Package 'shinybiocloader'

February 21, 2026

Title Use a Shiny Bioconductor CSS loader

Version 1.0.0

Description Add a Bioconductor themed CSS loader to your shiny app. It is based on the shinycustomloader R package. Use a spinning Bioconductor note loader to enhance your shiny app loading screen. This package is intended for developer use.

Depends htmltools

Imports shiny

Suggests shinydashboard, tinytest, quarto

VignetteBuilder quarto

SystemRequirements quarto

biocViews Software, Infrastructure, GUI

License Artistic-2.0

BugReports https://github.com/Bioconductor/shinybiocloader/issues

URL https://github.com/Bioconductor/shinybiocloader

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Author Marcel Ramos [aut, cre] (ORCID: <https://orcid.org/0000-0002-3242-0582>)

Maintainer Marcel Ramos <marcel.ramos@sph.cuny.edu>

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withLoader   *Add a loader to a Shiny UI element*

Description

Add a loader to a Shiny UI element

Usage

```
withLoader(ui_element, loader = "biocspin", proxy.height = "400px")
```

Arguments

ui_element   A Shiny UI element (e.g., uiOutput, plotOutput, etc.) for which to wrap with
                the loader.

loader   character(1) A string specifying the loader type. Default is "biocspin".

proxy.height   character(1) A string specifying the height of the proxy element. Default is
                "400px". If the ui_element already has a height specified, this will be set to
                "100%".

Value

A Shiny UI element wrapped with the Bioconductor loader

References

shinycustomloader https://github.com/emitanaka/shinycustomloader
dna spin https://codepen.io/knut/pen/ZopMWW

Examples

```
library(shiny)
library(shinydashboard)
library(shinybiocloader)

waitHist <- function() {
  waiting <- faithful[["waiting"]]
  Sys.sleep(3)  # Simulate loading
  hist(
    waiting, col = 'darkgray', border = 'white',
    main = 'Old Faithful Geyser Waiting Times Histogram',
    xlab = 'Waiting Time (min)'
  )
}

ui <- dashboardPage(
  dashboardHeader(title = "Bioconductor Loader"),
  dashboardSidebar(disable = TRUE),
  dashboardBody(
    h2("Bioconductor Spinning Loader"),
    HTML(
      paste0(
        "<pre><code class='language-r'>",
```

```
          "withLoader(plotOutput('distPlot'), loader='biocspin')",
          "</code></pre>"
      )
    ),
    fluidRow(
      box(
        title = "With Loader", status = "primary", solidHeader = TRUE,
        withLoader(plotOutput("distPlot"), loader = "biocspin")
      ),
      box(
        title = "Without Loader", status = "warning", solidHeader = TRUE,
        plotOutput("distPlot2")
      )
    )
  )
)

server <- function(input, output) {
  output$distPlot <- renderPlot(waitHist())
  output$distPlot2 <- renderPlot(waitHist())
}

shinyApp(ui = ui, server = server)
```

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