

Package ‘BiocHubsShiny’

November 25, 2024

Type Package

Title View AnnotationHub and ExperimentHub Resources Interactively

Version 1.7.1

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, 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

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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>

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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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