

Package ‘interactiveDisplayBase’

April 12, 2018

Type Package

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

Version 1.16.0

Date 2014-09-09

Author Shawn Balcome, Marc Carlson

Maintainer Shawn Balcome <balc0022@umn.edu>

Imports shiny

Depends R (>= 2.10), methods, BiocGenerics

Suggests knitr

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

NeedsCompilation no

R topics documented:

.runApp 2
display 3

Index 4

`.runApp`*Run a shiny app, capturing results to the R session*

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

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

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

| | |
|---------------------|---|
| <code>object</code> | data object to display |
| <code>...</code> | 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:
  mtcars2 <- display(mtcars)

}
```

Index

*Topic **manip**

.runApp, [2](#)

*Topic **methods**

display, [3](#)

.runApp, [2](#)

display, [3](#)

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

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

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