Package 'RTCGA.methylation'

November 10, 2026

Type Package

Title Methylation datasets from The Cancer Genome Atlas Project

Version 1.40.0

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

Author Marcin Kosinski [aut, cre], Witold Chodor [aut]

Maintainer Marcin Kosinski <m.p.kosinski@gmail.com>

git_url https://git.bioconductor.org/packages/RTCGA.methylation

git_branch RELEASE_3_23

git_last_commit dafcf06

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-10

Contents

methylation 2

Index 4

`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)
```

Index

∗ **datasets**
methylation, 2

BRCA.methylation *(*methylation*)*, 2
BRCA.methylation,COAD.methylation,COADREAD.methylation,GBM.methylation,GBMLGG.methylation,KIPAN.methyla
*(*methylation*)*, 2

COAD.methylation *(*methylation*)*, 2
COADREAD.methylation *(*methylation*)*, 2
convertTCGA, *2*

GBM.methylation *(*methylation*)*, 2
GBMLGG.methylation *(*methylation*)*, 2

KIPAN.methylation *(*methylation*)*, 2
KIRC.methylation *(*methylation*)*, 2
KIRP.methylation *(*methylation*)*, 2

LAML.methylation *(*methylation*)*, 2
LUAD.methylation *(*methylation*)*, 2
LUSC.methylation *(*methylation*)*, 2

methylation, 2

OV.methylation1 *(*methylation*)*, 2
OV.methylation2 *(*methylation*)*, 2

READ.methylation *(*methylation*)*, 2
RTCGA-package, *2*

STAD.methylation *(*methylation*)*, 2
STES.methylation *(*methylation*)*, 2

UCEC.methylation *(*methylation*)*, 2