates
advanced visualization functions, streamlining the process for faster and more convenient
data presentation.

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Encoding UTF-8

ByteCompile true

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

Imports clusterProfiler,
DOSE,
dplyr,
enrichplot,
ggplot2,
HGNChelper,
Hmisc,
httr,
jsonlite,
magrittr,
msigdbr,
openssl,
pathview,
png,
purrr,
ReactomePA,
stats,
vroom

R topics documented:

CMAPfromDSEATM   *A dataframe including drugs and their related genes*

Description

A dataframe including drugs and their related genes

Usage

```
CMAPfromDSEATM
```

Format

A dataframe with four columns from DSEATM

---

cols_brown_green *A vector of colors*

Description

A vector of colors

Usage

```
cols_brown_green
```

Format

A vector with 11 types of colors.

---

listEnrichMethod *List of enrichment methods*

Description

List of enrichment methods, including GO, KEGG, MKEGG, WikiPathways, Reactome, MsigDB, DO, CGN, DisGeNET, CellMarker, and CMAP.

Usage

```
listEnrichMethod()
```

Author(s)

Zaoqu Liu; E-mail: liuzaoqu@163.com

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lzq_getEF *Get enrichment factor from enrichResult*

Description

Get enrichment factor from enrichResult (clusterProfiler).

Usage

```
lzq_getEF(res)
```

Arguments

res   enrichResult from clusterProfiler.

Value

A new result with enrichment factor.

Author(s)

Zaoqu Liu; E-mail: liuzaoqu@163.com

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lzq_getGR_BR   *Get numeric GeneRatio and BgRatio from enrichResult*

Description

Get numeric GeneRatio and BgRatio from enrichResult (clusterProfiler).

Usage

```
lzq_getGR_BR(res)
```

Arguments

res   enrichResult from clusterProfiler.

Value

A new result with numeric GeneRatio and BgRatio.

Author(s)

Zaoqu Liu; E-mail: liuzaoqu@163.com

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lzq_GSEA   *Gene set enrichment analysis*

Description

Perform gene set enrichment analysis included GO, KEGG, WikiPathways, Reactome, MsigDB, Disease Ontoloty, Cancer Gene Network, DisGeNET, CellMarker, and CMAP.

Usage

```
lzq_GSEA(
  genes,
  gene.type = "SYMBOL",
  enrich.type,
  OrgDb = "org.Hs.eg.db",
  GO.ont = "BP",
  GO.simplify = T,
  KEGG.organism = "hsa",
  KEGG.use.internal.data = F,
  WikiPathways.organism = "Homo sapiens",
  Reactome.organism = "human",
  MsigDB.organism = "Homo sapiens",
  MsigDB.category = "H",
```

```
    CMAP.min.Geneset.Size = 3,
    pvalue.cutoff = 0.05,
    padjust.method = "BH",
    min.Geneset.Size = 10,
    max.Geneset.Size = 1000
)
```

Arguments

`genes`	An order ranked geneList.
`gene.type`	Keytype of input gene.
`enrich.type`	Select an enrichment method. One of GO, KEGG, MKEGG, WikiPathways, Reactome, MsigDB, DO, CGN, DisGeNET, CellMarker, and CMAP. WikiPathways can be replaced by WP, Reactome can be replaced by RP, and CellMarker can be replaced by CM.
`OrgDb`	OrgDb object or OrgDb name.
`GO.ont`	GO parameter. One of "BP", "MF", and "CC" subontologies, or "ALL" for all three.
`GO.simplify`	GO parameter. Whether to remove redundancy of enriched GO terms.
`KEGG.organism`	KEGG parameter. Supported organism listed in 'https://www.genome.jp/kegg/catalog/org_list.html'.
`KEGG.use.internal.data`	
	KEGG parameter. Logical, use KEGG.db or latest online KEGG data.
`WikiPathways.organism`	
	WP parameter. Supported organisms, which can be accessed via the get_wp_organisms() function.
`Reactome.organism`	
	Reactome parameter. One of "human", "rat", "mouse", "celegans", "yeast", "zebrafish", "fly".
`MsigDB.organism`	
	MsigDB parameter. Species name, such as Homo sapiens or Mus musculus.
`MsigDB.category`	
	MsigDB parameter. MSigDB collection abbreviation, such as All, H, C1, C2, C3, C4, C5, C6, C7.
`CMAP.min.Geneset.Size`	
	CMAP parameter. Minimal size of CMAP genes annotated for testing. Recommended use 3.
`pvalue.cutoff`	pvalue cutoff on enrichment tests to report as significant.
`padjust.method`	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
`min.Geneset.Size`	
	Minimal size of genes annotated for testing. Not suitable for CMAP.
`max.Geneset.Size`	
	Maximal size of genes annotated for testing.
`qvalue.cutoff`	qvalue cutoff on enrichment tests to report as significant.

Author(s)

Zaoqu Liu; E-mail: liuzaoqu@163.com

lzq_GSEA.barplot1   *Enrichment barplot for positive or negative GSEA results*

Description

Plot enrichment barplot for positive or negative GSEA results.

Usage

```
lzq_GSEA.barplot1(
  enrich.obj,
  type = "Positive",
  show.term.num = 15,
  Selct.P = "FDR",
  cutoff.P = 0.05,
  colors = rev(cols_brown_green),
  add.bar.border = T,
  bar.width = 0.6,
  y.label.position = "right",
  title = NULL,
  legend.position = "bottom",
  theme.plot = theme_bw(base_rect_size = 1.5),
  use.Chinese = F
)
```

Arguments

enrich.obj	A GSEA enrichment object from clusterProfiler.
type	Specify whether you want to show positive or negative results.
show.term.num	A number or a list of terms. If it is a number, the first n terms will be displayed. If it is a list of terms, the selected terms will be displayed.
Selct.P	Nominal P value (NP) or adjust P value (FDR) were selected to define significant terms.
cutoff.P	A cutoff value for Select_P.
colors	A color vector for the bars.
add.bar.border	Logical. Whether to add the black border of bars.
bar.width	Width of bar in the plot.
y.label.position	
	Y label position. right or left.
title	Title of the plot.
legend.position	
	Position of legend. 'none', 'right', 'left' or two numeric variables.
theme.plot	ggtheme of plot.
use.Chinese	Logical. Whether to use Chinese annotation in the barplot.

Author(s)

Zaoqu Liu; E-mail: liuzaoqu@163.com

`lzq_GSEA.barplot2`   *Enrichment barplot for positive and negative GSEA results*

Description

Plot enrichment barplot for positive and negative GSEA results.

Usage

```
lzq_GSEA.barplot2(
  enrich.obj,
  Selct.P = "FDR",
  cutoff.P = 0.05,
  types = c("Positive", "Negative"),
  type.colors = c("#ED6355", "#3E94B5"),
  pos.top.pathway.num = 10,
  neg.top.pathway.num = 10,
  bar.width = 0.6,
  add.bar.border = T,
  x.limit.fold = 1.05,
  label.size = 3.5,
  legend.position = "bottom",
  use.Chinese = F
)
```

Arguments

`enrich.obj`	A GSEA enrichment object from clusterProfiler.
`Selct.P`	Nominal P value (NP) or adjust P value (FDR) were selected to define significant terms.
`cutoff.P`	A cutoff value for Select_P.
`types`	Two characters for defining the types of two objects.
`type.colors`	Two colors for the types of two objects.
`pos.top.pathway.num`	
	The number of top pathways in positive terms. Based on the significant test.
`neg.top.pathway.num`	
	The number of top pathways in negative terms. Based on the significant test.
`bar.width`	Width of bar in the plot.
`add.bar.border`	Logical. Whether to add the black border of bars.
`x.limit.fold`	Specify the fold of x limitation. Because some terms is too long.
`label.size`	Fontsize of label.
`legend.position`	
	none, left, right, top, bottom; Or Two numeric variables indicated x and y positions, respectively.
`use.Chinese`	Logical. Whether to use Chinese annotation in the barplot.

Author(s)

Zaoqu Liu; E-mail: liuzaoqu@163.com

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lzq_GSEA.dotplot1   *Enrichment dotplot for positive or negative GSEA results*

Description

Plot enrichment dotplot for positive or negative GSEA results.

Usage

```
lzq_GSEA.dotplot1(
  enrich.obj,
  type = "neg",
  show.term.num = 15,
  Selct.P = "FDR",
  cutoff.P = 0.05,
  colors = rev(cols_brown_green),
  size.range = c(3, 8),
  y.label.position = "right",
  title = NULL,
  legend.position = "bottom",
  theme.plot = theme_bw(base_rect_size = 1.5),
  use.Chinese = F
)
```

Arguments

enrich.obj	A GSEA enrichment object from clusterProfiler.
type	Specify whether you want to show positive or negative results.
show.term.num	A number or a list of terms. If it is a number, the first n terms will be displayed. If it is a list of terms, the selected terms will be displayed.
Selct.P	Nominal P value (NP) or adjust P value (FDR) were selected to define significant terms.
cutoff.P	A cutoff value for Select_P.
colors	A color vector for the bars.
size.range	Two numeric variables, the first is minimal value and the first is maximal value.
y.label.position	
	Y label position. right or left.
title	Title of the plot.
legend.position	
	Position of legend. 'none', 'right', 'left' or two numeric variables.
theme.plot	ggtheme of plot.
use.Chinese	Logical. Whether to use Chinese annotation in the barplot.

Author(s)

Zaoqu Liu; E-mail: liuzaoqu@163.com

lzq_GSEA.integrated   *Integrate gene set enrichment analysis*

Description

Perform integrated gene set enrichment analysis included GO, KEGG, WikiPathways, Reactome, MsigDB, Disease Ontoloty, Cancer Gene Network, DisGeNET, CellMarker, and CMAP.

Usage

```
lzq_GSEA.integrated(
  genes,
  gene.type = "SYMBOL",
  OrgDb = "org.Hs.eg.db",
  GO.ont = "BP",
  KEGG.organism = "hsa",
  KEGG.use.internal.data = F,
  perform.WikiPathways = F,
  WikiPathways.organism = "Homo sapiens",
  perform.Reactome = F,
  Reactome.organism = "human",
  perform.MsigDB = F,
  MsigDB.organism = "Homo sapiens",
  MsigDB.category = "H",
  perform.disease.ontoloty = F,
  perform.Cancer.Gene.Network = F,
  perform.DisGeNET = F,
  perform.CellMarker = F,
  perform.CMAP = T,
  pvalue.cutoff = 0.05,
  qvalue.cutoff = 0.05,
  padjust.method = "BH",
  min.Geneset.Size = 10,
  max.Geneset.Size = 1000,
  CMAP.min.Geneset.Size = 3
)
```

Arguments

genes	A vector of gene id.
gene.type	Keytype of input gene.
OrgDb	OrgDb object or OrgDb name
GO.ont	One of "BP", "MF", and "CC" subontologies, or "ALL" for all three.
KEGG.organism	Supported organism listed in 'https://www.genome.jp/kegg/catalog/org_list.html'.
KEGG.use.internal.data	
	Logical, use KEGG.db or latest online KEGG data.
perform.WikiPathways	
	Whether to perform WikiPathways enrichment.

WikiPathways.organism

> Supported organisms, which can be accessed via the get_wp_organisms() function.

perform.Reactome

> Whether to perform Reactome enrichment.

Reactome.organism

> one of "human", "rat", "mouse", "celegans", "yeast", "zebrafish", "fly".

perform.MsigDB   Whether to perform MsigDB enrichment.

MsigDB.organism

> Species name, such as Homo sapiens or Mus musculus.

MsigDB.category

> MSigDB collection abbreviation, such as All, H, C1, C2, C3, C4, C5, C6, C7.

perform.disease.ontoloty

> Whether to perform DO enrichment.

perform.Cancer.Gene.Network

> Whether to perform CGN enrichment.

perform.DisGeNET

> Whether to perform DisGeNET enrichment.

perform.CellMarker

> Whether to perform CellMarker enrichment. Marker from cellmarker database.

perform.CMAP   Whether to perform CMAP enrichment. Marker from CMAP database (in DSEATM tool).

pvalue.cutoff   pvalue cutoff on enrichment tests to report as significant.

qvalue.cutoff   qvalue cutoff on enrichment tests to report as significant.

padjust.method   one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".

min.Geneset.Size

> Minimal size of genes annotated for testing. Not suitable for CMAP.

max.Geneset.Size

> Maximal size of genes annotated for testing.

CMAP.min.Geneset.Size

> Minimal size of CMAP genes annotated for testing. Recommended use 3.

Author(s)

Zaoqu Liu; E-mail: liuzaoqu@163.com

---

lzq_gseaplot   *Visualize analyzing result of GSEA.*

Description

Visualize analyzing result of GSEA.

Usage

```
lzq_gseaplot(
  GSEA.result,
  Pathway.ID,
  heatbar = T,
  rank = T,
  line.color = "#41A98E",
  rank.colors = viridis::viridis(10),
  heatbar.colors = c(rev(RColorBrewer::brewer.pal(5, "Blues")),
    RColorBrewer::brewer.pal(5, "Reds")),
  add.x.ann = T,
  x.lab = "Gene ranks",
  line.y.lab = "Enrichment score",
  rank.y.lab = "logFC",
  statistic.position = c(0.5, 0.2),
  statistic.face = "italic",
  statistic.size = 3.5,
  rel.heights = c(1.5, 0.2, 1),
  theme.plot = theme_bw(base_rect_size = 1.5)
)
```

Arguments

GSEA.result	GSEA results from clusterProfiler::GSEA() function.
Pathway.ID	Corresponding pathway term of the output plot.
heatbar	Whether to add heatbar. Default True.
rank	Whether to add Rank map. Default True.
line.color	Line color for running score.
rank.colors	Color scheme of rank lines. A vector.
heatbar.colors	Color scheme of heatbar. A vector.
add.x.ann	Whether to add the title, text, and ticks of X axis.
x.lab	X label.
line.y.lab	Y label of running score plot.
rank.y.lab	Y label of rank plot.
statistic.position	
	Position of statistics in the running score plot.
statistic.face	Font face of statistics.
statistic.size	Font size of statistics.
rel.heights	Relative heights of subplots.
theme.plot	A theme object from ggplot2.

Author(s)

Zaoqu Liu; E-mail: liuzaoqu@163.com

lzq_KEGGview   *KEGG pathway visualization*

Description

Simple visualization of KEGG pathway based on pathview package.

Usage

```
lzq_KEGGview(
  gene.data = NULL,
  gene.type = "SYMBOL",
  pathway.id,
  species = "hsa",
  figure.suffix = ""
)
```

Arguments

gene.data   either vector (single sample) or a matrix-like data (multiple sample). Vector
                should be numeric with gene IDs as names or it may also be character of gene
                IDs. Character vector is treated as discrete or count data. Matrix-like data struc-
                ture has genes as rows and samples as columns. Row names should be gene IDs.
                Here gene ID is a generic concepts, including multiple types of gene, transcript
                and protein uniquely mappable to KEGG gene IDs. KEGG ortholog IDs are also
                treated as gene IDs as to handle metagenomic data. Check details for mappable
                ID types. Default gene.data=NULL.

gene.type   character, ID type used for the gene.data, case insensitive. Default gene.idtype="entrez",
                i.e. Entrez Gene, which are the primary KEGG gene ID for many common
                model organisms. For other species, gene.idtype should be set to "KEGG" as
                KEGG use other types of gene IDs. For the common model organisms (to check
                the list, do: data(bods); bods), you may also specify other types of valid IDs. To
                check the ID list, do: data(gene.idtype.list); gene.idtype.list.

pathway.id   character vector, the KEGG pathway ID(s), usually 5 digit, may also include the
                3 letter KEGG species code.

species   character, either the kegg code, scientific name or the common name of the tar-
                get species. This applies to both pathway and gene.data or cpd.data. When
                KEGG ortholog pathway is considered, species="ko". Default species="hsa", it
                is equivalent to use either "Homo sapiens" (scientific name) or "human" (com-
                mon name).

figure.suffix   character, the suffix to be added after the pathway name as part of the output
                graph file. Sample names or column names of the gene.data or cpd.data are also
                added when there are multiple samples. Default out.suffix="pathview".

Author(s)

Zaoqu Liu; E-mail: liuzaoqu@163.com

---

lzq_ORA   *Over-representative analysis*

Description

Perform over-representative analysis included GO, KEGG, WikiPathways, Reactome, MsigDB, Disease Ontoloty, Cancer Gene Network, DisGeNET, CellMarker, and CMAP.

Usage

```
lzq_ORA(
  genes,
  background.genes = NULL,
  gene.type = "SYMBOL",
  enrich.type,
  OrgDb = "org.Hs.eg.db",
  GO.ont = "BP",
  GO.simplify = T,
  KEGG.organism = "hsa",
  KEGG.use.internal.data = F,
  WikiPathways.organism = "Homo sapiens",
  Reactome.organism = "human",
  MsigDB.organism = "Homo sapiens",
  MsigDB.category = "H",
  CMAP.min.Geneset.Size = 3,
  pvalue.cutoff = 0.05,
  qvalue.cutoff = 0.05,
  padjust.method = "BH",
  min.Geneset.Size = 10,
  max.Geneset.Size = 1000
)
```

Arguments

genes	A vector of gene id.
background.genes	Background genes. If missing, the all genes listed in the database (eg TERM2GENE table) will be used as background.
gene.type	Keytype of input gene.
enrich.type	Select an enrichment method. One of GO, KEGG, MKEGG, WikiPathways, Reactome, MsigDB, DO, CGN, DisGeNET, CellMarker, and CMAP. WikiPathways can be replaced by WP, Reactome can be replaced by RP, and CellMarker can be replaced by CM.
OrgDb	OrgDb object or OrgDb name.
GO.ont	GO parameter. One of "BP", "MF", and "CC" subontologies, or "ALL" for all three.
GO.simplify	GO parameter. Whether to remove redundancy of enriched GO terms.
KEGG.organism	KEGG parameter. Supported organism listed in 'https://www.genome.jp/kegg/catalog/org_list.html'.

KEGG.use.internal.data

    KEGG parameter. Logical, use KEGG.db or latest online KEGG data.

WikiPathways.organism

    WP parameter. Supported organisms, which can be accessed via the get_wp_organisms() function.

Reactome.organism

    Reactome parameter. One of "human", "rat", "mouse", "celegans", "yeast", "zebrafish", "fly".

MsigDB.organism

    MsigDB parameter. Species name, such as Homo sapiens or Mus musculus.

MsigDB.category

    MsigDB parameter. MSigDB collection abbreviation, such as All, H, C1, C2, C3, C4, C5, C6, C7.

CMAP.min.Geneset.Size

    CMAP parameter. Minimal size of CMAP genes annotated for testing. Recommended use 3.

pvalue.cutoff   pvalue cutoff on enrichment tests to report as significant.

qvalue.cutoff   qvalue cutoff on enrichment tests to report as significant.

padjust.method one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".

min.Geneset.Size

    Minimal size of genes annotated for testing. Not suitable for CMAP.

max.Geneset.Size

    Maximal size of genes annotated for testing.

Author(s)

Zaoqu Liu; E-mail: liuzaoqu@163.com

---

lzq_ORA.barplot1   *Enrichment barplot for one ORA enrichment object*

Description

Plot enrichment barplot for one ORA enrichment object.

Usage

```
lzq_ORA.barplot1(
  enrich.obj,
  x = "GeneRatio",
  show.term.num = 15,
  color.by = "p.adjust",
  colors = rev(cols_brown_green),
  color.title = color.by,
  bar.width = 0.6,
  add.bar.border = F,
  y.label.position = "right",
  title = NULL,
  legend.position = "bottom",
  theme.plot = theme_bw(base_rect_size = 1.5),
  use.Chinese = F
)
```

Arguments

enrich.obj	An object from clusterProfiler.
x	variable for x-axis, one of 'GeneRatio', 'pvalue', 'p.adjust', 'Count', EnrichmentFactor.
show.term.num	A number or a list of terms. If it is a number, the first n terms will be displayed. If it is a list of terms, the selected terms will be displayed.
color.by	variable that used to color enriched terms, one of 'GeneRatio', 'pvalue', 'p.adjust', 'Count', EnrichmentFactor.
colors	A color vector for the bars.
color.title	Title of color annotation legend.
bar.width	Width of bars.
add.bar.border	Logical. Whether to add the black border of bars.
y.label.position	Y label position. right or left.
title	Title of the plot.
legend.position	Position of legend. 'none', 'right', 'left' or two numeric variables.
theme.plot	ggtheme of plot.
use.Chinese	Logical. Whether to use Chinese annotation in the barplot.

Author(s)

Zaoqu Liu; E-mail: liuzaoqu@163.com

---

lzq_ORA.barplot2 *Enrichment barplot for two ORA enrichment objects*

Description

Plot enrichment barplot for two ORA enrichment objects.

Usage

```
lzq_ORA.barplot2(
  enrich.obj1,
  enrich.obj2,
  Selct.P = "FDR",
  cutoff.P = 0.05,
  obj.types = c("Up", "Down"),
  obj.type.colors = c("#ED6355", "#3E94B5"),
  obj1.top.pathway.num = 10,
  obj2.top.pathway.num = 10,
  bar.width = 0.6,
  add.bar.border = T,
  x.limit.fold = 1.05,
  label.size = 3.5,
  legend.position = "bottom",
  use.Chinese = F
)
```

Arguments

`enrich.obj1`	An object from clusterProfiler.
`enrich.obj2`	An object from clusterProfiler.
`Selct.P`	Nominal P value (NP) or adjust P value (FDR) were selected to define significant terms.
`cutoff.P`	A cutoff value for Select_P.
`obj.types`	Two characters for defining the types of two objects.
`obj.type.colors`	
	Two colors for the types of two objects.
`obj1.top.pathway.num`	
	The number of top pathways in object 1. Based on the significant test.
`obj2.top.pathway.num`	
	The number of top pathways in object 2. Based on the significant test.
`bar.width`	Width of bar in the plot.
`add.bar.border`	Logical. Whether to add the black border of bars.
`x.limit.fold`	Specify the fold of x limitation. Because some terms is too long.
`label.size`	Fontsize of label.
`legend.position`	
	none, left, right, top, bottom; Or Two numeric variables indicated x and y positions, respectively.
`use.Chinese`	Logical. Whether to use Chinese annotation in the barplot.

Author(s)

Zaoqu Liu; E-mail: liuzaoqu@163.com

`lzq_ORA.dotplot1`	*Enrichment dotplot for one ORA enrichment object*

Description

Plot enrichment dotplot for one ORA enrichment object.

Usage

```
lzq_ORA.dotplot1(
  enrich.obj,
  x = "GeneRatio",
  show.term.num = 15,
  color.by = "p.adjust",
  colors = rev(cols_brown_green),
  color.title = color.by,
  size.by = "Count",
  size.range = c(3, 8),
  size.title = size.by,
  y.label.position = "right",
  title = NULL,
```

```
    legend.position = "bottom",
    theme.plot = theme_bw(base_rect_size = 1.5),
    use.Chinese = F
)
```

Arguments

`enrich.obj`	An object from clusterProfiler.
`x`	variable for x-axis, one of 'GeneRatio', 'pvalue', 'p.adjust', 'Count', EnrichmentFactor.
`show.term.num`	A number or a list of terms. If it is a number, the first n terms will be displayed. If it is a list of terms, the selected terms will be displayed.
`color.by`	variable that used to color enriched terms, one of 'GeneRatio', 'pvalue', 'p.adjust', 'Count', EnrichmentFactor.
`colors`	A color vector for the bars.
`color.title`	Title of color annotation legend.
`size.by`	variable that used to size enriched terms, one of 'GeneRatio', 'pvalue', 'p.adjust', 'Count', EnrichmentFactor.
`size.range`	Two numeric variables, the first is minimal value and the first is maximal value.
`size.title`	Title of size annotation legend.
`y.label.position`	
	Y label position. right or left.
`title`	Title of the plot.
`legend.position`	
	Postion of legend. 'none', 'right', 'left' or two numeric variables.
`theme.plot`	ggtheme of plot.
`use.Chinese`	Logical. Whether to use Chinese annotation in the barplot.

Author(s)

Zaoqu Liu; E-mail: liuzaoqu@163.com

`lzq_ORA.integrated` *Integrate over-representative analysis*

Description

Perform integrated over-representative analysis included GO, KEGG, WikiPathways, Reactome, MsigDB, Disease Ontoloty, Cancer Gene Network, DisGeNET, CellMarker, and CMAP.

Usage

```
lzq_ORA.integrated(
  genes,
  background.genes = NULL,
  gene.type = "SYMBOL",
  OrgDb = "org.Hs.eg.db",
  GO.ont = "BP",
  KEGG.organism = "hsa",
  KEGG.use.internal.data = F,
  perform.WikiPathways = F,
  WikiPathways.organism = "Homo sapiens",
  perform.Reactome = F,
  Reactome.organism = "human",
  perform.MsigDB = F,
  MsigDB.organism = "Homo sapiens",
  MsigDB.category = "H",
  perform.disease.ontoloty = F,
  perform.Cancer.Gene.Network = F,
  perform.DisGeNET = F,
  perform.CellMarker = F,
  perform.CMAP = T,
  pvalue.cutoff = 0.05,
  qvalue.cutoff = 0.05,
  padjust.method = "BH",
  min.Geneset.Size = 10,
  max.Geneset.Size = 1000,
  CMAP.min.Geneset.Size = 3
)
```

Arguments

`genes`	A vector of gene id.
`background.genes`	
	Background genes. If missing, the all genes listed in the database (eg TERM2GENE table) will be used as background.
`gene.type`	Keytype of input gene.
`OrgDb`	OrgDb object or OrgDb name
`GO.ont`	One of "BP", "MF", and "CC" subontologies, or "ALL" for all three.
`KEGG.organism`	Supported organism listed in 'https://www.genome.jp/kegg/catalog/org_list.html'.
`KEGG.use.internal.data`	
	Logical, use KEGG.db or latest online KEGG data.
`perform.WikiPathways`	
	Whether to perform WikiPathways enrichment.
`WikiPathways.organism`	
	Supported organisms, which can be accessed via the get_wp_organisms() function.
`perform.Reactome`	
	Whether to perform Reactome enrichment.
`Reactome.organism`	
	one of "human", "rat", "mouse", "celegans", "yeast", "zebrafish", "fly".

perform.MsigDB   Whether to perform MsigDB enrichment.

MsigDB.organism
                 Species name, such as Homo sapiens or Mus musculus.

MsigDB.category
                 MSigDB collection abbreviation, such as All, H, C1, C2, C3, C4, C5, C6, C7.

perform.disease.ontoloty
                 Whether to perform DO enrichment.

perform.Cancer.Gene.Network
                 Whether to perform CGN enrichment.

perform.DisGeNET
                 Whether to perform DisGeNET enrichment.

perform.CellMarker
                 Whether to perform CellMarker enrichment. Marker from cellmarker database.

perform.CMAP   Whether to perform CMAP enrichment. Marker from CMAP database (in DSEATM
                 tool).

pvalue.cutoff   pvalue cutoff on enrichment tests to report as significant.

qvalue.cutoff   qvalue cutoff on enrichment tests to report as significant.

padjust.method   one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".

min.Geneset.Size
                 Minimal size of genes annotated for testing. Not suitable for CMAP.

max.Geneset.Size
                 Maximal size of genes annotated for testing.

CMAP.min.Geneset.Size
                 Minimal size of CMAP genes annotated for testing. Recommended use 3.

Author(s)

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lzq_translate   *Baidu translation*

Description

Perform Baidu translation.

Usage

```
lzq_translate(
  sentence,
  from = "en",
  to = "zh",
  appid = "20231122001888718",
  key = "5GpDqe8F3pmXfnOkEKGQ"
)
```

Arguments

sentence	A sentence or word need to be translated.
from	Input language type.
to	Output language type.
appid	User app id from baidu translation api. https://fanyi-api.baidu.com/manage/developer.
key	User Key from baidu translation api. https://fanyi-api.baidu.com/manage/developer.

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lzq_updateSymbol	*Title Identify outdated or Excel-mogrified gene symbols for a gene vector*

Description

Title Identify outdated or Excel-mogrified gene symbols for a gene vector

Usage

```
lzq_updateSymbol(genes, unmapGene_keep = F)
```

Arguments

genes	A gene vector.
unmapGene_keep	whether to keep unmapped genes.

Author(s)

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lzq_updateSymbolforDL	*Title Identify outdated or Excel-mogrified gene symbols for a dataframe*

Description

Title Identify outdated or Excel-mogrified gene symbols for a dataframe

Usage

```
lzq_updateSymbolforDL(data, unmapGene_keep = F)
```

Arguments

data	A expression dataframe with genename rows and sample columns.
unmapGene_keep	whether to keep unmapped genes.

Author(s)

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