

Package: geyser (via r-universe)

January 16, 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.

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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, 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>

Config/pak/sysreqs make libicu-dev libpng-dev libssl-dev perl zlib1g-dev

Repository <https://bioc.r-universe.dev>

RemoteUrl <https://github.com/bioc/geyser>

RemoteRef HEAD

RemoteSha 437a52d847cbcd7f8f896e8f6335af9251a3774a

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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)

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Examples

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

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