Package ‘CLLmethylation’

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Title  Methylation data of primary CLL samples in PACE project
Version  1.22.0
Author  Malgorzata Oles, Andreas Mock
Maintainer  Malgorzata Oles <dr.malgorzata.oles@gmail.com>, Andreas Mock <andreas.mock@embl.de>

Description  The package includes DNA methylation data for the primary Chronic Lymphocytic Leukemia samples included in the Primary Blood Cancer Encyclopedia (PACE) project. Raw data from the 450k DNA methylation arrays is stored in the European Genome-Phenome Archive (EGA) under accession number EGAS0000100174. For more information concerning the project please refer to the paper “Drug-perturbation-based stratification of blood cancer” by Dietrich S, Oles M, Lu J et al., J. Clin. Invest. (2018) and R/Bioconductor package BloodCancerMultiOmics2017.

Depends  R (>= 3.5.0)
Encoding  UTF-8
VignetteBuilder  knitr
Imports  SummarizedExperiment, ExperimentHub
Suggests  BiocStyle, ggplot2, knitr, rmarkdown
License  LGPL
biocViews  ExperimentData, DiseaseModel, CancerData, LeukemiaCancerData
LazyData  true
git_url  https://git.bioconductor.org/packages/CLLmethylation
git_branch  RELEASE_3_18
git_last_commit  78ee55d
git_last_commit_date  2023-10-24
Repository  Bioconductor 3.18
Date/Publication  2024-04-04

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DNA methylation data

Description

The data was produced with the use of either 450k or 850k methylation arrays. Preprocessing of raw IDAT files was made using minfi R/Bioconductor package version 1.19.16. Intensities were normalized using the functional normalization algorithm. CpG sites containing SNPs inside the probe body were removed. Data is a subset of CpG sites present in 450k methylation arrays.

Format

"RangedSummarizedExperiment" object with Features 435155 and Samples 196.

Author(s)

Andreas Mock, Malgorzata Oles

Examples

```r
library("SummarizedExperiment")
library("ExperimentHub")
eh = ExperimentHub()
meth = eh["EH1071"]
colData(meth)
assay(meth)[1:5,1:5]
head(rowData(meth))
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