Package ‘RTCGA.methylation’

April 4, 2024

Type Package

Title Methylation datasets from The Cancer Genome Atlas Project

Version 1.30.0

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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R topics documented:

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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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