Package 'Toolsets'

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Type Package

Title Toolsets

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Description Toolsets

License GPL (>= 2)

Depends R (>= 3.0)

LazyData true

Encoding UTF-8

RoxygenNote 6.1.1

R topics documented:

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example.function   *description of the example function*

Description

description of the example function

1

Usage

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

Arguments

param1   param1

Value

the return object

Examples

```
example.function()
```

---

gsea.GO.genes.keyWords

Get the genes of interested GO terms by some key words

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
GO KEGG GSEA analysis

Description

GO KEGG GSEA analysis

Usage

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

Arguments

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

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")
```

---

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	*Draw barplot for GO dataframe*

Description

Draw barplot for GO dataframe

Usage

```
## S3 method for class 'GO.barplot'
plot(barplot_df)
```

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'))
```

Index