

# 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	<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()
```

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plot.dotplot.SC3	<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.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)
```

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plot.GO.barplot	<i>Draw barplot for GO dataframe</i>
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**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)
```

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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'))
```

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toC\_get\_genes\_of\_GO\_by\_keyWords

*Get the genes of interested GO terms by some key words*

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**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**

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")
```

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