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
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biocViews AssayDomainData, TechnologyData, OrganismData
URL https://github.com/BioinformaticsFMRP/TCGAbiolinksGUI.data
BugReports https://github.com/BioinformaticsFMRP/TCGAbiolinksGUI.data/issues
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### GDCdisease

Contains all GDC projects with open data

#### Usage

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

#### Format

A named list with 39 projects

#### Source

Retrieved from GDC API

### gencode.v36.annotation.genes

GENCODE v36 gene information

#### Description

GENCODE v36 gene information

#### Usage

```r
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
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

**Description**

linkedOmics table with links

**Usage**

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

**Format**

A table

**Source**

Parsed from [http://linkedomics.org/login.php#dataSource](http://linkedomics.org/login.php#dataSource)

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### maf.tumor

**Description**

Contains the list of GDC project with open MAF files available

**Usage**

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


TCGAbiolinksGUI.data Auxilary 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.idhw.t.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.
- 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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