

Package: interactiveDisplayBase (via r-universe)

June 30, 2024

Type Package

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

Version 1.43.0

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, ShinyApps

RoxygenNote 7.1.1

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

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

RemoteRef HEAD

RemoteSha 4c333d5cee9858a4562a30dcd8e9483e1286d4c1

Contents

.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

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:  
  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](#)