Package 'raerdata'

May 2, 2024

Title A collection of datasets for use with raer package

Version 1.2.0

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

URL https://github.com/rnabioco/raerdata

Config/testthat/edition 3

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Contents

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()
```

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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-rea](#)

Examples

```
pbmc_10x()
```

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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

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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