Package ‘RTCGA.methylation’

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Type Package

Title Methylation datasets from The Cancer Genome Atlas Project

Version 1.35.0

Date 2015-12-23

Description Package provides methylation (humanmethylation27) datasets from The Cancer Genome Atlas Project for all available cohorts types from http://gdac.broadinstitute.org/. Data format is explained here https://wiki.nci.nih.gov/display/TCGA/DNA+methylation Data from 2015-11-01 snapshot.

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
```

`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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