

# Package ‘interactiveDisplayBase’

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**Type** Package

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

**Version** 1.47.1

**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

**PackageStatus** Deprecated

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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

|                     |                                                           |
|---------------------|-----------------------------------------------------------|
| <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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