Package 'DropletTestFiles'

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Title Test Files for Single-Cell Droplet Utilities

Version 1.22.0

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Description Assorted files generated from droplet-based single-cell protocols, to be used for testing functions in DropletUtils. Primarily intended for storing files that directly come out of processing pipelines like 10X Genomics' CellRanger software, prior to the formation of a SingleCellExperiment object. Unlike other packages, this is not designed to provide objects that are immediately ready for analysis.

License GPL-3

NeedsCompilation no

Imports utils, ExperimentHub, AnnotationHub, S4Vectors

Suggests BiocStyle, knitr, rmarkdown, testthat, DropletUtils

VignetteBuilder knitr

Encoding UTF-8

biocViews ExperimentHub, ExperimentData, ExpressionData, SequencingData, RNASeqData, SingleCellData

BuildResaveData no

RoxygenNote 7.1.1

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Contents

DropletTestFiles 2
listTestFiles 3

Index **5**

`DropletTestFiles` *The* **DropletTestFiles** *package*

Description

The **DropletTestFiles** package stores files for droplet-based single-cell protocols, such as those generated from 10X Genomics' CellRanger software. These files are primarily intended for testing of utilities (e.g., in **DropletUtils**) to handle raw pipeline output and are not (immediately) analysis-ready, unlike the SingleCellExperiment objects offered by **scRNAseq** and related packages. (After all, without these files, how else would we test the functions that are required to *make* such datasets analysis-ready?) We store these files on ExperimentHub as this has better long-term availability guarantees than sourcing them from the origin.

10X Genomics public datasets

A number of public datasets are taken from the 10X Genomics website (https://www.10xgenomics.com/resources/datasets/):

- `"tenx-2.0.1-nuclei_900"`, 1k brain nuclei from an E18 mouse, single cell gene expression dataset by CellRanger 2.0.1. https://support.10xgenomics.com/single-cell-gene-expression/datasets/2.0.1/nuclei_900.
- `"tenx-2.1.0-pbmc4k"`, 4k PBMCs from a healthy donor, single cell gene expression dataset by CellRanger 2.1.0. https://support.10xgenomics.com/single-cell-gene-expression/datasets/2.1.0/pbmc4k.
- `"tenx-3.0.0-pbmc_10k_protein_v3"`, 10k PBMCs from a healthy donor - gene expression and cell surface protein, single cell gene expression dataset by CellRanger 3.0.0. https://support.10xgenomics.com/single-cell-gene-expression/datasets/3.0.0/pbmc_10k_protein_v3.
- `"tenx-3.1.0-5k_pbmc_protein_v3"`, 5k Peripheral blood mononuclear cells (PBMCs) from a healthy donor with cell surface proteins (v3 chemistry), single cell gene expression dataset by CellRanger 3.1.0. https://support.10xgenomics.com/single-cell-gene-expression/datasets/3.1.0/5k_pbmc_protein_v3.
- `"tenx-4.0.0-SC3_v3_NextGem_DI_Neuron_10K"`, 10k mouse E18 combined cortex, hippocampus and subventricular zone cells, dual indexed, single cell gene expression dataset by CellRanger 4.0.0. https://support.10xgenomics.com/single-cell-gene-expression/datasets/4.0.0/SC3_v3_NextGem_DI_Neuron_10K.
- `"tenx-atac-1.2.0-atac_pbmc_1k_nextgem"`, 1k peripheral blood mononuclear cells (PBMCs) from a healthy donor (Next GEM v1.1), single cell ATAC dataset by CellRanger ATAC 1.2.0. https://support.10xgenomics.com/single-cell-atac/datasets/1.2.0/atac_pbmc_1k_nextgem.

Griffiths *et al.* barcode swapping files

The `"bach-mammary-swapping"` dataset provide the raw molecule information files from Griffiths et al. (2018). This contains 10X Genomics data from eight samples of the mouse mammary gland that were multiplexed for sequencing on either the HiSeq 2500 (`"hiseq_2500/*"` files) or the HiSeq 4000 (`"hiseq_4000/*"` files, where the swapping takes effect). Each sample is defined by its 10X library barcode (A1 - H1). In addition, a replicate experiment was performed with a different set of 8 replicate samples (A7 - H7) on the HiSeq 2500; these are represented by the `"hiseq_2500_exp2/*"` files.

Author(s)

Aaron Lun

References

Griffiths JA, Lun ATL, Richard AC, Bach K, Marioni JC (2018). Detection and removal of barcode swapping in single-cell RNA-seq data. *Nat. Commun.* 9, 1:2667.

Zheng GX, Terry JM, Belgrader P, and others (2017). Massively parallel digital transcriptional profiling of single cells. *Nat. Commun.* 8:14049.

See Also

`listTestFiles`, to see all files available for a particular dataset name.

`listTestFiles` *List available test files*

Description

List all test files managed by **DropletTestFiles** on **ExperimentHub**.

Usage

```
listTestFiles(
  hub = ExperimentHub(),
  dataset = NULL,
  version = NULL,
  latest = TRUE
)

getTestFile(path, hub = ExperimentHub(), prefix = TRUE)
```

Arguments

hub	An ExperimentHub object.
dataset	String specifying the dataset to search for, e.g., "tenx-2.1.0-pbmc4k". By default, files are listed for all datasets.
version	String specifying the version of the files to search for.
latest	Logical scalar indicating whether the latest version of each file should be presented. Only used if version=NULL; if FALSE, entries are returned for all versions.
path	String containing the RDataPath of the resource of interest.
prefix	Logical scalar indicating whether path should be prefixed with "DropletTestFiles/".

Details

Versions refer to those of the **DropletTestFiles** package itself, and refer to the version of the package in which a particular dataset was added.

Value

A DataFrame containing information on all relevant test files (one per row). Of particular interest are the columns file.dataset, file.version and file.name, containing the dataset, version and name of each test file.

Author(s)

Aaron Lun

Examples

```
# Getting everything:
listTestFiles()

# Getting all files for a particular dataset.
out <- listTestFiles(dataset="tenx-3.1.0-5k_pbmc_protein_v3")
out

# Downloading a resource to a local file, using an EH number:
library(ExperimentHub)
hub <- ExperimentHub()
hub[[rownames(out)[1]]]

# Downloading the same resource using an RDataPath:
getTestFile(out$rdatapath[1], prefix=FALSE)
```

Index

DataFrame, *4*
DropletTestFiles, 2

ExperimentHub, *4*

getTestFile *(*listTestFiles*)*, 3

listTestFiles, *3*, 3