

# Package: iSEEhub (via r-universe)

June 30, 2024

**Title** iSEE for the Bioconductor ExperimentHub

**Version** 1.7.0

**Date** 2023-07-02

**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, curatedTCGADData, DMRcatedata, DuoClustering2018, easierData, emtdata, epimutationsData, 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

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

**RemoteUrl** <https://github.com/bioc/iSEEhub>

**RemoteRef** HEAD

**RemoteSha** 3b25117ea2fd2bf0b831a75eb0a858aefb07f9c9

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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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