

# Package ‘SimBenchData’

June 27, 2024

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

**Version** 1.13.0

**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>

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**Author** Yue Cao [aut, cre],

Pengyi Yang [aut],

Jean Yee Hwa Yang [aut]

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

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showAdditionalDetail *Additional details on 35 datasets*

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### 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
```

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showMetaData	<i>Metadata of the 35 datasets</i>
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**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
```

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