Package ‘SeuratExplorer’

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Title An 'Shiny' App for Exploring scRNA-seq Data Processed in 'Seurat'

Version 0.1.0

Description A simple, one-command package which runs an interactive dashboard capable of common visualizations for single cell RNA-seq. 'SeuratExplorer' requires a processed 'Seurat' object, which is saved as 'rds' or 'qs2' file.

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Encoding UTF-8

RoxygenNote 7.3.2

Imports ggplot2, utils, Seurat, shiny, shinydashboard, DT, shinycssloaders, patchwork, tools, colourpicker, shinyWidgets, scales, SeuratObject, shinyjqui, shinyBS, ggalluvial, dplyr, ComplexHeatmap, qs2, circlize, reshape2, stats, htmltools

Depends R (>= 4.1.0)

Suggests BiocManager, DESeq2, MAST, roxygen2, devtools

NeedsCompilation no

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Repository CRAN

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Contents

`cellRatioPlot` *plot cell percentage barplot*

Description

support facet, codes refer to: https://github.com/junjunlab/scRNAtoolVis/blob/master/R/cellRatioPlot.R, with modification

Usage

```
cellRatioPlot(
  object = NULL,
  sample.name = NULL,
  sample.order = NULL,
  celltype.name = NULL,
  celltype.order = NULL,
  facet.name = NULL,
  facet.order = NULL,
  col.width = 0.7,
  flow.alpha = 0.25,
  flow.curve = 0,
  color.choice = NULL
)
```

Arguments

`object`	an Seurat object
`sample.name`	x axis
`sample.order`	order for x axis
`celltype.name`	column fill by
`celltype.order`	order for fill by
`facet.name`	column name for facet
`facet.order`	the order for facet
`col.width`	column width, from 0-1
`flow.alpha`	transparency for flow
`flow.curve`	curve for flow
`color.choice`	color choice for fill

Value

a ggplot2 object

Examples

```
#NULL
```

`explorer_body_ui` *generate the body UI for each menu item specified in* `explorer_sidebar_ui`

Description

generate the body UI for each menu item specified in `explorer_sidebar_ui`

Usage

```
explorer_body_ui(tab_list)
```

Arguments

`tab_list`	a tag list for the body UI of shiny dashboard

Value

a filled tag list for body UI

Examples

```
tab_list <- list()
tab_list <- explorer_body_ui(tab_list = tab_list)
```

`explorer_server` *server side functions related to* `explorer_sidebar_ui`

Description

server side functions related to `explorer_sidebar_ui`

Usage

```
explorer_server(input, output, session, data, verbose = FALSE)
```

Arguments

`input`	server input
`output`	server output
`session`	server session
`data`	the Seurat object and related parameters
`verbose`	for debug use

Value

server side functions related to `explorer_sidebar_ui`

`explorer_sidebar_ui` *some menu items of the dashboard sidebar*

Description

to generate some menu items for the dashboard, which can be integrated to other packages, such as 'fentouxungui/SeuratExplorerServer' from github.

Usage

```
explorer_sidebar_ui()
```

Value

return some menu items for the dashboard

Examples

```
explorer_sidebar_ui()
```

`getColors` *getColors*

Description

getColors

Usage

```
getColors(color.platte = NULL, choice = NULL, n = NULL)
```

Arguments

`color.platte`	predefined color list
`choice`	color name
`n`	how many colors to return

Value

a color list

Examples

```
# null
```

`launchSeuratExplorer` *Launch shiny app*

Description

Launch shiny app

Usage

```
launchSeuratExplorer(verbose = FALSE)
```

Arguments

`verbose`	for debug use

Value

In-browser Shiny Application launch

Examples

```
if(interactive()){launchSeuratExplorer()}
```

`server` *Server*

Description

Server

Usage

```
server(input, output, session)
```

Arguments

`input`	Input from the UI
`output`	Output to send back to UI
`session`	from shiny server function

Value

the server functions of shiny app

`top_genes` *Find Top Genes by Cell*

Description

for each cell, find genes that has high UMI percentage, for example, if a cell has 10000 UMIs, and the UMI percentage cutoff is set to 0.01, then all genes that has more than 10000 * 0.01 = 100 UMIs is thought to be the highly expressed genes for this cell.summary those genes for each cluster, firstly get all highly expressed genes in a cluster, some genes may has less cells, then for each gene, count cells in which this genes is highly expressed, and also calculate the mean and median UMI percentage in those highly expressed cells.

Usage

```
top_genes(SeuratObj, expr.cut = 0.01, group.by)
```

Arguments

`SeuratObj`	Seurat object
`expr.cut`	UMI percentage cutoff, in a cell, if a gene with UMIs ratio more than this cutoff, this gene will be assigned to highly expressed gene for this cell
`group.by`	how to group cells

Value

a data frame

`ui` *UI*

Description

UI

Usage

```
ui()
```

Value

the UI part of the shiny app

Examples

```
ui()
```

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