Package: BiocHubsShiny (via r-universe)

June 18, 2026

Type Package

Title View AnnotationHub and ExperimentHub Resources Interactively

Version 1.12.0

Description A package that allows interactive exploration of AnnotationHub and ExperimentHub resources. It uses DT / DataTable to display resources for multiple organisms. It provides template code for reproducibility and for downloading resources via the indicated Hub package.

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Encoding UTF-8

Depends R (>= 4.3.0), shiny

Imports AnnotationHub, ExperimentHub, DT, htmlwidgets, rclipboard, S4Vectors, shinyAce, shinybiocloader, shinyjs, shinythemes, utils

Suggests BiocManager, BiocStyle, curl, glue, knitr, rmarkdown, sessioninfo, shinytest2

biocViews Software, ShinyApps

BugReports `https://github.com/Bioconductor/BiocHubsShiny/issues`

URL `https://github.com/Bioconductor/BiocHubsShiny`

VignetteBuilder knitr

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

Date 2025-09-22

Config/pak/sysreqs cmake make libicu-dev libpng-dev libuv1-dev libssl-dev zlib1g-dev

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

Date/Publication 2026-04-28 12:59:43 UTC

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

RemoteRef RELEASE_3_23

RemoteSha 334f695dd85c7a78cad6260f67de8f1c1408df46

Contents

`BiocHubsShiny` *Initialize the shiny application for Bioconductor Hub resources*

Description

The shiny app will allow the user to view a table of either AnnotationHub or ExperimentHub resources depending on the sidebar selection. It provides example code for downloading the selected resources.

Usage

```
BiocHubsShiny(...)
```

Arguments

`...`	Further arguments to the `runApp` function

Details

Note. The code here was adapted from `interactiveDisplayBase` and `?'display,Hub-method'` which are now deprecated.

Value

Mainly called for the side effect of displaying the shiny app in a browser

Examples

```
if (interactive()) {
    BiocHubsShiny()
}
```

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