Package: shinybiocloader (via r-universe)

May 30, 2026

Title Use a Shiny Bioconductor CSS loader

Version 1.3.0

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`

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Config/pak/sysreqs cmake make libuv1-dev zlib1g-dev

Repository https://bioc.r-universe.dev

Date/Publication 2026-04-28 13:05:28 UTC

RemoteUrl https://github.com/bioc/shinybiocloader

RemoteRef HEAD

RemoteSha 18a48bd93bb7f99a013329dc8d29c50dfcf31b8d

Contents

`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)
```

Index