Package 'HCAData'

April 14, 2020

Type Package	
Title Accessing The Datasets Of The Human Cell Atlas in R/Bioconductor	
Version 1.2.0	
Maintainer Federico Marini <marinif@uni-mainz.de></marinif@uni-mainz.de>	
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, igraph, iSEE, testthat	
VignetteBuilder knitr	
RoxygenNote 6.1.1	
git_url https://git.bioconductor.org/packages/HCAData	
git_branch RELEASE_3_10	
git_last_commit ea8dc7b	
git_last_commit_date 2019-10-29	
Date/Publication 2020-04-14	
Author Federico Marini [aut, cre] (https://orcid.org/0000-0003-3252-7758)	
R topics documented:	
HCAData	2 2
Index	4

2 HCAData-pkg

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)
```

Arguments

dataset

A character string: which dataset should be retrieved?

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")</pre>
```

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>

HCAData-pkg 3

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.

Index

 $\label{eq:hcadata} \begin{array}{l} \mbox{HCAData}, \, 2 \\ \mbox{HCAData-pkg}, \, 2 \\ \mbox{HCAData-pkg-package (HCAData-pkg)}, \, 2 \\ \end{array}$