Package 'methyvimData'

March 29, 2021

Title Example experimental data for use with the methyvim package

Version 1.12.0

Description Contains a reduced set of simulated data inspired by data produced
by the Infinium EPIC BeadChip assays by Illumina. The example data set is made
available to highlight many of the key procedures that are available within
the core functions of the methyvim package.

Depends R (>= 3.4.0), minfi

Suggests Biobase, BiocStyle, SummarizedExperiment, knitr, rmarkdown

License file LICENSE

Encoding UTF-8

VignetteBuilder knitr

RoxygenNote 6.0.1

biocViews Clustering, DNAMethylation, DifferentialMethylation,
MethylationArray, MethylSeq

PackageStatus Deprecated

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R topics documented:

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grsExample   *Filtered Mock Epigenomics Data Set*

Description

A data set containing data that is similar in structure to that typically found in epigenomics studies.

Usage

```
grsExample
```

Format

An object of class `GenomicRatioSet` with 400 rows and 210 columns.

Details

This data set was simulated based on several key characteristics of data sets available to the package authors through collaborations in studies of differential methylation. It is based on data collected using the 850K (EPIC) Infinium arrays produced by Illumina, from samples collected on human subjects in studies of environmental epidemiology. The structure of the original data set (e.g., notable differences between the exposure and treatment conditions) were used to guide the simulation, and data was only produced for an arbitrary subset of sites. The phenotype-level exposure and outcome data (accessible via `colData`) were derived from the original data. The size of the subset was chosen such that the data package would be compliant with the standards outlined by Bioconductor. We emphasize that this is not real data and is not in any way suitable for scientific investigation. Please note that THIS IS NOT REAL DATA.

Value

A `GenomicRatioSet` containing pre-filtered CpG sites, ready to be used with the core function of the `methyvim` package.

Examples

```
# Load required packages and the data set
suppressMessages(library(SummarizedExperiment))
data(grsExample)
# Take a look at the data in the GenomicRatioSet object
grsExample
# Extract treatment/exposure values with colData
as.numeric(colData(grsExample)[, 1])
```

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