

Package: BiocHubsShiny (via r-universe)

July 15, 2024

Type Package

Title View AnnotationHub and ExperimentHub Resources Interactively

Version 1.5.0

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, 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

Date 2024-04-24

Repository <https://bioc.r-universe.dev>

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

RemoteRef HEAD

RemoteSha 6ea0f540d9020843bd93e4750934e2a8fcbd03ac

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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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