

Package ‘Toolsets’

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Description Toolsets

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example.function	<i>description of the example function</i>
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Description

description of the example function

Usage

```
example.function(param1 = NULL)
```

Arguments

param1	param1
--------	--------

Value

the return object

Examples

```
example.function()
```

gsea.GO.genes.keyWords	<i>Get the genes of interested GO terms by some key words</i>
------------------------	---

Description

Get the genes of interested GO terms by some key words

Usage

```
gsea.GO.genes.keyWords(organism = "hs", keyWords = "axon",
  returnAll = F)
```

Arguments

organism	organism (hs and mm)
keyWords	keyWords (for grey function, e.g. cell cycle DNA replication)
returnAll	if return all the GO terms

Value

a list with the GO terms and genes

Examples

```
tmpList <- toC_get_genes_of_GO_by_keyWords(organism = "hs", keyWords = "axon", returnAll = F)
tmpList <- toC_get_genes_of_GO_by_keyWords(organism = "hs",
  keyWords = "cell cycle|DNA replication|cell division|segregation")
```

```
gsea.go.kegg.clusterProfiler
```

GSEA analysis by newest fgsea

Description

GSEA analysis by newest fgsea

Usage

```
gsea.go.kegg.clusterProfiler(geneList = DEGs_list_full,
  use.score = "cor", organism = "hs", pvalueCutoff = 0.05)
```

Arguments

geneList	a gene list
use.score	the score used for the GSEA analysis
organism	organism (hs and mm)
pvalueCutoff	pvalueCutoff

Value

a list with GO and KEGG GSEA annotation result (clusterProfiler format)

Examples

```
gsea_list <- gsea.go.kegg.clusterProfiler(geneList = pheno_DEGs, use.score = "cor", organism="mm")
```

```
gsea.ID2gene
```

transfer the ID string to gene vector or string

Description

transfer the ID string to gene vector or string

Usage

```
gsea.ID2gene(ID, organism = "hs", returnVector = T)
```

Arguments

ID	the ID string, like 4171/4175/5422/4172
organism	organism (hs and mm)
returnVector	return vector or string

Value

a transformed gene name list or string

Examples

```
tmpgenes <- gsea.ID2gene("4171/4175/5422/4172", organism="hs")
```

```
ora.go.kegg.clusterProfiler
```

GO KEGG ORA analysis

Description

GO KEGG ORA analysis

Usage

```
ora.go.kegg.clusterProfiler(geneList = markerList, organism = "hs")
```

Arguments

geneList	a gene list
organism	organism (hs and mm)

Value

a list with GO and KEGG annotation result (clusterProfiler format)

Examples

```
result <- ora.go.kegg.clusterProfiler(geneList = new_moduleList, organism="mm")
```

```
plot.dotplot.SC3
```

Draw dotplot for human SC3 object

Description

Draw dotplot for human SC3 object

Usage

```
## S3 method for class 'dotplot.SC3'
plot(sce, genes.plot, use = "cellGroup2",
     xAngle = 60, cols.use = c("lightgrey", "blue"), col.min = -2.5,
     col.max = 2.5, dot.min = 0, dot.scale = 6, group.order = c(),
     scale.by = "radius", scale.min = NA, scale.max = NA, group.by,
     title = "", plot.legend = FALSE, do.return = FALSE,
     x.lab.rot = FALSE)
```

Arguments

sce	SC3 object
genes.plot	genes
use	group used in SC3 object
xAngle	angle of x title
cols.use	colors used
col.min	col.min
col.max	col.max
dot.min	dot.min
dot.scale	whether to scale or not
group.order	group.order
scale.by	scale.by
scale.min	scale.min
scale.max	scale.max
group.by	group.by
title	title
plot.legend	plot legend or not
do.return	return object or not
x.lab.rot	rotate x title or not

Value

a ggplot dotplot

Examples

```
options(repr.plot.width=4, repr.plot.height=6)
plot.dotplot.human(sce = sce_HSCR_pure, genes.plot = uniquegenes2, use="cellGroup", group.order = group.order,
  scale.min=0, scale.max=100, title="", plot.legend = T, xAngle=90)
```

plot.GO.barplot	<i>Draw barplot for GO dataframe</i>
-----------------	--------------------------------------

Description

Draw barplot for GO dataframe

Usage

```
## S3 method for class 'GO.barplot'
plot(barplot_df, color = "random")
```

Arguments

barplot_df	GO dataframe from clusterProfiler
------------	-----------------------------------

Value

a ggplot barplot object

Examples

```
options(repr.plot.width=4, repr.plot.height=9)
plot.GO.barplot(df)
```

```
plot.gsea.GO.KEGG.barplot.batch
```

Draw GSEA GO KEGG barplot for a gene list

Description

Draw GSEA GO KEGG barplot for a gene list

Usage

```
## S3 method for class 'gsea.GO.KEGG.barplot.batch'
plot(anno_list = gsea_list$go_list,
      type)
```

Arguments

anno_list	a gene list
type	type of the input data

Value

a dataframe

Examples

```
options(repr.plot.width=10, repr.plot.height=6)
go_list <- plot.gsea.GO.KEGG.barplot.batch(gsea_list$go_list, type = "GO")
kegg_list <- plot.gsea.GO.KEGG.barplot.batch(gsea_list$kegg_list, type = "KEGG")
```

```
plot.ora.GO.KEGG.barplot.batch
```

Draw GO KEGG barplot for a gene list

Description

Draw GO KEGG barplot for a gene list

Usage

```
## S3 method for class 'ora.GO.KEGG.barplot.batch'  
plot(anno_list = go_list, type)
```

Arguments

anno_list	a gene list
type	type of the input data

Value

a dataframe

Examples

```
options(repr.plot.width=4, repr.plot.height=9)  
go_list <- plot.GO.KEGG.barplot.batch(result$go_list, type="GO")
```

```
plot.violin
```

Draw violin plot

Description

Draw violin plot

Usage

```
## S3 method for class 'violin'  
plot(exprData, cellAnno, genes, use, direction = "h",  
      showGroup = T, groupOrder = NULL)
```

Arguments

exprData	the expression matrix to be used
cellAnno	the annotation of the cells
genes	genes wanted to show
use	the group selected in the cellAnno
direction	direction of the violin plot
showGroup	whether to show the group names
groupOrder	the order of the group

Value

a ggplot violin object

Examples

```
options(repr.plot.width=4, repr.plot.height=9)
plot.violin(exprData=seuset@data, cellAnno=all_tsne_2, genes=key_genes, use="final", direction = "h")

all_tsne_3 <- subset(all_tsne_2, final %in% c('ctrl:c4','kif7:c4','ctrl:c6','kif7:c6'))
options(repr.plot.width=4, repr.plot.height=4)
plot.violin(exprData=seuset@data, cellAnno=all_tsne_3, genes=key_genes, use="final", direction = "h",
            groupOrder = c('ctrl:c4','kif7:c4','ctrl:c6','kif7:c6'))
```


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