

Package ‘interactiveDisplayBase’

October 18, 2022

Type Package

Title Base package for enabling powerful shiny web displays of
Bioconductor objects

Version 1.34.0

Date 2021-07-30

Imports shiny, DT

Depends R (>= 2.10), methods, BiocGenerics

Suggests knitr, markdown

Enhances rstudioapi

Description The interactiveDisplayBase package contains the the basic
methods needed to generate interactive Shiny based display
methods for Bioconductor objects.

License Artistic-2.0

Collate interactiveDisplayBase.R dataframe.R dot_runApp.R zzz.R

VignetteBuilder knitr

biocViews GO, GeneExpression, Microarray, Sequencing, Classification,
Network, QualityControl, Visualization, Visualization,
Genetics, DataRepresentation, GUI, AnnotationData

RoxygenNote 7.1.1

git_url <https://git.bioconductor.org/packages/interactiveDisplayBase>

git_branch RELEASE_3_15

git_last_commit fafbb13

git_last_commit_date 2022-04-26

Date/Publication 2022-10-18

Author Bioconductor Package Maintainer [cre],
Shawn Balcome [aut],
Marc Carlson [ctb],
Marcel Ramos [ctb]

Maintainer Bioconductor Package Maintainer <maintainer@bioconductor.org>

R topics documented:

| | |
|-------------------|---|
| .runApp | 2 |
| display | 3 |

| | |
|--------------|----------|
| Index | 5 |
|--------------|----------|

| | |
|---------|--|
| .runApp | <i>Run a shiny app, capturing results to the R session</i> |
|---------|--|

Description

This utility function launches a shiny visualization application, either in the RStudio viewer pane (if run under RStudio) or in the browser.

Usage

```
.runApp(app, ...)
```

Arguments

| | |
|-----|---|
| app | The shiny application definition, see ?shiny::runApp. |
| ... | additional arguments passed to shiny::runApp(). |

Value

The return value of shiny::runApp.

Author(s)

Martin Morgan

Examples

```
if (interactive()) {
  require(shiny)

  app <- list(
    ui = fluidPage(
      title="Who Am I?",
      sidebarLayout(
        position="left",
        sidebarPanel(
          h1("Your name"),
          textInput("your_name", "Your name?", "Anonymous"),
          actionButton("done", "Done")),
        mainPanel(
          "Hi", textOutput("your_name", inline=TRUE))
      )),
  )
```

```
server = function(input, output) {
  output$your_name <- renderText(input$your_name)
  observe({
    if (input$done > 0)
      isolate(stopApp(returnValue = input$your_name))
  })
})

.runApp(app)
}
```

display

display: Open a Shiny application for a Bioconductor object

Description

This opens a shiny visualization application in the browser based on the submitted object.

Usage

```
display(object, ...)
```

Arguments

| | |
|--------|---|
| object | data object to display |
| ... | additional arguments passed to methods; currently unused. |

Value

Usually some variation of the initial input object, but it may be altered by the display widget (subset for example).

Author(s)

Shawn Balcome and Marc Carlson

See Also

<http://bioconductor.org/packages/2.13/bioc/html/interactiveDisplayBase.html>

Examples

```
if(interactive()) {
  ## draw a data.frame
  display(mtcars)

  ## subset a data.frame:
```

4

display

```
mtcars2 <- display(mtcars)
```

```
}
```

Index

* **manip, internal**

[.runApp, 2](#)

* **methods**

[display, 3](#)

[.runApp, 2](#)

[display, 3](#)

[display, ANY-method \(display\), 3](#)

[display, data.frame-method \(display\), 3](#)

[display, missing-method \(display\), 3](#)