Package ‘interactiveDisplay’

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Type Package

Title Package for enabling powerful shiny web displays of Bioconductor objects

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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.

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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, ShinyApps

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Author Bioconductor Package Maintainer [cre],
Shawn Balcome [aut],
Marc Carlson [ctb]

Maintainer Bioconductor Package Maintainer <maintainer@bioconductor.org>

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`altgr` *altgr: Open a Shiny Application for ...*

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

http://bioconductor.org/packages/2.13/bioc/html/interactiveDisplay.html

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

http://bioconductor.org/packages/2.13/bioc/html/interactiveDisplay.html

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(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, ...)
```

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/interactiveDisplay.html

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` *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

```
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

```
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

http://bioconductor.org/packages/2.13/bioc/html/interactiveDisplay.html

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)

}
```

---

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

http://bioconductor.org/packages/2.13/bioc/html/interactiveDisplay.html

Examples

```
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

```
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

```
data(mmgrl)
```

---

se *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

http://bioconductor.org/packages/2.13/bioc/html/interactiveDisplay.html

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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