Package 'SingleCellMultiModal'

Type Package

Title Integrating Multi-modal Single Cell Experiment datasets

Version 1.0.0

Description SingleCellMultiModal is an ExperimentHub package
that serves multiple datasets obtained from GEO and other sources and
represents them as MultiAssayExperiment objects. The current focus is
on datasets that use new technologies such as scNMT and scM&T.

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BugReports https://github.com/waldronlab/SingleCellMultiModal/issues

Depends R (>= 4.0.0), MultiAssayExperiment

Imports AnnotationHub, BiocFileCache, ExperimentHub, rappdirs, utils

Suggests knitr

VignetteBuilder knitr

biocViews ExperimentData, SingleCellData, ReproducibleResearch,
ExperimentHub, GEO

Encoding UTF-8

LazyData true

RoxygenNote 7.1.0

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R topics documented:

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Description

The SingleCellMultiModal package provides a convenient and user-friendly representation of multi-modal data from project such as 'scNMT' for mouse gastrulation.

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See Also

Useful links:

- Report bugs at `https://github.com/waldronlab/SingleCellMultiModal/issues`

Examples

```
help(package = "SingleCellMultiModal")
```

scmmCache   *Manage cache / download directories for study data*

Description

Managing data downloads is important to save disk space and re-downloading data files. This can be done effortlessly via the integrated `BiocFileCache` system.

Usage

```
scmmCache(...)

setCache(
  directory = rappdirs::user_cache_dir("SingleCellMultiModal"),
  verbose = TRUE,
  ask = interactive()
)

removeCache(accession)
```

Arguments

`...`	For scmmCache, arguments passed to setCache
`directory`	The file location where the cache is located. Once set future downloads will go to this folder.
`verbose`	Whether to print descriptive messages
`ask`	logical (default TRUE when interactive session) Confirm the file location of the cache directory
`accession`	character(1) A single string indicating the accession number of the study

Value

The directory / option of the cache location

scmmCache

Get the directory location of the cache. It will prompt the user to create a cache if not already created. A specific directory can be used via setCache.

setCache

Specify the directory location of the data cache. By default, it will got to the user's home/.cache and "appname" directory as specified by user_cache_dir. (default appname: 'SingleCellMultiModal')

removeCache

Some files may become corrupt when downloading, this function allows the user to delete the tarball associated with a study number in the cache.

Examples

```
getOption("scmmCache")
scmmCache()
```

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scNMT   *Single-cell Nucleosome, Methylation and Transcription sequencing*

Description

scNMT assembles data on-the-fly from 'ExperimentHub' to provide a MultiAssayExperiment container. The 'dataType' argument provides access to the 'mouse_gastrulation' dataset as obtained from Argelaguet et al. (2019). Pre-processing code can be seen at `https://github.com/rarguelaguet/mouse_gastrulation`. Protocol information for this dataset is available at Clark et al. (2018). See the vignette for the full citation.

Usage

```
scNMT(
  dataType = "mouse_gastrulation",
  modes = "*",
  dry.run = TRUE,
  verbose = TRUE,
  ...
)
```

Arguments

dataType	character(1) Indicates study that produces this type of data (default: 'mouse_gastrulation')
modes	character() The assay types or modes of data to obtain these include single cell Chromatin Accessibilty ("acc"), Methylation ("met"), RNA-seq ("rna") by default.
dry.run	logical(1) Whether to return the dataset names before actual download (default TRUE)
verbose	logical(1) Whether to show the dataset currently being (down)loaded (default TRUE)
...	Additional arguments passed on to the [ExperimentHub-class](#) constructor

Details

scNMT is a combination of RNA-seq (transcriptome) and an adaptation of Nucleosome Occupancy and Methylation sequencing (NOMe-seq, the methylome and chromatin accessibility) technologies. For more information, see Reik et al. (2018) DOI: 10.1038/s41467-018-03149-4

- mouse_gastrulation:
  - rna - RNA-seq
  - acc_* - chromatin accessibility
  - met_* - DNA methylation
    * cgi - CpG islands
    * CTCF - footprints of CTCF binding
    * DHS - DNase Hypersensitive Sites
    * genebody - gene bodies
    * p300 - p300 binding sites
    * promoter - gene promoters

Value

A single cell multi-modal [MultiAssayExperiment](#)

Source

http://ftp.ebi.ac.uk/pub/databases/scnmt_gastrulation/

References

Argelaguet et al. (2019)

See Also

SingleCellMultiModal-package

Examples

```
scNMT(dataType = "mouse_gastrulation", modes = "*", dry.run = TRUE)
```

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