

# Package ‘iSEEhub’

May 17, 2024

**Title** iSEE for the Bioconductor ExperimentHub

**Version** 1.6.0

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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.

**License** Artistic-2.0

**URL** <https://github.com/iSEE/iSEEhub>

**BugReports** <https://support.bioconductor.org/t/iSEEhub>

**biocViews** DataImport, ImmunoOncology Infrastructure, ShinyApps, SingleCell, Software

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.2.1

**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,

TabulaMurisSenisData, TENxVisiumData, tissueTreg,  
VectraPolarisData, xcoredata

**Config/testthat/edition** 3

**VignetteBuilder** knitr

**git\_url** <https://git.bioconductor.org/packages/iSEEhub>

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### 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 <- iSEHub(ehub)

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

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