

Package ‘TCGAWorkflowData’

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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 pack-
ages''.

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	<i>A gene expression matrix for 10 GBM and 10 LGG samples prepared for the creation of an ELMER object.</i>
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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	<i>A gene expression matrix with 20 GBM samples</i>
---------	---

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	<i>A gene expression matrix with 20 LGG samples</i>
---------	---

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	<i>Identifiers for the 10 GBM samples in the ELMER objects</i>
-------------	--

Description

Identifiers for the 10 GBM samples in the ELMER objects

Format

A vector of 10 barcodes

Examples

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

genes	<i>A data frame object with gene information (hg19)</i>
-------	---

Description

A data frame object with gene information (hg19)

Format

A dataframe object

Examples

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

genes_GR	<i>A GRanges object with gene information (hg19)</i>
----------	--

Description

A GRanges object with gene information (hg19)

Format

A GRanges object

Examples

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

gistic_allbygene	<i>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</i>
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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	<i>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</i>
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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	<i>histone marks specific for brain tissue from the Roadmap database.</i>
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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	<i>Identifiers for the 10 LGG samples in the ELMER objects</i>
-------------	--

Description

Identifiers for the 10 LGG samples in the ELMER objects

Format

A vector of 10 barcodes

Examples

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

maf	<i>Merged LGG and GBM GDC MAF files from GDC workflow: Aliquot Ensemble Somatic Variant Merging and Masking</i>
-----	---

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	<i>A SummarizedExperiment containing TCGA data: DNA methylation platform 450K chromosome 9 for 10 LGG samples and 10 GBM samples</i>
-----	--

Description

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

Format

A SumarrizedExperiment with 9861 rows and 20 samples

Examples

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

TCGAWorkflowData	<i>Data for TCGA Workflow</i>
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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 chromosome 9 in order to make the example of the workflow faster
- elmerExample: Contains a DNA methylation matrix (only probes in chromosome 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 TCGA Biolinks
- 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 following 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	<i>Biogrid information</i>
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Description

Biogrid information

Format

Two matrices with 24776 rows and 580 columns

Examples

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

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