Package 'iSEEhub'

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Title iSEE for the Bioconductor ExperimentHub

Version 1.14.0

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Description This package defines a custom landing page for an iSEE app interfacing with the Bioconductor ExperimentHub. The landing page allows users to browse the ExperimentHub, select a data set, download and cache it, and import it directly into a Bioconductor iSEE app.

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URL https://github.com/iSEE/iSEEhub

BugReports https://support.bioconductor.org/t/iSEEhub

biocViews DataImport, ImmunoOncology Infrastructure, ShinyApps, SingleCell, Software

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Depends SummarizedExperiment, SingleCellExperiment, ExperimentHub

Imports AnnotationHub, BiocManager, DT, iSEE, methods, rintrojs, S4Vectors, shiny, shinydashboard, shinyjs, utils

Suggests BiocStyle, covr, knitr, RefManageR, rmarkdown, sessioninfo, testthat (>= 3.0.0), nullrangesData

Enhances BioPlex, biscuiteerData, bodymapRat, CLLmethylation, CopyNeutralIMA, curatedAdipoArray, curatedAdipoChIP, curatedMetagenomicData, curatedTCGAData, DMRcatedata, DuoClustering2018, easierData, emtdata, epimutacionsData, FieldEffectCrc, GenomicDistributionsData, GSE103322, GSE13015, GSE62944, HDCytoData, HMP16SData, HumanAffyData, imcdatasets, mcsurvdata, MetaGxBreast, MetaGxOvarian, MetaGxPancreas, MethylSeqData, muscData, NxtIRFdata, ObMiTi, quantiseqr, restfulSEData, RLHub, sesameData, SimBenchData, SingleCellMultiModal, SingleMoleculeFootprintingData, spatialDmelxsim, STexampleData, TabulaMurisData,

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`iSEEhub` *iSEEhub app*

Description

iSEEhub app

Usage

```
iSEEhub(ehub, runtime_install = FALSE)
```

Arguments

`ehub`	An `ExperimentHub()` object.
`runtime_install`	A logical scalar indicating whether the app may allow users whether to install data set dependencies at runtime using `BiocManager::install()` through a modal prompt.

Value

An `iSEE()` app with a custom landing page interfacing with ehub.

Examples

```
library(ExperimentHub)
ehub <- ExperimentHub()

app <- iSEEhub(ehub)

if (interactive()) {
  shiny::runApp(app, port = 1234)
}
```

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