

Package ‘interactiveDisplayBase’

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Type Package

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

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Imports shiny

Depends R (>= 2.10), methods, BiocGenerics

Suggests knitr

Enhances rstudio

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

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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)

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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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