Package ‘RTCGA.methylation’

May 30, 2024

Type Package
Title Methylation datasets from The Cancer Genome Atlas Project
Version 1.32.0
Date 2015-12-23
License GPL-2
LazyData TRUE
BugReports https://github.com/RTCGA/RTCGA/issues
Depends R (>= 3.3.0), RTCGA
Suggests knitr, rmarkdown
biocViews AnnotationData
VignetteBuilder knitr
NeedsCompilation no
RoxygenNote 7.1.1
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methylation  Methylation datasets from TCGA project

Description

Package provides methylation (humanmethylation27) datasets from The Cancer Genome Atlas Project for all cohorts types from http://gdac.broadinstitute.org/. Data were downloaded using RTCGA-package and contain snapshots for the date: 2015-11-01. The process is described here: http://rtcga.github.io/RTCGA/. Use cases, examples and information about datasets in RTCGA.data family can be found here: browseVignettes("RTCGA"). Methylation data format is explained here https://wiki.nci.nih.gov/display/TCGA/DNA+methylation. Converting RTCGA.methylation datasets from data.frames to Bioconductor classes is explained here convertTCGA.

Usage

BRCA.methylation
COAD.methylation
COADREAD.methylation
GBM.methylation
GBMLGG.methylation
KIPAN.methylation
KIRC.methylation
KIRP.methylation
LAML.methylation
LUAD.methylation
LUSC.methylation
OV.methylation2
OV.methylation1
READ.methylation
STAD.methylation
methylation

STES.methylation

UCEC.methylation

Details

browseVignettes("RTCGA")

Value

Data frames with methylation data.

Source

http://gdac.broadinstitute.org/

Examples

## Not run:
browseVignettes("RTCGA")

## End(Not run)
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