Package ‘geyser’

April 21, 2025

Title Gene Expression displaYer of SummarizedExperiment in R

Version 1.0.0

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, 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`

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Contents

`.exp_plot` *exp_plot*

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
```

`.hm_plot` *hm_plot*

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
```

`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

`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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