

Package ‘BiocHubsShiny’

January 29, 2026

Type Package

Title View AnnotationHub and ExperimentHub Resources Interactively

Version 1.10.0

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

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

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

Contents

BiocHubsShiny	2
Index	3

BiocHubsShiny	<i>Initialize the shiny application for Bioconductor Hub resources</i>
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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()
}
```

Index

AnnotationHub, [2](#)

BiocHubsShiny, [2](#)

ExperimentHub, [2](#)