Package ‘TCGAbiolinksGUI.data’

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Title Data for the TCGAbiolinksGUI package
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License GPL-3
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GDCdisease  GDC projects

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

Description
GENCODE v36 gene information

Usage
data("genencode.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

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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 into 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 into 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

**Description**

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

**Usage**

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

**Format**

A list with 977 probes

**Source**


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### 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.
  
- **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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