

# Package ‘interactiveDisplayBase’

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**Type** Package

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

**Version** 1.6.1

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**Imports** shiny

**Depends** R (>= 2.10), methods, BiocGenerics

**Suggests** knitr

**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' 'zzz.R'

**VignetteBuilder** knitr

**biocViews** GO, GeneExpression, Microarray, Sequencing, Classification,  
Network, QualityControl, Visualization, Visualization,  
Genetics, DataRepresentation, GUI, AnnotationData

**NeedsCompilation** no

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

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