

Package ‘TCGAbiolinksGUI.data’

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Title Data for the TCGAbiolinksGUI package

Version 1.24.0

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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>

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Contents

| | |
|---------------------------------------|---|
| GDCdisease | 2 |
| encode.v36.annotation.genes | 2 |
| gene.location.hg19 | 3 |
| gene.location.hg38 | 3 |
| glioma.gcimp.model | 4 |
| glioma.idh.model | 4 |

| | |
|--------------------------------|---|
| glioma.idhmut.model | 5 |
| glioma.idhwt.model | 5 |
| linkedOmics.data | 6 |
| maf.tumor | 6 |
| probes2rm | 7 |
| TCGAbiolinksGUI.data | 7 |

Index 8

| | |
|------------|---------------------|
| GDCdisease | <i>GDC projects</i> |
|------------|---------------------|

Description

Contains all GDC projects with open data

Usage

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

Format

A named list with 39 projects

Source

Retrieved from GDC API

| | |
|------------------------------|-------------------------------------|
| gencode.v36.annotation.genes | <i>GENCODE v36 gene information</i> |
|------------------------------|-------------------------------------|

Description

GENCODE v36 gene information

Usage

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

Format

A Granges object

Source

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

`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](http://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](http://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](http://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](http://www.cell.com/cell/abstract/S0092-8674(15)01692-X)

| | |
|------------------|--------------------------|
| linkedOmics.data | <i>linkedOmics table</i> |
|------------------|--------------------------|

Description

linkedOmics table with links

Usage

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

Format

A table

Source

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

| | |
|-----------|---------------------------|
| maf.tumor | <i>GDC open MAF files</i> |
|-----------|---------------------------|

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

Index

* datasets

- GDCdisease, [2](#)
- gencode.v36.annotation.genes, [2](#)
- gene.location.hg19, [3](#)
- gene.location.hg38, [3](#)
- glioma.gcimp.model, [4](#)
- glioma.idh.model, [4](#)
- glioma.idhmut.model, [5](#)
- glioma.idhwt.model, [5](#)
- linkedOmics.data, [6](#)
- maf.tumor, [6](#)
- probes2rm, [7](#)

* utilities

- TCGAbiolinksGUI.data, [7](#)

- GDCdisease, [2](#), [7](#)
- gencode.v36.annotation.genes, [2](#)
- gene.location.hg19, [3](#)
- gene.location.hg38, [3](#)
- glioma.gcimp.model, [4](#), [7](#)
- glioma.idh.model, [4](#), [7](#)
- glioma.idhmut.model, [5](#), [7](#)
- glioma.idhwt.model, [5](#), [7](#)

- linkedOmics.data, [6](#)

- maf.tumor, [6](#), [7](#)

- probes2rm, [7](#), [7](#)

- TCGAbiolinksGUI.data, [7](#)