Package 'HCAData'

November 10, 2026

Type Package

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

Version 1.28.0

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/HCAData

VignetteBuilder knitr

RoxygenNote 7.3.2

Roxygen list(markdown = TRUE)

git_url https://git.bioconductor.org/packages/HCAData

git_branch RELEASE_3_23

git_last_commit 76cb236

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-10

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

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

Contents

HCAData 2
HCAData-pkg 3

Index **4**

`HCAData` *Download data from the HCA via ExperimentHub*

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

```
HCAData(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

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

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

Description

HCAData 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/HCAData

Index

∗ **internal**
HCAData-pkg, 3

HCAData, 2
HCAData-package *(*HCAData-pkg*)*, 3
HCAData-pkg, 3