Package ‘RTCGA.CNV’

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Type Package

Title CNV (Copy-number variation) datasets from The Cancer Genome Atlas Project

Version 1.2.0

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Description Package provides CNV (based on Merge snp) datasets from The Cancer Genome Atlas Project for all cohorts types from http://gdac.broadinstitute.org/. Data format is explained here https://wiki.nci.nih.gov/display/TCGA/Retrieving+Data+Using+the+Data+Matrix. 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

R topics documented:

`CNV` *CNV datasets from TCGA project*

Description

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

Usage

```
ACC.CNV

BLCA.CNV

BRCA.CNV

CESC.CNV

CHOL.CNV

COAD.CNV

COADREAD.CNV

DLBC.CNV

ESCA.CNV

GBM.CNV

GBMLGG.CNV

HNSC.CNV

KICH.CNV

KIPAN.CNV

KIRC.CNV

KIRP.CNV

LAML.CNV

LGG.CNV
```

`LIHC.CNV`

`LUAD.CNV`

`LUSC.CNV`

`MESO.CNV`

`OV.CNV`

`PAAD.CNV`

`PCPG.CNV`

`PRAD.CNV`

`READ.CNV`

`SARC.CNV`

`SKCM.CNV`

`STAD.CNV`

`STES.CNV`

`TGCT.CNV`

`THCA.CNV`

`THYM.CNV`

`UCEC.CNV`

`UCS.CNV`

`UVM.CNV`

Details

`browseVignettes("RTCGA")`

Value

Data frames with CNV data.

Source

`http://gdac.broadinstitute.org/`

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