

# Package ‘interactiveDisplayBase’

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**Type** Package

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

**Version** 1.42.0

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**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

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

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

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

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)  
}
```

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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

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:
```

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*display*

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

```
}
```

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