

Package ‘Toolsets’

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Type Package

Title Toolsets

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Author Zhixin Li

Maintainer Zhixin Li <zxlee@hku.hk>

Description Toolsets

License GPL (>= 2)

Depends R (>= 3.0)

LazyData true

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RoxygenNote 6.1.1

R topics documented:

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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
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Value

the return object

Examples

```
example.function()
```

plot.dotplot.human	<i>Draw dotplot for human SC3 object</i>
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Description

Draw dotplot for human SC3 object

Usage

```
## S3 method for class 'dotplot.human'
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.violin	<i>Draw violin plot</i>
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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'))
```

`toC_get_genes_of_GO_by_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

```
toC_get_genes_of_GO_by_keyWords(organism = "hs", keyWords = "axon",  
  returnAll = F)
```

Arguments

<code>organism</code>	organism (hs and mm)
<code>keyWords</code>	keyWords (for grey function, e.g. cell cycle DNA replication)
<code>returnAll</code>	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")
```

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