

# Package ‘geyser’

April 10, 2025

**Title** Gene Expression displaYer of SummarizedExperiment in R

**Version** 0.99.8

**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, tidyr

**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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.exp_plot	<i>exp_plot</i>
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### Description

draws the expression box plot

### Usage

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

### Arguments

input	From ui.R
rse	The rse object
slot	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	<i>geyser</i>
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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**

rse	SummarizedExperiment object
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

**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)  
}
```

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\* **internal**

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