Package 'raerdata'

March 6, 2025

```
Version 1.4.0

Description raerdata is an ExperimentHub package that provides a collection of files useful for demostrating functionality in the raer package. Datasets include 10x genomics scRNA-seq, bulk RNA-seq, and paired whole-genome and RNA-seq data. Additionally databases of human and mouse RNA editing sites are provided.

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```

```
Imports ExperimentHub, Rsamtools, BiocGenerics, rtracklayer, SingleCellExperiment
```

Suggests rmarkdown, knitr, BiocStyle, testthat (>= 3.0.0)

Title A collection of datasets for use with raer package

VignetteBuilder knitr

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

Encoding UTF-8

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

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Config/testthat/edition 3

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GSE99249

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GSE99249

RNA sequencing data from study GSE99249

Description

Study GSE99249 examined RNA editing in WT, ADAR1KO, and ADAR1-p150 HEK293T cells treated with and without interferon beta.

Usage

GSE99249()

Details

GSE99249() will download BAM and BAM index files from 6 RNA-seq libraries. 3 libraries are ADAR1 knockout cells treated with interferon beta and 3 libraries are wild type cells treated with interferon beta. The BAM files contain alignments from chromosome 18.

Value

A list containing:

- bams A BamFileList object, indicating the BAM file paths and BAI indexes.
- fasta A path to a fasta file from chr18 of hg38
- snps a GRanges object containing known SNPs from the REDIportal database (hg38)

Examples

GSE99249()

NA12878 3

NA12878

Whole genome and RNA sequencing data from NA12878 cell line

Description

Whole genome and RNA sequencing data from NA12878 cell line

Usage

NA12878()

Details

Will download BAM and BAM index files from whole genome and RNA sequencing of the NA12878 cell line, The data is from the first megabase of chromosome 4. Additionally a fasta file and a database of known SNPs will be downloaded.

Value

A list containing:

- bams A BamFileList object, indicating the BAM file paths and BAI indexes.
- fasta A path to a fasta file containing the genome sequence of the first megabase of chr4 (hg38)
- snps a GRanges object containing SNPs from the first megabase of chr4

Examples

NA12878()

pbmc_10x

single cell RNA sequencing data from human PBMCs

Description

A 10x Genomics 3' single cell RNA-seq library from 10k PBMCs. The BAM file contains alignments from chr16. A SingleCellExperiment is also provided with pre-processed gene expression data, a UMAP projection and cell type annotations.

Usage

pbmc_10x()

Details

pbmc_10x() will download a BAM, BAM index file, REDIportal RNA editing sites, and a Single-CellExperiment object from the ExperimentHub.

Value

A list containing:

- bam a BamFile object indicating the BAM and BAI file paths. Contains alignments from only chr16 (hg38).
- sites a GRanges object containing known RNA editing sites from the REDIportal database (hg38).
- sce a SingleCellExperiment object containing gene expression data, a UMAP projection and cell type annotations.

See Also

https://www.10xgenomics.com/resources/datasets/10k-human-pbmcs-3-v3-1-chromium-x-with-intronic-

Examples

pbmc_10x()

raerdata

raerdata

Description

A collection of datasets and databases to demonstrate RNA-editing analysis approaches using the raer package.

Details

atlases a collection of RNA editing databases

NA12878 Whole genome and RNA sequencing data from the NA12878 cell line

GSE99249 RNA sequencing data from a study that examined RNA editing in WT, ADAR1KO, and ADAR1-p150 HEK293T cells treated with and without interferon beta.

pbmc_10x single cell RNA sequencing data from human PBMCs from 10x Genomics

rediportal_full_mm10 Databases of known RNA editing sites

Description

Databases of known RNA editing sites

rediportal_full_mm10

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Usage

```
rediportal_full_mm10()
rediportal_coords_mm10()
rediportal_full_hg38()
rediportal_coords_hg38()
gabay_sites_mm10()
gabay_sites_hg38()
```

Details

rediportal_full_hg38() will download the human REDIportal database for hg38 which has been converted into a GRanges object. The GRanges is supplemented with additional columns of information provided by the REDIportal database, including gene location, repeat type, dbSNP annotation, and potential for amino-acid recoding.

rediportal_coords_hg38() will download the human REDIportal database for hg38 which has been converted into a GRanges object, which only contains the coordinates of the editing site.

rediportal_full_mm10() will download the mouse REDIportal database for mm10 which has been converted into a GRanges object. The GRanges is supplemented with additional columns of information provided by the REDIportal database, including gene location, repeat type, dbSNP annotation, and potential for amino-acid recoding.

rediportal_coords_mm10()will download the mouse REDIportal database for mm10 which has been converted into a GRanges object, which only contains the coordinates of the editing site.

gabay_sites_hg38() will download high-confidence human CDS editing sites (hg38).

gabay_sites_mm10() will download high-confidence mouse CDS editing sites (lifted-over from hg38 to mm10).

Value

A GRanges object.

Examples

```
gabay_sites_hg38()
```

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