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, DT

Depends R (>= 2.10), methods, BiocGenerics

Suggests knitr, markdown

Enhances rstudioapi

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 dot_runApp.R zzz.R

VignetteBuilder knitr

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

RoxygenNote 7.1.1

PackageStatus Deprecated

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.runApp *Run a shiny app, capturing results to the R session*

Description

This utility function launches a shiny visualization application, either in the RStudio viewer pane (if run under RStudio) or in the browser.

Usage

```
.runApp(app, ...)
```

Arguments

app	The shiny application definition, see ?shiny::runApp.
...	additional arguments passed to shiny::runApp().

Value

The return value of shiny::runApp.

Author(s)

Martin Morgan

Examples

```
if (interactive()) {
    require(shiny)

    app <- list(
        ui = fluidPage(
          title="Who Am I?",
          sidebarLayout(
              position="left",
              sidebarPanel(
                  h1("Your name"),
                  textInput("your_name", "Your name?", "Anonymous"),
                  actionButton("done", "Done")),
              mainPanel(
                  "Hi", textOutput("your_name", inline=TRUE))
              )),

        server = function(input, output) {
            output$your_name <- renderText(input$your_name)
            observe({
                if (input$done > 0)
```

```
                    isolate(stopApp(returnValue = input$your_name))
                })

            })

        .runApp(app)
    }
```

`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/interactiveDisplayBase.html

Examples

```
if(interactive()) {

## draw a data.frame
display(mtcars)

## subset a data.frame:
mtcars2 <- display(mtcars)

}
```

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