

Package ‘BioEnricher’

November 23, 2023

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

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

Imports clusterProfiler,

DOSE,
dplyr,
enrichplot,
ggplot2,
HGNCHELPER,
Hmisc,
httr,
jsonlite,
magrittr,
msigdb,
openssl,
pathview,
png,
purrr,
ReactomePA,
stats,
vroom

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listEnrichMethod	<i>List of enrichment methods</i>
------------------	-----------------------------------

Description

List of enrichment methods

Usage

```
listEnrichMethod()
```

Author(s)

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

lzq_getEF	<i>Get enrichment factor from enrichResult</i>
-----------	--

Description

Get enrichment factor from enrichResult (clusterProfiler).

Usage

```
lzq_getEF(res)
```

Arguments

res enrichResult from clusterProfiler.

Value

A new res with enrichment factor.

Author(s)

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

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 res with numeric GeneRatio and BgRatio.

Author(s)

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

lzq_GSEA

Gene set enrichment analysis

Description

Perform gene set enrichment analysis included GO, KEGG, WikiPathways, Reactome, MsigDB, Disease Ontology, 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 <code>get_wp_organisms()</code> 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	<i>Enrichment barplot for positive or negative GSEA results</i>
-------------------	---

Description

Plot enrichment barplot or positive and 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 = "right",
  theme.plot = theme_bw(base_rect_size = 1.5),
  use.Chinese = F
)
  
```

Arguments

<code>enrich.obj</code>	A GSEA enrichment object from clusterProfiler.
<code>type</code>	Specify whether you want to show positive or negative results.
<code>show.term.num</code>	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.
<code>Selct.P</code>	Nominal P value (NP) or adjust P value (FDR) were selected to define significant terms.
<code>cutoff.P</code>	A cutoff value for Select_P.
<code>colors</code>	A color vector for the bars.
<code>add.bar.border</code>	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	<i>Enrichment barplot for positive and negative GSEA results</i>
-------------------	--

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 = "right",
  legend.justification = c(0, 0.5),
  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.
legend.justification	Justification of legend; masked from ggplot2.
use.Chinese	Logical. Whether to use Chinese annotation in the barplot.

Author(s)

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

lzq_GSEA.dotplot1	<i>Enrichment dotplot for positive or negative GSEA results</i>
-------------------	---

Description

Plot enrichment dotplot or positive and 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 = "right",
  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	<i>Integrate gene set enrichment analysis</i>
---------------------	---

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

<code>genes</code>	A vector of gene id.
<code>gene.type</code>	Keytype of input gene.
<code>OrgDb</code>	OrgDb object or OrgDb name
<code>GO.ont</code>	One of "BP", "MF", and "CC" subontologies, or "ALL" for all three.
<code>KEGG.organism</code>	Supported organism listed in ' https://www.genome.jp/kegg/catalog/org_list.html '.
<code>KEGG.use.internal.data</code>	Logical, use KEGG.db or latest online KEGG data.
<code>perform.WikiPathways</code>	Whether to perform WikiPathways enrichment.
<code>WikiPathways.organism</code>	Supported organisms, which can be accessed via the <code>get_wp_organisms()</code> function.
<code>perform.Reactome</code>	Whether to perform Reactome enrichment.
<code>Reactome.organism</code>	one of "human", "rat", "mouse", "celegans", "yeast", "zebrafish", "fly".
<code>perform.MsigDB</code>	Whether to perform MsigDB enrichment.
<code>MsigDB.organism</code>	Species name, such as <i>Homo sapiens</i> or <i>Mus musculus</i> .
<code>MsigDB.category</code>	MSigDB collection abbreviation, such as All, H, C1, C2, C3, C4, C5, C6, C7.
<code>perform.disease.ontoloty</code>	Whether to perform DO enrichment.
<code>perform.Cancer.Gene.Network</code>	Whether to perform CGN enrichment.
<code>perform.DisGeNET</code>	Whether to perform DisGeNET enrichment.
<code>perform.CellMarker</code>	Whether to perform CellMarker enrichment. Marker from cellmarker database.
<code>perform.CMAP</code>	Whether to perform CMAP enrichment. Marker from CMAP database (in DSEATM tool).
<code>pvalue.cutoff</code>	pvalue cutoff on enrichment tests to report as significant.
<code>qvalue.cutoff</code>	qvalue cutoff on enrichment tests to report as significant.
<code>padjust.method</code>	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
<code>min.Geneset.Size</code>	Minimal size of genes annotated for testing. Not suitable for CMAP.
<code>max.Geneset.Size</code>	Maximal size of genes annotated for testing.
<code>CMAP.min.Geneset.Size</code>	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)

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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 structure 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 target 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" (common 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 Ontology, 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 = "right",
  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.
Select.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	<i>Enrichment dotplot for one ORA enrichment object</i>
------------------	---

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 = "right",
theme.plot = theme_bw(base_rect_size = 1.5),
use.Chinese = F
)

```

Arguments

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

Author(s)

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

lzq_ORA.integrated	<i>Integrate over-representative analysis</i>
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Description

Perform integrated over-representative analysis included GO, KEGG, WikiPathways, Reactome, MsigDB, Disease Ontology, 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.ontology = 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

<code>genes</code>	A vector of gene id.
<code>background.genes</code>	Background genes. If missing, the all genes listed in the database (eg TERM2GENE table) will be used as background.
<code>gene.type</code>	Keytype of input gene.
<code>OrgDb</code>	OrgDb object or OrgDb name
<code>GO.ont</code>	One of "BP", "MF", and "CC" subontologies, or "ALL" for all three.
<code>KEGG.organism</code>	Supported organism listed in ' https://www.genome.jp/kegg/catalog/org_list.html '.
<code>KEGG.use.internal.data</code>	Logical, use KEGG.db or latest online KEGG data.
<code>perform.WikiPathways</code>	Whether to perform WikiPathways enrichment.
<code>WikiPathways.organism</code>	Supported organisms, which can be accessed via the <code>get_wp_organisms()</code> function.
<code>perform.Reactome</code>	Whether to perform Reactome enrichment.
<code>Reactome.organism</code>	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 = "5GpDqe8F3pmXfn0kEKGQ"
)

```

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 .

Author(s)

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lzq_updateSymbol	<i>Title Identify outdated or Excel-mogrified gene symbols for a gene vector</i>
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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)

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

lzq_updateSymbolforDL	<i>Title Identify outdated or Excel-mogrified gene symbols for a dataframe</i>
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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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