

Package ‘geyser’

July 9, 2025

Title Gene Expression displaYer of SummarizedExperiment in R

Version 1.1.0

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 (gene) expression grouped from the sample metadata columns (in the `colData` slot). Feature expression can either be viewed with a box plot or a heatmap.

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LazyData false

biocViews Software, ShinyApps, GUI, GeneExpression

Imports bslib (>= 0.6.0), BiocStyle, ComplexHeatmap, dplyr, DT, ggbeeswarm, ggplot2, htmltools, magrittr, shiny, SummarizedExperiment, tibble, tidyselect, tidy

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Suggests airway, knitr, DESeq2, recount3, rmarkdown, stringr, testthat (>= 3.0.0)

Config/testthat/edition 3

VignetteBuilder knitr

URL <https://github.com/davemcg/geyser>

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

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Contents

<code>.exp_plot</code>	2
<code>.hm_plot</code>	3
<code>geyser</code>	4
Index	5

<code>.exp_plot</code>	<i>exp_plot</i>
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Description

draws the expression box plot

Usage

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

Arguments

<code>input</code>	From ui.R
<code>rse</code>	The rse object
<code>slot</code>	which slot to pull the count data from the rse assay

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'
geyser:::exp_plot(input, tiny_rse, 'counts')$plot
```

<i>.hm_plot</i>	<i>hm_plot</i>
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Description

draws the expression heatmap

Usage

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

Arguments

<code>input</code>	From ui.R
<code>rse</code>	rse object
<code>slot</code>	which slot to pull the count data from the rse assay

Details

Makes the heatmap for the geyser 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$col_clust <- TRUE
geyser:::hm_plot(input, tiny_rse, 'counts')$plot
```

*geyser**geyser*

Description

Run shiny app to use SummarizedExperiment object to display genomics data

Usage

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

Arguments

<code>rse</code>	SummarizedExperiment object
<code>app_name</code>	Title name that goes on the top left of the Shiny app
<code>primary_color</code>	The title bar color
<code>secondary_color</code>	The plot action button color

Details

Shiny app uses the `rowData` rownames to define the genes. The `colData` field is made fully available to make custom plot groupings.

Value

Shiny app

Author(s)

David McGaughey

Examples

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

Index

- * **internal**
 - .exp_plot, [2](#)
 - .hm_plot, [3](#)
- .exp_plot, [2](#)
- .hm_plot, [3](#)
- geyser, [4](#)