

Package ‘TCGAWorkflowData’

November 7, 2024

Title Data for TCGA Workflow

Version 1.30.0

Author Tiago Chedraoui Silva <tiagochst@gmail.com>

Maintainer Tiago Chedraoui Silva <tiagochst@gmail.com>

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

git_url <https://git.bioconductor.org/packages/TCGAWorkflowData>

git_branch RELEASE_3_20

git_last_commit ceef0c4

git_last_commit_date 2024-10-29

Repository Bioconductor 3.20

Date/Publication 2024-11-07

Contents

exp	2
exp_gbm	2
exp_lgg	3
gbm.samples	3
genes	3

genes_GR	4
gistic_allbygene	4
gistic_thresholedbygene	4
histone.marks	5
lgg.samples	5
maf	5
met	6
TCGAWorkflowData	6
tmp.biogrid	7

Index	8
--------------	----------

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

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`*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	<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>
------------------	---

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>
-------------------------	---

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>
---------------	---

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>
------------------	-------------------------------

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 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 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>
-------------	----------------------------

Description

Biogrid information

Format

Two matrices with 24776 rows and 580 columns

Examples

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

Index

* **internal**

- exp, [2](#)
- exp_gbm, [2](#)
- exp_lgg, [3](#)
- gbm.samples, [3](#)
- genes, [3](#)
- genes_GR, [4](#)
- gistic_allbygene, [4](#)
- gistic_thresholedbygene, [4](#)
- histone.marks, [5](#)
- lgg.samples, [5](#)
- maf, [5](#)
- met, [6](#)
- tmp.biogrid, [7](#)

* **utilities**

- TCGAWorkflowData, [6](#)

exp, [2](#)

exp_gbm, [2](#)

exp_lgg, [3](#)

gbm.samples, [3](#)

genes, [3](#)

genes_GR, [4](#)

gistic_allbygene, [4](#)

gistic_thresholedbygene, [4](#)

histone.marks, [5](#)

lgg.samples, [5](#)

maf, [5](#)

met, [6](#)

TCGAWorkflowData, [6](#)

tmp.biogrid, [7](#)