

# Package ‘interactiveDisplay’

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**Type** Package

**Title** Package for enabling powerful shiny web displays of Bioconductor objects

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**Author** Shawn Balcome, Marc Carlson

**Maintainer** Shawn Balcome <balc0022@umn.edu>

**Imports** shiny, GenomicRanges, Gviz, RColorBrewer, ggplot2, reshape2, tracklayer, GO.db, plyr, gridSVG, XML

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

**Suggests** RUnit, hgu95av2.db, knitr

**Description** The interactiveDisplay package contains the methods needed to generate interactive Shiny based display methods for Bioconductor objects.

**License** Artistic-2.0

**biocViews** GO GeneExpression Microarray Sequencing Classification  
Networks QualityControl Visualization NetworkVisualization  
Genetics DataRepresentation GUI AnnotationData

**Collate** 'interactiveDisplay.R' 'ExpressionSet.R' 'GRanges.R'  
'GRangesList.R' 'SummarizedExperiment.R' 'gridsvgjs.R'

**VignetteBuilder** knitr

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display	<i>display: Open a Shiny application for a Bioconductor object</i>
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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).

**See Also**

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

**Examples**

```
if(interactive()) {  
  
  ## draw a SummarizedExperiment object  
  data(se)  
  display(se)  
  
  ## draw a GRanges object  
  data(mmgr)  
  display(mmgr)  
  
  ## draw a GRangesList object  
  data(mmgrl)  
  display(mmgrl)  
  
  ## draw an ExpressionSet object  
  data(expr)  
  display(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**

```
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**

<code>object</code>	a grid based plot to display in browser
<code>...</code>	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)  
  
}
```

---

mmgr

*An Example GRanges Object*

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## 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 SummarizedExperiment Object*

---

**Description**

A toy SummarizedExperiment object for demonstration purposes.

**Examples**

```
data(se)
```

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