

Package ‘RTCGA.methylation’

January 22, 2026

Type Package

Title Methylation datasets from The Cancer Genome Atlas Project

Version 1.39.0

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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