Package 'RTCGA.methylation'

October 12, 2020

Type Package

Title Methylation datasets from The Cancer Genome Atlas Project

Version 1.16.0

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

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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R topics documented:

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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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