

Package ‘scaeData’

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Type Package

Title Data Package for SingleCellAlleleExperiment

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Description Contains default datasets used by the Bioconductor package SingleCellAlleleExperiment. The raw FASTQ files were sourced from publicly accessible datasets provided by 10x Genomics. Subsequently, our scIGD snakemake workflow was employed to process these FASTQ files. The resulting output from scIGD constitutes to the contents of this data package.

Depends R (>= 4.4.0)

Imports ExperimentHub

Suggests knitr, rmarkdown, markdown, SingleCellAlleleExperiment, Matrix, BiocStyle

biocViews ExperimentHub, ExperimentData, Homo_sapiens_Data, SingleCellData

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VignetteBuilder knitr

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.1

URL <https://github.com/AGImkeller/scaeData>

BugReports <https://github.com/AGImkeller/scIGD/issues>

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demo_dir_file	<i>Split getter output</i>
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Description

Internal function used by ehoub_out() that splits the output from the getter into a file path and the corresponding file name. This is necessary as the read-in function read_allele_counts() from the SingleCellAlleleExperiment package expects a directory path as well as the names of each expected file.

Usage

```
demo_dir_file(ehub_dir, dir = TRUE)
```

Arguments

- ehub_dir character string that is retrieved by the getters
- dir binary if the output should contain file path and file name or only file name

Value

list containing (file path) and file name

ehub_out	<i>Build output list per dataset</i>
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Description

Internal function used by `scaeDataGet()` to build a list containing the file path

Usage

```
ehub_out(bc_dir, feature_dir, mtx_dir)
```

Arguments

<code>bc_dir</code>	character string containing full path to barcode file
<code>feature_dir</code>	character string containing full path to feature file
<code>mtx_dir</code>	character string containing full path to matrix file

Value

list with four elements containing file path to the directory containing all files and each file name for barcodes, features and matrix

<code>get_barcodes_10k</code>	<i>Get barcode identifiers for pbmc-10k dataset</i>
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Description

Internal getter function that retrieves the `pbmc_10k_barcodes.txt` from ExperimentHub (`eh[["EH9456"]]`). This is one out of 3 files that are necessary to load for using the data in a *SingleCellAlleleExperiment* data structure. File is generated with the *scIGD* workflow.

Usage

```
get_barcodes_10k()
```

Value

character string containing the file path of the barcode file

get_barcodes_20k	<i>Get barcode identifiers for pbmc-20k dataset</i>
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Description

Internal getter function that retrieves the pbmc_20k_barcodes.txt from ExperimentHub (eh[["EH9459"]]). This is one out of 3 files that are necessary to load for using the data in a *SingleCellAlleleExperiment* data structure. File is generated with the *scIGD* workflow.

Usage

```
get_barcodes_20k()
```

Value

character string containing the file path of the barcode file

get_barcodes_5k	<i>Get barcode identifiers for pbmc-5k dataset</i>
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Description

Internal getter function that retrieves the pbmc_5k_barcodes.txt from ExperimentHub (eh[["EH9453"]]). This is one out of 3 files that are necessary to load for using the data in a *SingleCellAlleleExperiment* data structure. File is generated with the *scIGD* workflow.

Usage

```
get_barcodes_5k()
```

Value

character string containing the file path of the barcode file

get_counts_10k	<i>Get quantification matrix for pbmc-10k dataset</i>
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Description

Internal getter function that retrieves the pbmc_10k_count_mtx.mtx from ExperimentHub (eh[["EH9458"]]). This is one out of 3 files that are necessary to load for using the data in a *SingleCellAlleleExperiment* data structure. File is generated with the *scIGD* workflow.

Usage

```
get_counts_10k()
```

Value

character string containing the file path of the matrix file

get_counts_20k	<i>Get quantification matrix for pbmc-20k dataset</i>
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Description

Internal getter function that retrieves the pbmc_20k_count_mtx.mtx from ExperimentHub (eh[["EH9461"]]). This is one out of 3 files that are necessary to load for using the data in a *SingleCellAlleleExperiment* data structure. File is generated with the *scIGD* workflow.

Usage

```
get_counts_20k()
```

Value

character string containing the file path of the matrix file

get_counts_5k	<i>Get quantification matrix for pbmc-5k dataset</i>
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Description

Internal getter function that retrieves the pbmc_5k_count_mtx.mtx from ExperimentHub (eh[["EH9455"]]). This is one out of 3 files that are necessary to load for using the data in a *SingleCellAlleleExperiment* data structure. File is generated with the *scIGD* workflow.

Usage

```
get_counts_5k()
```

Value

character string containing the file path of the matrix file

get_features_10k	<i>Get feature identifiers for pbmc-10k dataset</i>
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Description

Internal getter function that retrieves the pbmc_10k_features.txt from ExperimentHub (eh[["EH9457"]]). This is one out of 3 files that are necessary to load for using the data in a *SingleCellAlleleExperiment* data structure. File is generated with the *scIGD* workflow.

Usage

```
get_features_10k()
```

Value

character string containing the file path of the feature file

get_features_20k	<i>Get feature identifiers for pbmc-20k dataset</i>
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Description

Internal getter function that retrieves the `pbmc_20k_features.txt` from ExperimentHub (`eh[["EH9460"]]`). This is one out of 3 files that are necessary to load for using the data in a *SingleCellAlleleExperiment* data structure. File is generated with the *scIGD* workflow.

Usage

```
get_features_20k()
```

Value

character string containing the file path of the feature file

get_features_5k	<i>Get feature identifiers for pbmc-5k dataset</i>
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Description

Internal getter function that retrieves the `pbmc_5k_features.txt` from ExperimentHub (`eh[["EH9454"]]`). This is one out of 3 files that are necessary to load for using the data in a *SingleCellAlleleExperiment* data structure. File is generated with the *scIGD* workflow.

Usage

```
get_features_5k()
```

Value

character string containing the file path of the features file

scaeData-pkg	<i>scaeData</i>
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Description

scaeData: Data Package for SingleCellAlleleExperiment

Details

This package contains some exemplary datasets used by the Bioconductor package *SingleCellAlleleExperiment*. The raw FASTQ files were sourced from publicly accessible datasets provided by 10x Genomics. Subsequently, our *scIGD* snakemake workflow was employed to process these FASTQ files in order to obtain allele-level quantifications. The resulting output from *scIGD* constitutes to the contents of this data package.

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See Also

<https://github.com/AGImkeller/scIGD/> for the definition of the quantification workflow.

scaeDataGet

Download and process demo dataset

Description

Wrapper function used to retrieve a list containing the file path and file names for the chosen dataset. The corresponding dataset is retrieved from ExperimentHub. The following demo datasets are available:

- **pbmc_5k**: using the following ExperimentHub entries: **barcodes**(EH9453); **features**(EH9454); **counts matrix**(EH9455)
- **pbmc_10k**: using the following ExperimentHub entries: **barcodes**(EH9456); **features**(EH9457); **counts matrix**(EH9458)
- **pbmc_20k**: using the following ExperimentHub entries: **barcodes**(EH9459); **features**(EH9460); **counts matrix**(EH9461)

Usage

```
scaeDataGet(dataset = c("pbmc_5k", "pbmc_10k", "pbmc_20k"))
```

Arguments

dataset character vector describing which dataset should be retrieved. Choose one as input.

Value

list with four elements containing file path and file names for the chosen dataset

Examples

```
if (interactive()) {
  scae_data_5k <- scaeDataGet(dataset = "pbmc_5k")
  scae_data_5k
}
```

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