

# Package ‘interactiveDisplayBase’

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**Type** Package

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

**Version** 1.20.0

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**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

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

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

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### 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*

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**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)

}
```

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