

Package ‘raerdata’

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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 demonstrating 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>

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Contents

GSE99249	2
NA12878	3
pbmc_10x	3
raerdata	4
redportal_full_mm10	5
Index	6

GSE99249	<i>RNA sequencing data from study GSE99249</i>
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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 REDportal 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, REDportal 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 REDportal 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-reads>

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

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()
```

Index

* atlases

 redportal_full_mm10, [5](#)

atlases, [4](#)

BamFile, [4](#)

BamFileList, [2](#), [3](#)

ExperimentHub, [4](#)

gabay_sites_hg38

 (redportal_full_mm10), [5](#)

gabay_sites_mm10

 (redportal_full_mm10), [5](#)

GSE99249, [2](#), [4](#)

NA12878, [3](#), [4](#)

pbmc_10x, [3](#), [4](#)

raerdata, [4](#)

redportal_coords_hg38

 (redportal_full_mm10), [5](#)

redportal_coords_mm10

 (redportal_full_mm10), [5](#)

redportal_full_hg38

 (redportal_full_mm10), [5](#)

redportal_full_mm10, [5](#)

SingleCellExperiment, [3](#), [4](#)