Package 'TCGAWorkflowData'

Title Data for TCGA Workflow

Version 1.34.0

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Description This experimental data package contains 11 data sets necessary to follow the ``TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages".

Depends R (>= 3.5.0)

Imports SummarizedExperiment

License GPL-3

VignetteBuilder knitr

biocViews ExperimentData, Homo_sapiens_Data, MicroarrayData, CancerData

NeedsCompilation no

URL https://f1000research.com/articles/5-1542/v2

BugReports https://github.com/BioinformaticsFMRP/TCGAWorkflow/issues

RoxygenNote 7.2.3

Suggests knitr, rmarkdown, pander, testthat, BiocStyle

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exp	*A gene expression matrix for 10 GBM and 10 LGG samples prepared for the creation of an ELMER object.*

Description

A gene expression matrix for 10 GBM and 10 LGG samples prepared for the creation of an ELMER object.

Format

A matrix with 21022 rows and 20 samples

Examples

```
data("elmerExample")
```

---

exp_gbm	*A gene expression matrix with 20 GBM samples*

Description

A gene expression matrix with 20 GBM samples

Format

Gene expression: A SummarizedExperiment object with 21022 rows and 20 columns

Examples

```
data("TCGA_GBM_Transcriptome_20_samples")
```

---

exp_lgg	*A gene expression matrix with 20 LGG samples*

Description

A gene expression matrix with 20 LGG samples

Format

Gene expression: A SummarizedExperiment object with 21022 rows and 20 columns

Examples

```
data("TCGA_LGG_Transcriptome_20_samples")
```

---

gbm.samples	*Identifiers for the 10 GBM samples in the ELMER objects*

Description

Identifiers for the 10 GBM samples in the ELMER objects

Format

A vector of 10 barcodes

Examples

```
data("elmerExample")
```

---

genes	*A data frame object with gene information (hg19)*

Description

A data frame object with gene information (hg19)

Format

A dataframe object

Examples

```
data("genes_GR")
```

---

genes_GR   *A GRanges object with gene information (hg19)*

Description

A GRanges object with gene information (hg19)

Format

A GRanges object

Examples

```
data("genes_GR")
```

---

gistic_allbygene   *A subset of GBM GISTIC2 results, which is used to identify genes tar-*
                          geted by somatic copy-number alterations (SCNAs) From: GDAC fire-
                          hose, downloaded with RTCGAtoolbox

Description

A subset of GBM GISTIC2 results, which is used to identify genes targeted by somatic copy-number alterations (SCNAs) From: GDAC firehose, downloaded with RTCGAtoolbox

Format

A matrix with 24776 rows and 580 columns

Examples

```
data("gbm_gistic")
```

---

gistic_thresholedbygene

                          A subset of GBM GISTIC2 results, which is used to identify genes tar-
                          geted by somatic copy-number alterations (SCNAs) From: GDAC fire-
                          hose, downloaded with RTCGAtoolbox

Description

A subset of GBM GISTIC2 results, which is used to identify genes targeted by somatic copy-number alterations (SCNAs) From: GDAC firehose, downloaded with RTCGAtoolbox

Format

A matrix with 24776 rows and 580 columns

Examples

```
data("gbm_gistic")
```

| histone.marks | *histone marks specific for brain tissue from the Roadmap database.* |

Description

histone marks specific for brain tissue from the Roadmap database.

Format

A matrix with 72102 rows and 114 columns

Examples

```
data("histoneMarks")
```

| lgg.samples | *Identifiers for the 10 LGG samples in the ELMER objects* |

Description

Identifiers for the 10 LGG samples in the ELMER objects

Format

A vector of 10 barcodes

Examples

```
data("elmerExample")
```

| maf | *Merged LGG and GBM GDC MAF files from GDC workflow: Aliquot Ensemble Somatic Variant Merging and Masking* |

Description

Merged LGG and GBM GDC MAF files from GDC workflow: Aliquot Ensemble Somatic Variant Merging and Masking

Format

A matrix with 87957 rows and 141 columns

Examples

```
data("maf_lgg_gbm")
```

met	*A SummarizedExperiment containing TCGA data: DNA methylation platform 450K chromossome 9 for 10 LGG samples and 10 GBM samples*

Description

A SummarizedExperiment containing TCGA data: DNA methylation platform 450K chromossome 9 for 10 LGG samples and 10 GBM samples

Format

A SumarrizedExperiment with 9861 rows and 20 samples

Examples

```
data("elmerExample")
```

TCGAWorkflowData	*Data for TCGA Workflow*

Description

This experimental data package has the data necessary to follow the TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. It contains the following files:

- met20SamplesGBMLGGchr9: DNA methylation matrix from Infinium HumanMethylation450 platform for 10 LGG (Lower grade glioma) and 10 GBM (Glioblastoma multiforme). It has only probes in chromossome 9 in order to make the example of the workflow faster

- elmerExample: Contains a DNA methylation matrix (only probes in chromossome 9) and a gene expression matrix for 10 LGG (Lower grade glioma) and 10 GBM (Glioblastoma multiforme) in the required format for to execute the R/Bioconductor ELMER package analysis and a vector identifying which sample belongs to each tumor type.

- biogrid: biogrid information

- maf_lgg_gbm: Mutation annotation files for LGG (Lower grade glioma) and GBM (Glioblastoma multiforme) samples merged into a single matrix. The GDC Somatic Mutation Calling Workflow mutect2 was used to create this MAF files.

- histoneMarks: histone marks specific for brain tissue using from Roadmap database.

- genes_GR: A GRanges Object and a dataframe with gene information (hg19) downloaded from ENSEMBLE database using biomart via TCGAbiolinks

- TCGA_GBM_Transcriptome_20_samples: a matrix with raw expression signal for expression of a gene for 20 GBM (Glioblastoma multiforme) samples

- TCGA_LGG_Transcriptome_20_samples: a matrix with raw expression signal for expression of a gene for 20 LGG (low grade glioma) samples

For more information how to create these objects please read the vignette of this package with the follwing command: browseVignettes("TCGAWorkflowData")

Examples

```
data("elmerExample")
data("TCGA_LGG_Transcriptome_20_samples")
data("TCGA_GBM_Transcriptome_20_samples")
data("histoneMarks")
data("biogrid")
data("genes_GR")
data("maf_lgg_gbm")
```

---

tmp.biogrid *Biogrid information*

Description

Biogrid information

Format

Two matrices with 24776 rows and 580 columns

Examples

```
data("biogrid")
```

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