Package ‘interactiveDisplay’

December 21, 2016

Type Package

Title Package for enabling powerful shiny web displays of Bioconductor objects

Version 1.12.0

Date 2015-06-16

Author Shawn Balcome, Marc Carlson

Maintainer Shawn Balcome <balc0022@umn.edu>

Imports interactiveDisplayBase (>= 1.7.3), shiny, RColorBrewer,
    ggplot2, reshape2, plyr, gridSVG, XML, Category, AnnotationDbi

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

Collate 'interactiveDisplay.R' 'ExpressionSet.R' 'GRanges.R'
    'GRangesList.R' 'SummarizedExperiment.R' 'gridsvgjs.R'
    'bicgo.R' 'gridtweak.R' 'simplenet.R' 'MRexperiment.R'
    'altgr.R' 'zzz.R'

VignetteBuilder knitr

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

NeedsCompilation no

R topics documented:

altgr ................................................................. 2
bicgo ............................................................. 3
display ........................................................... 3
expr ................................................................. 5
gridsvgjs .......................................................... 5
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

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
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 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, ...)

display

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)

}
expr

---

**expr**  
_An Example ExpressionSet object_

**Description**

The expression data are real but anonymized. The data are from an experiment that used Affymetrix U95v2 chips. The data were processed by dChip and then exported to R for analysis. The data illustrate ExpressionSet-class, with assayData containing the required matrix element exprs and an additional matrix se.exprs. se.exprs has the same dimensions as exprs. The phenoData and standard error estimates (se.exprs) are made up. The information in the "description" slot is fake.

**Details**

The data for 26 cases, labeled A to Z and 500 genes. Each case has three covariates: sex (male/female); type (case/control); and score (testing score).

**Examples**

```r
data(expr)
```

---

**gridsvgjs**  
_gridsvgjs: Open a Shiny Application for a Grid Plot_

**Description**

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

**Usage**

```r
gridsvgjs(object, ...)
```

**Arguments**

- `object`  
data object to display  
- `...`  
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

```r
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)
}
```

Description

This opens a shiny visualization application in the browser.

Usage

```r
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

```r
if(interactive()) {

## Send a grid based plot to a browser as a Javascript interactive SVG

gridtweak()

}```
An Example GRanges Object

Description

A toy GRanges object for demonstration purposes.

Examples

data(mmgr)

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

data(mmgrl)

An Example RangedSummarizedExperiment Object

Description

A toy RangedSummarizedExperiment object for demonstration purposes.

Examples

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

```r
if(interactive()) {
  ## Open a browser application for the purpose of manually biclustering an
  ## ExpressionSet object and obtaining a GO summary for a specific bicluster.
  simplenet(mtcars)
}
```
Index

«Topic datasets
  expr, 5
  mmgr, 7
  mmgrl, 7
  se, 7
» Topic methods
  altgr, 2
  bicgo, 3
  display, 3
  gridsvgjs, 5
  gridtweak, 6
  simplenet, 8

altgr, 2
altgr, ANY-method (altgr), 2
bicgo, 3
bicgo, ANY-method (bicgo), 3
display, 3
display, ANY-method (display), 3
display, ExpressionSet-method (display), 3
display, GRanges-method (display), 3
display, GRangesList-method (display), 3
display, missing-method (display), 3
display, MRexperiment-method (display), 3
display, RangedSummarizedExperiment-method (display), 3
expr, 5

gridsvgjs, 5
gridsvgjs, ANY-method (gridsvgjs), 5
gridtweak, 6
gridtweak, ANY-method (gridtweak), 6

mmgr, 7
mmgrl, 7

se, 7
simplenet, 8
simplenet, ANY-method (simplenet), 8