Package ‘RTCGA.methylation’

February 1, 2017

Type Package

Title Methylation datasets from The Cancer Genome Atlas Project

Version 1.2.0

Date 2015-12-23


License GPL-2

LazyData TRUE

Repository Bioconductor

BugReports https://github.com/RTCGA/RTCGA/issues

Depends R (>= 3.3.0), RTCGA

Suggests knitr

biocViews AnnotationData

VignetteBuilder knitr

NeedsCompilation no

RoxygenNote 5.0.1

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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/](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/](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](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
STES.methylation
UCEC.methylation
```
methylations

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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