

Package ‘SeuratExplorer’

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

Version 0.1.8

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.

License GPL (>= 3)

URL <https://CRAN.R-project.org/package=SeuratExplorer>,
<https://github.com/fentouxngui/SeuratExplorer>

BugReports <https://github.com/fentouxngui/SeuratExplorer/issues>

Encoding UTF-8

RoxygenNote 7.3.3

Imports utils, tools, stats, methods, Seurat (>= 5.4.0), SeuratObject (>= 5.3.0), ggplot2 (>= 4.0.1), shinydashboard, DT, shinycssloaders, colourpicker, shinyWidgets, scales, shinyjqui, shinyBS, ggalluvial, dplyr, qs2, circlize, reshape2, knitr, markdown, shinyjs, rlang

Depends R (>= 4.1.0), shiny

Suggests ComplexHeatmap, patchwork (>= 1.3.2), MAST, limma, DESeq2, Signac

NeedsCompilation no

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cellRatioPlot	<i>plot cell percentage barplot</i>
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Description

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

Usage

```
cellRatioPlot(  
  object = NULL,  
  idents = 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
- idents idents used, default all idents
- 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	<i>generate the body UI for each menu item specified in explorer_sidebar_ui</i>
------------------	---

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
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Value

a filled tag list for body UI

Examples

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

explorer_server	<i>server side functions related to explorer_sidebar_ui</i>
-----------------	---

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	<i>some menu items of the dashboard sidebar</i>
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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 = "default", n = NULL)
```

Arguments

<code>color.platte</code>	predefined color list
<code>choice</code>	color name
<code>n</code>	how many colors to return

Value

a color list

Examples

```
# null
```

`get_counts_matrix`*Helper function to extract counts matrix with proper handling*

Description

Helper function to extract counts matrix with proper handling

Usage

```
get_counts_matrix(SeuratObj, assay = "RNA")
```

Arguments

<code>SeuratObj</code>	A Seurat object
<code>assay</code>	Assay name

Value

A counts matrix

get_data_matrix	<i>Helper function to extract data matrix with proper handling</i>
-----------------	--

Description

Helper function to extract data matrix with proper handling

Usage

```
get_data_matrix(SeuratObj, assay = "RNA")
```

Arguments

SeuratObj	A Seurat object
assay	Assay name

Value

A data matrix

join_layers_if_needed	<i>Helper function to join layers for Assay5 objects</i>
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Description

Helper function to join layers for Assay5 objects

Usage

```
join_layers_if_needed(SeuratObj, assay = "RNA")
```

Arguments

SeuratObj	A Seurat object
assay	Assay name

Value

Seurat object with joined layers

launchSeuratExplorer *Launch shiny app*

Description

used to launch the shiny app in a web browser.

Usage

```
launchSeuratExplorer(
  verbose = FALSE,
  ReductionKeyWords = c("umap", "tsne", "pca"),
  SplitOptionMaxLevel = 12,
  MaxInputFileSize = 20 * 1024^3
)
```

Arguments

verbose for debug use

ReductionKeyWords key words used for prepare Reduction options

SplitOptionMaxLevel max level cutoff for prepare Split options

MaxInputFileSize set the limited upload file size

Value

In-browser Shiny Application launch

Examples

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

param_group_collapse *Create a collapsible parameter group for Plot Settings*

Description

Creates a styled, collapsible parameter group for the Plot Settings sidebar. Clicking the header toggles visibility of the content area. The group preserves the existing color-coded left border styling.

Usage

```
param_group_collapse(id, title, icon_name, color = "#3b82f6", ...)
```

Arguments

id	A unique identifier for the collapse target (used as the div ID).
title	Character string for the group header title.
icon_name	Character string passed to <code>shiny::icon()</code> .
color	Hex color string for the left border and title accent. Default: "#3b82f6".
...	UI elements to place inside the collapsible content area. Groups always start expanded.

Value

A `shiny.tag` div representing the collapsible parameter group.

`prepare_gene_annotations`

extract the features from row names or annotation slot of assays

Description

extract the features from row names or annotation slot of assays

Usage

```
prepare_gene_annotations(obj, verbose = FALSE)
```

Arguments

obj	a Seurat object
verbose	whether output messages

Value

a list with `data.frames`

Examples

```
#NULL
```

server	<i>Server</i>
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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	<i>Find Top Genes by Cell</i>
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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, percent.cut = 0.01, group.by, assay = "RNA")

Arguments

SeuratObj	Seurat object
percent.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
assay	which assay used

Value

a data frame

<code>ui</code>	<i>UI</i>
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Description

UI

Usage

`ui()`

Value

the UI part of the shiny app

Examples

`ui()`

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