Package ‘TCGAbiolinksGUI.data’

April 30, 2026

Title Data for the TCGAbiolinksGUI package

Version 1.33.0

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Description Supporting data for the TCGAbiolinksGUI package.

License GPL-3

LazyData false

Depends R (>= 3.5.0)

Suggests BiocStyle, knitr, rmarkdown, readr, DT

biocViews AssayDomainData, TechnologyData, OrganismData

URL `https://github.com/BioinformaticsFMRP/TCGAbiolinksGUI.data`

BugReports `https://github.com/BioinformaticsFMRP/TCGAbiolinksGUI.data/issues`

VignetteBuilder knitr

RoxygenNote 7.1.2

git_url https://git.bioconductor.org/packages/TCGAbiolinksGUI.data

git_branch devel

git_last_commit a2c4747

git_last_commit_date 2026-04-28

Repository Bioconductor 3.24

Date/Publication 2026-04-30

Contents

`GDCdisease` *GDC projects*

Description

Contains all GDC projects with open data

Usage

```
data("GDCdisease")
```

Format

A named list with 39 projects

Source

Retrivied from GDC API

`gencode.v36.annotation.genes` *GENCODE v36 gene information*

Description

GENCODE v36 gene information

Usage

```
data("gencode.v36.annotation.genes")
```

Format

A Granges object

Source

Downloaded from GENCODE v36 https://www.gencodegenes.org/human/release_36.html Comprehensive gene annotation and filtered to genes

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`gene.location.hg19` *Biomart hg19 gene information*

Description

Biomart hg19 gene information

Usage

```
data("gene.location.hg19")
```

Format

A table

Source

Downloaded with biomart

`gene.location.hg38` *Biomart hg38 gene information*

Description

Biomart hg38 gene information

Usage

```
data("gene.location.hg38")
```

Format

A table

Source

Downloaded with biomart

`glioma.gcimp.model` *gcimp RF model*

Description

A RF model able to classify DNA methylation samples in to GCIMP groups

Usage

```
data("glioma.gcimp.model")
```

Format

A random forest model with 276 samples and 145 predictors classifying into 3 classes

Source

RF model created from DNA methylation signatures retrieved from `www.cell.com/cell/abstract/S0092-8674(15)01692-X`

`glioma.idh.model` *IDH RF model*

Description

A RF model able to classify DNA methylation samples in to IDH groups

Usage

```
data("glioma.idh.model")
```

Format

A random forest model with 880 samples and 1205 predictors classifying into 6 classes

Source

RF model created from DNA methylation signatures retrieved from `www.cell.com/cell/abstract/S0092-8674(15)01692-X`

`glioma.idhmut.model` *IDHmut RF model*

Description

A RF model able to classify DNA methylation samples in to IDHmut groups

Usage

```
data("glioma.idhmut.model")
```

Format

A random forest model with 450 samples and 1216 predictors classifying into 3 classes

Source

RF model created from DNA methylation signatures retrieved from `www.cell.com/cell/abstract/S0092-8674(15)01692-X`

`glioma.idhwt.model` *IDHwt RF model*

Description

A RF model able to classify DNA methylation samples in to IDHwt groups

Usage

```
data("glioma.idhwt.model")
```

Format

A random forest model with 430 samples and 843 predictors classifying into 3 classes

Source

RF model created from DNA methylation signatures retrieved from `www.cell.com/cell/abstract/S0092-8674(15)01692-X`

`linkedOmics.data` *linkedOmics table*

Description

linkedOmics table with links

Usage

```
data("linkedOmics.data")
```

Format

A table

Source

Parsed from `http://linkedomics.org/login.php#dataSource`

`maf.tumor` *GDC open MAF files*

Description

Contains the list of GDC project with open MAF files available

Usage

```
data(maf.tumor)
```

Format

A named list with 33 tumors

Source

`https://gdc-docs.nci.nih.gov/Data/Release_Notes/Manifests/GDC_open_MAFs_manifest.txt`

`probes2rm` *EPIC probes removed from newer versions*

Description

EPIC probes removed from newer versions that should not be used in the analysis

Usage

```
data("probes2rm")
```

Format

A list with 977 probes

Source

`https://support.illumina.com/downloads/infinium-methylationepic-v1-0-product-files.html`

`TCGAbiolinksGUI.data` *Auxiliary data for TCGAbiolinksGUI package.*

Description

Package: TCGAbiolinksGUI.data provide the necessary data for TCGAbiolinksGUI glioma classifier menu. It includes the following objects:

glioma.gcimp.model A train model for GCIMP DNA methylation signatures.

glioma.idhwt.model A train model for IDHwt DNA methylation signatures

glioma.idhmut.model A train model for IDHmut DNA methylation signatures

glioma.idh.model A train model for IDH DNA methylation signatures

probes2rm List of probes that should be removed from EPIC array due to different versions of the platform.
Source: https://support.illumina.com/downloads/infinium-methylationepic-v1-0-product-files.html

maf.tumor TCGA projects with open MAF files retrieved from the NCI's Genomic Data Commons (GDC).
Source: https://gdc-docs.nci.nih.gov/Data/Release_Notes/Manifests/GDC_open_MAFs_manifest.txt

GDCdisease The NCI's Genomic Data Commons (GDC) projects list

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