

# Package ‘BiocHubsShiny’

April 15, 2024

**Type** Package

**Title** View AnnotationHub and ExperimentHub Resources Interactively

**Version** 1.2.0

**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.

**License** Artistic-2.0

**Encoding** UTF-8

**Depends** R (>= 4.3.0), shiny

**Imports** AnnotationHub, ExperimentHub, DT, htmlwidgets, S4Vectors, shinyAce, shinyjs, shinythemes, shinytoastr, utils

**Suggests** BiocManager, BiocStyle, 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** 7.2.3

**git\_url** <https://git.bioconductor.org/packages/BiocHubsShiny>

**git\_branch** RELEASE\_3\_18

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**Repository** Bioconductor 3.18

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BioHubsShiny	<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

```
BioHubsShiny(...)
```

### 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()) {
  BioHubsShiny()
}
```

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