Package 'RTCGA.mRNA'

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Type Package

Title mRNA datasets from The Cancer Genome Atlas Project

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Author Witold Chodor <witoldchodor@gmail.com>

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

Description Package provides mRNA 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/Gene+expression+data 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

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

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mRNA *mRNA datasets from TCGA project*

Description

Package provides mRNA 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")`. mRNA data format is explained here https://wiki.nci.nih.gov/display/TCGA/Gene+expression+data. Converting **RTCGA.mRNA** datasets from `data.frames` to Bioconductor classes is explained here convertTCGA.

Usage

```
BRCA.mRNA

COAD.mRNA

COADREAD.mRNA

GBMLGG.mRNA

KIPAN.mRNA

KIRC.mRNA

KIRP.mRNA

LGG.mRNA

LUAD.mRNA

LUSC.mRNA

OV.mRNA

READ.mRNA

UCEC.mRNA
```

Details

```
browseVignettes("RTCGA")
```

Value

Data frames with mRNA data.

Source

http://gdac.broadinstitute.org/

Examples

```
## Not run:
browseVignettes("RTCGA")

## End(Not run)
```

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