Package ‘raerdata’

June 12, 2025

Title A collection of datasets for use with raer package

Version 1.6.0

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)

VignetteBuilder knitr

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

Encoding UTF-8

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

BugReports https://github.com/rnabioco/raerdata/issues

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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` *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 SingleCellExperiment 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-rea`

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

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`rediportal_full_mm10` *Databases of known RNA editing sites*

Description

Databases of known RNA editing sites

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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