Package ‘clustifyrdatahub’

November 26, 2024

Title External data sets for clustifyr in ExperimentHub

Version 1.16.0

Description References made from external single-cell mRNA sequencing data sets, stored as average gene expression matrices. For use with clustifyr <`https://bioconductor.org/packages/clustifyr`> to assign cell type identities.

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URL `https://rnabioco.github.io/clustifyrdatahub/`

Depends R (>= 4.0), ExperimentHub

Imports utils

Suggests clustifyr, Seurat, usethis, rmarkdown, knitr, tidyr, BiocStyle

VignetteBuilder knitr

Encoding UTF-8

LazyData true

RoxygenNote 7.2.1

biocViews SingleCellData, SequencingData, MicroarrayData, ExperimentHub, RNASeqData, PackageTypeData, ExpressionData

BugReports `https://github.com/rnabioco/clustifyrdatahub/issues`

Config/Needs/website pkgdown, rnabioco/rbitemplate

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

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Contents

`clustifyrdatahub` *clustifyrdatahub: reference scRNA-seq data for clustifyr*

Description

The clustifyrdatahub package provides access to the summarized reference count matrix data from multiple datasets used in the clustifyr manuscript and tutorial. They are provided for future users of clustifyr, for automated cell type classification of scRNA-seq experiments.

Details

Available datasets:

+ Mouse Cell Atlas - [ref_MCA()] + Tabula Muris (10X) - [ref_tabula_muris_drop()] + Tabula Muris (SmartSeq2) - [ref_tabula_muris_facs()] + Mouse RNA-seq from 28 cell types - [ref_mouse.rnaseq()] + Mouse Organogenesis Cell Atlas (main cell types) - [ref_moca_main()] + Mouse sorted immune cells - [ref_immgen()] + Human hematopoietic cell microarray - [ref_hema_microarray()] + Human cortex development scRNA-seq - [ref_cortex_dev()] + Human pancreatic cell scRNA-seq (inDrop) - [ref_pan_indrop()] + Human pancreatic cell scRNA-seq (SmartSeq2) - [ref_pan_smartseq2()]

`ref_cortex_dev` *Matrix of average gene detection on cortex development cell types*

Description

47 distinct annotated clusters of human neuronal subtypes

Usage

```
ref_cortex_dev
```

Format

An object of class `function` of length 1.

Source

<https://cells.ucsc.edu/?ds=cortex-dev#>

See Also

Other ref: `ref_MCA()`, `ref_hema_microarray()`, `ref_immgen()`, `ref_moca_main()`, `ref_mouse.rnaseq()`, `ref_mouse_atlas()`, `ref_pan_indrop()`, `ref_pan_smartseq2()`, `ref_tabula_muris_drop()`, `ref_tabula_muris_facs()`

Examples

```
ref_cortex_dev(metadata = TRUE)
```

`ref_hema_microarray` *Matrix of average gene detection by microarray on sorted immune cell populations*

Description

38 distinct purified populations of human hematopoietic cells

Usage

```
ref_hema_microarray
```

Format

An object of class `function` of length 1.

Source

[https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE24759]

See Also

Other ref: `ref_MCA()`, `ref_cortex_dev()`, `ref_immgen()`, `ref_moca_main()`, `ref_mouse.rnaseq()`, `ref_mouse_atlas()`, `ref_pan_indrop()`, `ref_pan_smartseq2()`, `ref_tabula_muris_drop()`, `ref_tabula_muris_facs()`

Examples

```
ref_hema_microarray(metadata = TRUE)
```

`ref_immgen` *Matrix of average gene expression from immgen data*

Description

253 mouse immune cell types

Usage

```
ref_immgen
```

Format

An object of class `function` of length 1.

Source

["SingleR"]

See Also

Other ref: `ref_MCA()`, `ref_cortex_dev()`, `ref_hema_microarray()`, `ref_moca_main()`, `ref_mouse.rnaseq()`, `ref_mouse_atlas()`, `ref_pan_indrop()`, `ref_pan_smartseq2()`, `ref_tabula_muris_drop()`, `ref_tabula_muris_facs()`

Examples

```
ref_immgen(metadata = TRUE)
```

`ref_MCA` *Matrix of average gene expression for single-cell RNA-seq.*

Description

from mouse cell atlas project

Usage

```
ref_MCA
```

Format

An object of class `function` of length 1.

Source

<https://figshare.com/s/865e694ad06d5857db4b>

See Also

Other ref: `ref_cortex_dev()`, `ref_hema_microarray()`, `ref_immgen()`, `ref_moca_main()`, `ref_mouse.rnaseq()`, `ref_mouse_atlas()`, `ref_pan_indrop()`, `ref_pan_smartseq2()`, `ref_tabula_muris_drop()`, `ref_tabula_muris_facs()`

Examples

```
ref_MCA(metadata = TRUE)
```

`ref_moca_main` *Matrix of average gene expression per cluster from single-cell sci-RNA-seq3 from Mouse Organogenesis Cell Atlas.*

Description

100,000 cells

Usage

```
ref_moca_main
```

Format

An object of class `function` of length 1.

Source

<http://atlas.gs.washington.edu/mouse-rna/>

See Also

Other ref: `ref_MCA()`, `ref_cortex_dev()`, `ref_hema_microarray()`, `ref_immgen()`, `ref_mouse.rnaseq()`, `ref_mouse_atlas()`, `ref_pan_indrop()`, `ref_pan_smartseq2()`, `ref_tabula_muris_drop()`, `ref_tabula_muris_facs()`

Examples

```
ref_moca_main(metadata = TRUE)
```

`ref_mouse.rnaseq` *Matrix of average gene expression from general mouse cell type data*

Description

28 general cell types

Usage

```
ref_mouse.rnaseq
```

Format

An object of class `function` of length 1.

Source

["SingleR"]

See Also

Other ref: `ref_MCA()`, `ref_cortex_dev()`, `ref_hema_microarray()`, `ref_immgen()`, `ref_moca_main()`, `ref_mouse_atlas()`, `ref_pan_indrop()`, `ref_pan_smartseq2()`, `ref_tabula_muris_drop()`, `ref_tabula_muris_facs()`

Examples

```
ref_mouse.rnaseq(metadata = TRUE)
```

`ref_mouse_atlas` *Atlas matrix of average gene expression aggregated from scRNA-seq data of mouse organisms*

Description

Data aggregated from NCBI Gene Expression Omnibus

Usage

```
ref_mouse_atlas
```

Format

An object of class `function` of length 1.

Source

<https://github.com/rnabioco/scRNA-seq-Cell-Ref-Matrix/blob/master/atlas/musMusculus/MouseAtlas.rds>

See Also

Other ref: `ref_MCA()`, `ref_cortex_dev()`, `ref_hema_microarray()`, `ref_immgen()`, `ref_moca_main()`, `ref_mouse.rnaseq()`, `ref_pan_indrop()`, `ref_pan_smartseq2()`, `ref_tabula_muris_drop()`, `ref_tabula_muris_facs()`

Examples

```
ref_mouse_atlas(metadata = TRUE)
```

`ref_pan_indrop` *Matrix of average gene expression per cluster from single-cell RNA-seq pancreas data using indrop method.*

Description

A sample of 8569 pancreas cells

Usage

```
ref_pan_indrop
```

Format

An object of class `function` of length 1.

Source

<https://hemberg-lab.github.io/scRNA.seq.datasets/human/pancreas/>

See Also

Other ref: `ref_MCA()`, `ref_cortex_dev()`, `ref_hema_microarray()`, `ref_immgen()`, `ref_moca_main()`, `ref_mouse.rnaseq()`, `ref_mouse_atlas()`, `ref_pan_smartseq2()`, `ref_tabula_muris_drop()`, `ref_tabula_muris_facs()`

Examples

```
ref_pan_indrop(metadata = TRUE)
```

`ref_pan_smartseq2` *Matrix of average gene expression per cluster from single-cell RNA-seq pancreas data using smartseq2 method.*

Description

A sample of 2209 pancreas cells

Usage

```
ref_pan_smartseq2
```

Format

An object of class `function` of length 1.

Source

<https://hemberg-lab.github.io/scRNA.seq.datasets/human/pancreas/>

See Also

Other ref: `ref_MCA()`, `ref_cortex_dev()`, `ref_hema_microarray()`, `ref_immgen()`, `ref_moca_main()`, `ref_mouse.rnaseq()`, `ref_mouse_atlas()`, `ref_pan_indrop()`, `ref_tabula_muris_drop()`, `ref_tabula_muris_f`

Examples

```
ref_pan_smartseq2(metadata = TRUE)
```

`ref_tabula_muris_drop` *Matrix of average gene expression per cluster from single-cell RNA-seq from Tabula Muris (10x genomics).*

Description

422,803 droplet libraries, 55,656 of which passed a QC cutoff of 500 genes and 1000 UMI

Usage

```
ref_tabula_muris_drop
```

Format

An object of class `function` of length 1.

Source

<https://tabula-muris.ds.czbiohub.org/>

See Also

Other ref: `ref_MCA()`, `ref_cortex_dev()`, `ref_hema_microarray()`, `ref_immgen()`, `ref_moca_main()`, `ref_mouse.rnaseq()`, `ref_mouse_atlas()`, `ref_pan_indrop()`, `ref_pan_smartseq2()`, `ref_tabula_muris_facs(`

Examples

```
ref_tabula_muris_drop(metadata = TRUE)
```

`ref_tabula_muris_facs` *Matrix of average gene expression per cluster from single-cell RNA-seq from Tabula Muris (SMART-Seq2).*

Description

53,760 cells from 20 tissues from 8 mice

Usage

```
ref_tabula_muris_facs
```

Format

An object of class `function` of length 1.

Source

<https://tabula-muris.ds.czbiohub.org/>

See Also

Other ref: `ref_MCA()`, `ref_cortex_dev()`, `ref_hema_microarray()`, `ref_immgen()`, `ref_moca_main()`, `ref_mouse.rnaseq()`, `ref_mouse_atlas()`, `ref_pan_indrop()`, `ref_pan_smartseq2()`, `ref_tabula_muris_drop(`

Examples

```
ref_tabula_muris_facs(metadata = TRUE)
```

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