

# Package ‘interactiveDisplayBase’

December 7, 2023

**Type** Package

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

**Version** 1.41.0

**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

**git\_url** <https://git.bioconductor.org/packages/interactiveDisplayBase>

**git\_branch** devel

**git\_last\_commit** 6c22db7

**git\_last\_commit\_date** 2023-10-24

**Repository** Bioconductor 3.19

**Date/Publication** 2023-12-07

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

**Maintainer** Bioconductor Package Maintainer <maintainer@bioconductor.org>

## Table of contents:

.runApp . . . . .	2
display . . . . .	3
<b>Index</b>	<b>5</b>

---

.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](#)