Package 'SeuratExplorer'

January 19, 2026

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

Version 0.1.2

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/fentouxungui/SeuratExplorer

BugReports https://github.com/fentouxungui/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, shinydashboardPlus, DT, shinycssloaders, patchwork (>= 1.3.2), colourpicker, shinyWidgets, scales, shinyjqui, shinyBS, ggalluvial, dplyr, qs2, circlize, reshape2, knitr, markdown

Depends R (>= 4.1.0), shiny

Suggests ComplexHeatmap, MAST, limma, DESeq2, Signac

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,
  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` *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 = "default", n = NULL)
```

Arguments

`color.platte`	predefined color list
`choice`	color name
`n`	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

`SeuratObj`	A Seurat object
`assay`	Assay name

Value

A counts matrix

get_data_matrix *Helper function to extract data matrix with proper handling*

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 *Helper function to join layers for Assay5 objects*

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

Launch shiny app

Usage

```
launchSeuratExplorer(
  verbose = FALSE,
  ReductionKeyWords = c("umap", "tsne"),
  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()}
```

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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 *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, 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

ui *UI*

Description

UI

Usage

```
ui()
```

Value

the UI part of the shiny app

Examples

```
ui()
```

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