Package ‘interactiveDisplay’

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Type Package
Title Package for enabling powerful shiny web displays of Bioconductor objects
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Depends R (>= 2.10), methods, BiocGenerics, grid
Suggests RUnit, hgu95av2.db, knitr, GenomicRanges, SummarizedExperiment, GOstats, ggbio, GO.db, Gviz, rtracklayer, metagenomeSeq, gplots, vegan, Biobase
Enhances rstudio
Description The interactiveDisplay package contains the methods needed to generate interactive Shiny based display methods for Bioconductor objects.
License Artistic-2.0
VignetteBuilder knitr
biocViews GO, GeneExpression, Microarray, Sequencing, Classification, Network, QualityControl, Visualization, Visualization, Genetics, DataRepresentation, GUI, AnnotationData, ShinyApps
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altgr

Description
This opens a shiny visualization application in the browser based on ...

Usage

altgr(object, ...)

Arguments

object data object to display
... additional arguments passed to methods; currently unused.

Value
Any ...

See Also

bicgo

Examples

if(interactive()) {

## Open an browser application for the purpose of manually biclustering an
## ExpressionSet object and obtaining a GO summary for a specific bicluster.

data(mmgr)
altgr(mmgr)

}

bicgo: Open a Shiny Application for manual/interactive biclustering
and GO exploration

Description

This opens a shiny visualization application in the browser based on the submitted ExpressionSet
object.

Usage

bicgo(object, ...)

Arguments

object     data object to display
...        additional arguments passed to methods; currently unused.

Value

Any ExpressionSet object.

See Also


Examples

if(interactive()) {

## Open a browser application for the purpose of manually biclustering an
## ExpressionSet object and obtaining a GO summary for a specific bicluster.

data(expr)
bicgo(expr)

}
display

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

Examples
if(interactive()) {

  ## draw a RangedSummarizedExperiment object
  data(se)
  display(se)

  ## draw a GRanges object
  data(mmgr)
  display(mmgr)

  ## some display methods allow subsetting.
  ## To take advantage, just use an assignment operator like this:
  mmgr2 <- display(mmgr)

  ## draw a GRangesList object
  data(mmgrl)
  display(mmgrl)
## draw an ExpressionSet object

data(expr)
display(expr)

## draw an MRexperiment object (placeholder!!)

data(mr)
display(mr)

}
gridtweak

gridtweak: Open a Shiny Application for the purpose of tweaking grid plots

Description

This opens a shiny visualization application in the browser.

Usage

gridtweak(...)

Arguments

... additional arguments passed to methods; currently unused.

Value

Any grid based plot. For example: a plot produced with lattice, ggplot2 or biobase libraries.

See Also


Examples

if(interactive()) {
  ## Send a grid based plot to a browser as a Javascript interactive SVG
  library(ggplot2)
  data(mtcars)
  qp <- qplot(mpg, data=mtcars, geom="density", fill=factor(cyl), alpha=I(.4))
  gridsvgjs(qp)
}
Examples

```r
if(interactive()) {

  ## Send a grid based plot to a browser as a Javascript interactive SVG
  gridtweak()
}
```

---

**mmgr**

*An Example GRanges Object*

**Description**

A toy GRanges object for demonstration purposes.

**Examples**

```r
data(mmgr)
```

---

**mmgrl**

*An Example GRangesList Object*

**Description**

A toy GRangesList dataset derived from the GRanges dataset in this package for purposes of demonstration.

**Details**

The GRanges dataset was submitted to `display()`, subsetted and several iterations of the results were fused into a GRangesList object. This is fake data.

**Examples**

```r
data(mmgrl)
```

---

**se**

*An Example RangedSummarizedExperiment Object*

**Description**

A toy RangedSummarizedExperiment object for demonstration purposes.

**Examples**

```r
data(se)
```
simplenet

simplenet: Open a Shiny Application for ...

Description
This opens a shiny visualization application in the browser based on ...

Usage
simplenet(object, ...)

Arguments
object
data object to display
...
additional arguments passed to methods; currently unused.

Value
Any ...

See Also

Examples
if(interactive()) {

## Open an browser application for the purpose of manually biclustering an
## ExpressionSet object and obtaining a GO summary for a specific bicluster.

simplenet(mtcars)

}
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