

Package ‘geyser’

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Title Gene Expression displaYer of SummarizedExperiment in R

Version 1.5.0

Description Lightweight Expression displaYer (plotter / viewer) of SummarizedExperiment object in R. This package provides a quick and easy Shiny-based GUI to empower a user to use a SummarizedExperiment object to view

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LazyData false

biocViews Software, ShinyApps, GUI, GeneExpression

Imports bslib (>= 0.6.0), BiocStyle, ComplexHeatmap, cowplot, dplyr, DT, ggbeeswarm, ggplot2, ggrepel, ggh4x, htmltools, magrittr, pals, RColorBrewer, rlang, R.utils, shiny, shinyjs, S4Vectors, SummarizedExperiment, tibble, tidyselect, tidy, yaml

Suggests airway, knitr, DESeq2, rmarkdown, stringr, testthat (>= 3.0.0)

Config/testthat/edition 3

VignetteBuilder knitr

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BugReports <https://github.com/davemcg/geyser/issues>

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.exp_plot	<i>exp_plot</i>
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Description

draws the expression box plot

Usage

```
.exp_plot(input, rse, data_source_name)
```

Arguments

input	From ui.R
rse	The rse object
data_source_name	The name of the loaded dataset for the caption

Details

Makes the box plot for the geyser Shiny app

Value

Returns a list with the \$plot slot holding ggplot object and \$grouping_length contains the number of features to scale the plot

Author(s)

David McGaughey

Examples

```
load(system.file('extdata/tiny_rse.Rdata', package = 'geyser'))
input <- list()
input$feature_col <- "row names"
input$features <- c("TYRP1 (ENSG00000107165.12)", "OPN1LW (ENSG00000102076.9)")
input$groupings <- c('disease')
input$slot <- 'counts'
input$expression_scale <- TRUE
input$color_by <- 'tissue'
input$color_palette <- 'polychrome'
input$show_points <- TRUE
geyser:::exp_plot(input, tiny_rse, "tiny_rse.Rdata")$plot
```

*.hm_plot**hm_plot*

Description

draws the expression heatmap

Usage

```
.hm_plot(input, rse, data_source_name)
```

Arguments

<code>input</code>	From ui.R
<code>rse</code>	rse object
<code>data_source_name</code>	The name of the loaded dataset for the caption

Details

Makes the heatmap for the geysers Shiny app

Value

Returns a ComplexHeatmap object

Author(s)

David McGaughey

Examples

```
load(system.file('extdata/tiny_rse.Rdata', package = 'geyser'))
input <- list()
input$feature_col <- 'row names'
input$features <- c("TYRP1 (ENSG00000107165.12)", "OPN1LW (ENSG00000102076.9)")
input$groupings <- c('disease')
input$slot <- 'counts'
input$expression_scale <- TRUE
input$row_clust <- TRUE
```

```
input$col_clust <- TRUE
geyser:::hm_plot(input, tiny_rse, "tiny_rse.Rdata")$plot
```

`apply_config`*Configuration Helper Functions for Geyser*

Description

Functions to handle loading, saving, and applying configurations

Apply a configuration to the Shiny session

Usage

```
apply_config(config, session, rv)
```

Arguments

<code>config</code>	List containing configuration parameters
<code>session</code>	Shiny session object
<code>rv</code>	reactiveValues object containing app state

`apply_embedded_config` *Apply embedded config from SummarizedExperiment if present*

Description

Apply embedded config from SummarizedExperiment if present

Usage

```
apply_embedded_config(rse, session, rv)
```

Arguments

<code>rse</code>	SummarizedExperiment object
<code>session</code>	Shiny session object
<code>rv</code>	reactiveValues object

`apply_pending_group_filters`*Apply pending group filters to dynamic UI*

Description

Apply pending group filters to dynamic UI

Usage

```
apply_pending_group_filters(rv, input, session)
```

Arguments

<code>rv</code>	reactiveValues object
<code>input</code>	Shiny input object
<code>session</code>	Shiny session object

`apply_pending_sample_filter`*Apply pending sample filter to table*

Description

Apply pending sample filter to table

Usage

```
apply_pending_sample_filter(rv, input)
```

Arguments

<code>rv</code>	reactiveValues object
<code>input</code>	Shiny input object

`create_config_download_handler`*Create configuration download handler*

Description

Create configuration download handler

Usage

```
create_config_download_handler(input)
```

Arguments

<code>input</code>	Shiny input object
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```
extract_config_from_metadata
```

Extract geyser config from SummarizedExperiment metadata

Description

Extract geyser config from SummarizedExperiment metadata

Usage

```
extract_config_from_metadata(rse)
```

Arguments

`rse` SummarizedExperiment object

Value

List containing config or NULL if not found

```
geyser
```

geyser

Description

Run shiny app to use SummarizedExperiment object to display genomics data

Usage

```
geyser(
  rse = NULL,
  app_name = "geyser",
  primary_color = "#3A5836",
  secondary_color = "#d5673e",
  computer_data_dir = NULL
)
```

Arguments

`rse` SummarizedExperiment object. If NULL (the default), the app will start with a file upload screen.

`app_name` Title name that goes on the top left of the Shiny app

`primary_color` The title bar color

`secondary_color` The plot action button color

`computer_data_dir` Optional folder path to existing SummarizedExperiment RDS files.

Value

A Shiny app object

Examples

```
if (interactive()) {  
  load(system.file('extdata/tiny_rse.Rdata', package = 'geyser'))  
  geyser(tiny_rse, "Test RSE")  
}
```

setup_config_preset_observer

Setup configuration preset observer

Description

Setup configuration preset observer

Usage

```
setup_config_preset_observer(input, session, rv)
```

Arguments

input	Shiny input object
session	Shiny session object
rv	reactiveValues object

setup_config_upload_observer

Setup configuration upload observer

Description

Setup configuration upload observer

Usage

```
setup_config_upload_observer(input, session, rv)
```

Arguments

input	Shiny input object
session	Shiny session object
rv	reactiveValues object

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