# Package 'interactiveDisplayBase'

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**Type** Package

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

**Version** 1.44.0

**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

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.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

| | |
|---|---|
| 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:
mtcars2 <- display(mtcars)

}
```

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