

Package ‘shinybiocloader’

September 24, 2025

Title Use a Shiny Bioconductor CSS loader

Version 0.99.1

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

git_url <https://git.bioconductor.org/packages/shinybiocloader>

git_branch devel

git_last_commit 7a0f44f

git_last_commit_date 2025-08-19

Repository Bioconductor 3.22

Date/Publication 2025-09-23

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

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

Contents

withLoader	2
Index	4

withLoader	<i>Add a loader to a Shiny UI element</i>
------------	---

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

`withLoader`, [2](#)