

Package ‘HCADData’

August 21, 2025

Type Package

Title Accessing The Datasets Of The Human Cell Atlas in R/Bioconductor

Version 1.24.0

Description This package allows a direct access to the dataset generated by the Human Cell Atlas project for further processing in R and Bioconductor, in the comfortable format of SingleCellExperiment objects (available in other formats here: <http://preview.data.humancellatlas.org/>).

License MIT + file LICENSE

Encoding UTF-8

biocViews RNASeqData, SingleCellData, ExperimentData, ExpressionData, ExperimentHub

Depends R (>= 3.6), SingleCellExperiment

Imports ExperimentHub, AnnotationHub, HDF5Array, utils

Suggests knitr, rmarkdown, BiocStyle, scran (>= 1.11.4), BiocSingular, scater, scuttle, Rtsne, igraph, iSEE, testthat

URL <https://github.com/federicomarini/HCADData>

VignetteBuilder knitr

RoxygenNote 7.3.2

Roxygen list(markdown = TRUE)

git_url <https://git.bioconductor.org/packages/HCADData>

git_branch RELEASE_3_21

git_last_commit 08c299a

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-08-21

Author Federico Marini [aut, cre] (ORCID:
<<https://orcid.org/0000-0003-3252-7758>>)

Maintainer Federico Marini <marinif@uni-mainz.de>

Contents

HCADData	2
HCADData-pkg	3
Index	4

HCADData	<i>Download data from the HCA via ExperimentHub</i>
----------	---

Description

Download HDF5 (dense assay) and RDS (row and column annotations) files from the HCA via ExperimentHub, composing them together as a SingleCellExperiment object

Usage

```
HCADData(dataset = NULL, as.sparse = TRUE)
```

Arguments

dataset	A character string: which dataset should be retrieved?
as.sparse	Logical, specifies whether the underlying HDF5 dataset should be treated as sparse or not - will be passed to the call to HDF5Array(). Defaults to TRUE, i.e. by using the DelayedArray infrastructure.

Details

This current release includes the following datasets:

Census of Immune Cells - Umbilical cord blood UMI counts from the 10x (droplet) single-cell RNA-seq data. The object contains counts for 33694 genes in 384000 cells.

Census of Immune Cells - Bone marrow UMI counts from the 10x (droplet) single-cell RNA-seq data. The object contains counts for 33694 genes in 378000 cells.

Value

A SingleCellExperiment object with a HDF5Matrix in the counts assay, containing the UMI counts for each gene in each cell. Row- and column-level metadata are also provided.

Examples

```
HCADData()
sce_cordblood <- HCADData("ica_cord_blood")
```

HCADData-pkg*HCADData: Accessing The Datasets Of The Human Cell Atlas in R/Bioconductor*

Description

HCADData is an ExperimentHub package which provides access to the single-cell RNA-seq data from the Human Cell Atlas project (<https://www.humancellatlas.org>)

Author(s)

Federico Marini <marinif@uni-mainz.de>

References

If you use the data in this package, please refer to the original sources (Human Cell Atlas Data Portal, <https://preview.data.humancellatlas.org>) as well (plus the related publications, which will be listed here when they will be out), which are licensed under a Creative Commons Attribution 4.0 International License.

See Also

Useful links:

- <https://github.com/federicomarini/HCADData>

Index

* **internal**

HCADData-pkg, [3](#)

HCADData, [2](#)

HCADData-package (HCADData-pkg), [3](#)

HCADData-pkg, [3](#)