Package: BiocHubsShiny (via r-universe)

August 22, 2024

Type Package

Title View AnnotationHub and ExperimentHub Resources Interactively

Version 1.5.1

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.

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

Date 2024-08-22

Repository https://link-ny.r-universe.dev

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

RemoteRef HEAD

RemoteSha da4eb352251da0f349fc9e1700af99589dd8141f

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()
}
```

Index