

# Package ‘TCGAWorkflowData’

April 16, 2024

**Title** Data for TCGA Workflow

**Version** 1.26.0

**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\_18

**git\_last\_commit** 556a052

**git\_last\_commit\_date** 2023-10-24

**Repository** Bioconductor 3.18

**Date/Publication** 2024-04-16

**R topics documented:**

exp . . . . .	2
exp_gbm . . . . .	2
exp_lgg . . . . .	3
gbm.samples . . . . .	3
genes . . . . .	3
genes_GR . . . . .	4
gistic_allbygene . . . . .	4
gistic_thresoledbygene . . . . .	5
histone.marks . . . . .	5
lgg.samples . . . . .	6
maf . . . . .	6
met . . . . .	6
TCGAWorkflowData . . . . .	7
tmp.biogrid . . . . .	8

<b>Index</b>	<b>9</b>
--------------	----------

---

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

*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*

---

### **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	<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

*Biogrid information*

---

**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, [5](#)
- histone.marks, [5](#)
- lgg.samples, [6](#)
- maf, [6](#)
- met, [6](#)
- tmp.biogrid, [8](#)

## \* **utilities**

- TCGAWorkflowData, [7](#)

exp, [2](#)

exp\_gbm, [2](#)

exp\_lgg, [3](#)

gbm.samples, [3](#)

genes, [3](#)

genes\_GR, [4](#)

gistic\_allbygene, [4](#)

gistic\_thresholedbygene, [5](#)

histone.marks, [5](#)

lgg.samples, [6](#)

maf, [6](#)

met, [6](#)

TCGAWorkflowData, [7](#)

tmp.biogrid, [8](#)