

Package ‘Toolsets’

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Description Toolsets

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`add.background.point` *for facet plot, add background point*

Description

for facet plot, add background point

Usage

```
add.background.point(all_tsne, cluster = "cluster", group = "group",  
  cor1 = "X", cor2 = "Y", sample.order, group.order)
```

Arguments

<code>all_tsne</code>	<code>all_tsne</code>
<code>cluster</code>	<code>cluster</code>
<code>group</code>	<code>group</code>
<code>cor1</code>	<code>x</code>
<code>cor2</code>	<code>y</code>
<code>sample.order</code>	<code>sample.order</code>
<code>group.order</code>	<code>group.order</code>

Value

a merged dataframe

Examples

```
merged_df <- add.background.point(all_tsne, sample.order = sample.order, group.order = group.order)
```

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

description of the example function

Usage

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

Arguments

<code>param1</code>	<code>param1</code>
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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

<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")
```

```
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

<code>geneList</code>	a gene list
<code>use.score</code>	the score used for the GSEA analysis
<code>organism</code>	organism (hs and mm)
<code>pvalueCutoff</code>	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")
```

<code>gsea.ID2gene</code>	<i>transfer the ID string to gene vector or string</i>
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Description

transfer the ID string to gene vector or string

Usage

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

Arguments

<code>ID</code>	the ID string, like 4171/4175/5422/4172
<code>organism</code>	organism (hs and mm)
<code>returnVector</code>	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

<code>geneList</code>	a gene list
<code>organism</code>	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>
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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
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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")
```

<code>plot.violin</code>	<i>Draw violin plot</i>
--------------------------	-------------------------

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'))
```

pre.pheatmap.anno	<i>prepare the annotation for the pheatmap</i>
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Description

prepare the annotation for the pheatmap

Usage

```
pre.pheatmap.anno(sce = sce, group.order = group.order,
  sample.order = sample.order, Cluster = "impute_cluster",
  Sample = "cellGroup")
```

Arguments

sce	sce object
group.order	group.order
sample.order	sample.order
Cluster	the feature take as Cluster
Sample	the feature take as Sample

Value

anno list

Examples

```
options(repr.plot.width=8, repr.plot.height=7)
pheatmap(scale.data[sc3_marker$name, rownames(anno$col)], cluster_rows = F, cluster_cols = F, border_
  color = colorRampPalette(c("#FF00FF", "#000000", "#FFFF00"))(100),
  show_colnames=F, show_rownames=F, annotation_col = anno$col, annotation_colors = anno$colors)
```

pre.scale.data	<i>scale the matrix</i>
----------------	-------------------------

Description

scale the matrix

Usage

```
pre.scale.data(raw.data = logcounts(sce_HSCR), max.value = 2)
```

Arguments

raw.data	raw.data
max.value	max.value after scale

Value

scale.data

Examples

```
scale.data <- pre.scale.data(logcounts(sce_HSCR))
```

rep.col	<i>repeat the col or row for n times</i>
---------	--

Description

repeat the col or row for n times

Usage

```
## S3 method for class 'col'  
rep(x, n)
```

Arguments

x	x
n	n

Value

df

Examples

```
rep.df <- rep.col(all_tsne[,cluster], length(groups))
```

rep.row	<i>repeat the col or row for n times</i>
---------	--

Description

repeat the col or row for n times

Usage

```
## S3 method for class 'row'  
rep(x, n)
```

Arguments

x	x
n	n

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Value

df

Examples

```
rep.df <- rep.col(all_tsne[,cluster], length(groups))
```

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