Package ‘SimBenchData’

January 20, 2026

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

Version 1.19.0

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

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

git_branch devel

git_last_commit e762a0f

git_last_commit_date 2025-10-29

Repository Bioconductor 3.23

Date/Publication 2026-01-20

Author Yue Cao [aut, cre],
Pengyi Yang [aut],
Jean Yee Hwa Yang [aut]

Maintainer Yue Cao <`ycao6928@uni.sydney.edu.au`>

Contents

`showAdditionalDetail` *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, tissues 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.
- `Mutiple cell types/conditions ?`, whether the dataset contains multiple cell types or conditions (eg, treated vs untreated).

Author(s)

Yue Cao

Examples

```
showAdditionalDetail
```

`showMetaData` *Metadata of the 35 datasets*

Description

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

Usage

```
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 Rda or Rds data.
- `RDataPath`, the corresponding file in this package.

Author(s)

Yue Cao

Examples

```
showMetaData
```

Index