

# Package ‘geyser’

April 17, 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.

**License** CC0

**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>

**git\_url** <https://git.bioconductor.org/packages/geyser>

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## Contents

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

<b>Index</b>	<b>5</b>
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<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
```

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.hm\_plot                      *hm\_plot*

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### Description

draws the expression heatmap

### Usage

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

### Arguments

input	From ui.R
rse	rse object
slot	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
```

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`geyser``geyser`

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## 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