Package ‘BiocHubsShiny’

May 3, 2024

**Type** Package

**Title** View AnnotationHub and ExperimentHub Resources Interactively

**Version** 1.4.0

**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

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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()
}

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