Package ‘SimBenchData’

May 21, 2024

Title  SimBenchData: a collection of 35 single-cell RNA-seq data covering a wide range of data characteristics

Version  1.12.0

Description  The SimBenchData package contains a total of 35 single-cell RNA-seq datasets covering a wide range of data characteristics, including major sequencing protocols, multiple tissue types, and both human and mouse sources.

Depends  ExperimentHub

Imports  S4Vectors, utils

biocViews  ExperimentHub, ExperimentData, SingleCellData, RNASeqData, Tissue, SequencingData

VignetteBuilder  knitr

Suggests  BiocStyle, knitr, rmarkdown, Seurat

License  GPL-3

Encoding  UTF-8

LazyData  true

Roxygen  list(markdown = TRUE)

RoxygenNote  7.1.1

Date  2021-03-02

NeedsCompilation  no

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Additional details on 35 datasets

Description
This shows the additional details for the 35 datasets in the SimBenchData package.

Usage
showAdditionalDetail()

Details
This package contains a total of 35 curated datasets, covering a range of sequencing protocols, tissue types (including different cell lines) and from both mouse and human.

Value
A DataFrame, containing the following fields
- ExperimentHub ID, accession ID.
- Name, short name of this data.
- Species, whether human or mouse.
- Protocol, sequencing protocol.
- Number of cells, number of cells.
- Multiple cell types/conditions ?, whether the dataset contains multiple cell types or conditions (eg, treated vs untreated).

Author(s)
Yue Cao

Examples
showAdditionalDetail
**Description**

This displays the metadata for all available datasets in the **SimBenchData** package.

**Usage**

```r
showMetaData()
```

**Details**

This package contains a total of 35 curated datasets, covering a range of sequencing protocols, tissues types (including different cell lines) and from both mouse and human.

**Value**

A **DataFrame**, containing the following fields

- Name, short name of this data.
- Description, description of the data.
- BiocVersion, the first Bioconductor version the resource was made available for.
- Genome, Genome build.
- SourceType, Format of original data.
- SourceUrl, link of the original data.
- SourceVersion, version of the original data.
- Species, whether it is human or mouse.
- TaxonomyId, taxonomy ID.
- Coordinate_1_based, TRUE if data are 1-based.
-DataProvider, organisation or company that provided the original data.
- Maintainer, maintainer name and email.
- RDataClass, R / Bioconductor class the data are stored in.
- DispatchClass, whether Rd or Rds data.
- RDataPath, the corresponding file in this package.

**Author(s)**

Yue Cao

**Examples**

```r
showMetaData
```
Index

DataFrame, 2, 3
showAdditionalDetail, 2
showMetaData, 3