

# Package ‘TCGAbiolinks’

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**Type** Package

**Title** TCGAbiolinks: An R/Bioconductor package for integrative analysis with GDC data

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**Author** Antonio Colaprico,  
Tiago Chedraoui Silva,  
Catharina Olsen,  
Luciano Garofano,  
Davide Garolini,  
Claudia Cava,  
Thais Sabedot,  
Tathiane Malta,  
Stefano M. Pagnotta,  
Isabella Castiglioni,  
Michele Ceccarelli,  
Gianluca Bontempi,  
Houtan Noushmehr

**Maintainer** Tiago Chedraoui Silva <tiagochst@gmail.com>,  
Antonio Colaprico <axc1833@med.miami.edu>

**Depends** R (>= 4.0)

**Imports** downloader (>= 0.4), grDevices, biomaRt, dplyr, graphics, tibble, GenomicRanges, XML (>= 3.98.0), data.table, jsonlite (>= 1.0.0), plyr, knitr, methods, ggplot2, stringr (>= 1.0.0), IRanges, rvest (>= 0.3.0), stats, utils, S4Vectors, R.utils, SummarizedExperiment (>= 1.4.0), TCGAbiolinksGUI.data (>= 1.15.1), readr, tools, tidyr, purrr, xml2, httr (>= 1.2.1)

**Description** The aim of TCGAbiolinks is : i) facilitate the GDC open-access data retrieval, ii) prepare the data using the appropriate pre-processing strategies, iii) provide the means to carry out different standard analyses and iv) to easily reproduce earlier research results. In more detail, the package provides multiple methods for analysis (e.g., differential expression analysis, identifying differentially methylated regions) and methods for visualization (e.g., survival plots, volcano plots, starburst plots) in order to easily develop complete analysis pipelines.

**License** GPL (>= 3)

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**Suggests** jpeg, png, BiocStyle, rmarkdown, devtools, maftools, parmigene, c3net, minet, Biobase, affy, testthat, sesame, AnnotationHub, ExperimentHub, pathview, clusterProfiler, Seurat, ComplexHeatmap, circlize, ConsensusClusterPlus, igraph, supraHex, limma, edgeR, sva, EDASeq, survminer, genefilter, gridExtra, survival, doParallel, parallel, ggrepel ( $\geq 0.6.3$ ), scales, grid, DT

**VignetteBuilder** knitr

**LazyData** true

**URL** <https://github.com/BioinformaticsFMRP/TCGAbiolinks>

**BugReports** <https://github.com/BioinformaticsFMRP/TCGAbiolinks/issues>

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TCGAbiolinks-package    *The aim of TCGAbiolinks is : i) facilitate the TCGA open-access data retrieval, ii) prepare the data using the appropriate pre-processing strategies, iii) provide the means to carry out different standard analyses and iv) allow the user to download a specific version of the data and thus to easily reproduce earlier research results. In more detail, the package provides multiple methods for analysis (e.g., differential expression analysis, identifying differentially methylated regions) and methods for visualization (e.g., survival plots, volcano plots, starburst plots) in order to easily develop complete analysis pipelines.*

---

**Description**

The functions you're likely to need from **TCGAbiolinks** is [GDCdownload](#), [GDCquery](#). Otherwise refer to the vignettes to see how to format the documentation.

**See Also**

Useful links:

- <https://github.com/BioinformaticsFMRP/TCGAbiolinks>
- Report bugs at <https://github.com/BioinformaticsFMRP/TCGAbiolinks/issues>

---

batch.info	<i>TCGA batch information from Biospecimen Metadata Browser</i>
------------	---

---

**Description**

TCGA batch information from Biospecimen Metadata Browser

**Format**

A data frame with 11382 rows and 3 variables

---

bcgsc.ca_CHOL.IlluminaHiSeq_DNASeq.1.somatic.maf	<i>TCGA CHOL MAF</i>
--	----------------------

---

**Description**

TCGA CHOL MAF

**Format**

A tibble: 3,555 x 34

---

chol_maf	<i>TCGA CHOL MAF transformed to maftools object</i>
----------	---

---

**Description**

TCGA CHOL MAF transformed to maftools object

**Format**

An object of class MAF

---

classification	<i>Result of gliomaclassifier function</i>
----------------	--

---

**Description**

Result of gliomaclassifier function

**Format**

A list of data frames



---

dataBRCA	<i>TCGA data matrix BRCA</i>
----------	------------------------------

---

**Description**

TCGA data matrix BRCA

**Format**

A data frame with 20531 rows (genes) and 50 variables (samples)

---

dataDEGsFiltLevel	<i>TCGA data matrix BRCA DEGs</i>
-------------------	-----------------------------------

---

**Description**

TCGA data matrix BRCA DEGs

**Format**

A data frame with 3649 rows and 6 variables

---

dataREAD	<i>TCGA data SummarizedExperiment READ</i>
----------	--

---

**Description**

TCGA data SummarizedExperiment READ

**Format**

A SummarizedExperiment of READ with 2 samples

---

dataREAD_df	<i>TCGA data matrix READ</i>
-------------	------------------------------

---

**Description**

TCGA data matrix READ

**Format**

A data frame with 20531 rows (genes) and 2 variables (samples)

---

DE_PCBC_stemSig	<i>A numeric vector with SC-derived definitive endoderm (DE) signature trained on PCBC's dataset</i>
-----------------	--

---

**Description**

A numeric vector with SC-derived definitive endoderm (DE) signature trained on PCBC's dataset

**Format**

A numeric vector with 12956 genes

---

dmc.non.parametric	<i>Perform non-parametrix wilcoxon test</i>
--------------------	---

---

**Description**

Perform non-parametrix wilcoxon test

**Usage**

```
dmc.non.parametric(
  matrix,
  idx1 = NULL,
  idx2 = NULL,
  paired = FALSE,
  adj.method = "BH",
  alternative = "two.sided",
  cores = 1
)
```

**Arguments**

matrix	A matrix
idx1	Index columns group1
idx2	Index columns group2
paired	Do a paired wilcoxon test? Default: True
adj.method	P-value adjustment method. Default:"BH" Benjamini-Hochberg
alternative	wilcoxon test alternative
cores	Number of cores to be used

**Value**

Data frame with p-values and diff mean



**Examples**

```
nrows <- 200; ncols <- 20
counts <- matrix(
  runif(nrows * ncols, 1, 1e4), nrows,
  dimnames = list(paste0("cg",1:200),paste0("S",1:20))
)
TCGAbiolinks:::dmc.non.parametric(counts,1:10,11:20)
```

---

dmc.non.parametric.se *Calculate pvalues*

---

**Description**

Calculate pvalues using wilcoxon test

**Usage**

```
dmc.non.parametric.se(
  data,
  groupCol = NULL,
  group1 = NULL,
  group2 = NULL,
  paired = FALSE,
  adj.method = "BH",
  alternative = "two.sided",
  cores = 1
)
```

**Arguments**

data	SummarizedExperiment obtained from the TCGAPrepare
groupCol	Columns with the groups inside the SummarizedExperiment object. (This will be obtained by the function colData(data))
group1	In case our object has more than 2 groups, you should set the groups
group2	In case our object has more than 2 groups, you should set the groups
paired	Do a paired wilcoxon test? Default: True
adj.method	P-value adjustment method. Default:"BH" Benjamini-Hochberg
alternative	wilcoxon test alternative
cores	Number of cores to be used

**Details**

Verify if the data is significant between two groups. For the methylation we search for probes that have a difference in the mean methylation and also a significant value. Input: A SummarizedExperiment object that will be used to compared two groups with wilcoxon test, a boolean value to do a paired or non-paired test Output: p-values (non-adj/adj) histograms, p-values (non-adj/adj)

**Value**

Data frame with cols p values/p values adjusted

Data frame with two cols p-values/p-values adjusted

**Examples**

```
nrows <- 200; ncols <- 20
counts <- matrix(runif(nrows * ncols, 1, 1e4), nrows,
  dimnames = list(paste0("cg", 1:200), LETTERS[1:20]))
rowRanges <- GenomicRanges::GRanges(rep(c("chr1", "chr2"), c(50, 150)),
  IRanges::IRanges(floor(runif(200, 1e5, 1e6)), width=100),
  strand=sample(c("+", "-"), 200, TRUE),
  feature_id=sprintf("ID%03d", 1:200))
colData <- S4Vectors::DataFrame(Treatment=rep(c("ChIP", "Input"), 10),
  row.names=LETTERS[1:20],
  group=rep(c("group1", "group2"), c(10, 10)))
data <- SummarizedExperiment::SummarizedExperiment(
  assays=S4Vectors::SimpleList(counts=counts),
  rowRanges=rowRanges,
  colData=colData)
results <- TCGAbiolinks::dmc.non.parametric.se(data, "group")
```

---

EB_PCBC_stemSig	<i>A numeric vector with stem cell (SC)-derived embryoid bodies (EB) signature trained on PCBC's dataset</i>
-----------------	--

---

**Description**

A numeric vector with stem cell (SC)-derived embryoid bodies (EB) signature trained on PCBC's dataset

**Format**

A numeric vector with 12956 genes

---

ECTO_PCBC_stemSig	<i>A numeric vector with SC-derived ectoderm (ECTO) signature trained on PCBC's dataset</i>
-------------------	---

---

**Description**

A numeric vector with SC-derived ectoderm (ECTO) signature trained on PCBC's dataset

**Format**

A numeric vector with 12956 genes

---

gaiaCNVplot	<i>Creates a plot for GAIA output (all significant aberrant regions.)</i>
-------------	---

---

**Description**

This function is a auxiliary function to visualize GAIA output (all significant aberrant regions.)

**Usage**

```
gaiaCNVplot(calls, threshold = 0.01)
```

**Arguments**

calls	A matrix with the following columns: Chromosome, Aberration Kind Region Start, Region End, Region Size and score
threshold	Score threshold (orange horizontal line in the plot)

**Value**

A plot with all significant aberrant regions.

**Examples**

```
call <- data.frame("Chromosome" = rep(9,100),
                  "Aberration Kind" = rep(c(-2,-1,0,1,2),20),
                  "Region Start [bp]" = 18259823:18259922,
                  "Region End [bp]" = 18259823:18259922,
                  "score" = rep(c(1,2,3,4),25))
gaiaCNVplot(call,threshold = 0.01)
call <- data.frame("Chromosome" = rep(c(1,9),50),
                  "Aberration Kind" = rep(c(-2,-1,0,1,2),20),
                  "Region Start [bp]" = 18259823:18259922,
                  "Region End [bp]" = 18259823:18259922,
                  "score" = rep(c(1,2,3,4),25))
gaiaCNVplot(call,threshold = 0.01)
```

---

gbm.exp.harmonized	<i>A RangedSummarizedExperiment two samples with gene expression data from vignette aligned against hg38</i>
--------------------	--

---

**Description**

A RangedSummarizedExperiment two samples with gene expression data from vignette aligned against hg38

**Format**

A RangedSummarizedExperiment: 56963 genes, 2 samples

---

gbm.exp.legacy	<i>A RangedSummarizedExperiment two samples with gene expression data from vignette aligned against hg19</i>
----------------	--

---

**Description**

A RangedSummarizedExperiment two samples with gene expression data from vignette aligned against hg19

**Format**

A RangedSummarizedExperiment: 21022 genes, 2 samples

---

GDCdownload	<i>Download GDC data</i>
-------------	--------------------------

---

**Description**

Uses GDC API or GDC transfer tool to download gdc data The user can use query argument The data from query will be save in a folder: project/data.category

**Usage**

```
GDCdownload(
  query,
  token.file,
  method = "api",
  directory = "GDCdata",
  files.per.chunk = NULL
)
```

**Arguments**

query	A query for GDCquery function
token.file	Token file to download controlled data (only for method = "client")
method	Uses the API (POST method) or gdc client tool. Options "api", "client". API is faster, but the data might get corrupted in the download, and it might need to be executed again
directory	Directory/Folder where the data was downloaded. Default: GDCdata
files.per.chunk	This will make the API method only download n (files.per.chunk) files at a time. This may reduce the download problems when the data size is too large. Expected a integer number (example files.per.chunk = 6)

**Value**

Shows the output from the GDC transfer tools

**Author(s)**

Tiago Chedraoui Silva

**Examples**

```
## Not run:
# Download clinical data from XML
query <- GDCquery(project = "TCGA-COAD", data.category = "Clinical")
GDCdownload(query, files.per.chunk = 200)
query <- GDCquery(
  project = "TARGET-AML",
  data.category = "Transcriptome Profiling",
  data.type = "miRNA Expression Quantification",
  workflow.type = "BCGSC miRNA Profiling",
  barcode = c("TARGET-20-PARUDL-03A-01R", "TARGET-20-PASRRB-03A-01R")
)
# data will be saved in:
# example_data_dir/TARGET-AML/harmonized/Transcriptome_Profiling/miRNA_Expression_Quantification
GDCdownload(query, method = "client", directory = "example_data_dir")
query_acc_gbm <- GDCquery(
  project = c("TCGA-ACC", "TCGA-GBM"),
  data.category = "Transcriptome Profiling",
  data.type = "Gene Expression Quantification",
  workflow.type = "STAR - Counts"
)
GDCdownload(
  query = query_acc_gbm,
  method = "api",
  directory = "example",
  files.per.chunk = 50
)

## End(Not run)
```

GDCprepare

*Prepare GDC data***Description**

Reads the data downloaded and prepare it into an R object

**Usage**

```
GDCprepare(
  query,
  save = FALSE,
  save.filename,
  directory = "GDCdata",
  summarizedExperiment = TRUE,
  remove.files.prepared = FALSE,
  add.gistic2.mut = NULL,
  mutant_variant_classification = c("Frame_Shift_Del", "Frame_Shift_Ins",
    "Missense_Mutation", "Nonsense_Mutation", "Splice_Site", "In_Frame_Del",
```

```
    "In_Frame_Ins", "Translation_Start_Site", "Nonstop_Mutation")
  )
```

### Arguments

```
query          A query for GDCquery function
save           Save result as RData object?
save.filename  Name of the file to be save if empty an automatic will be created
directory     Directory/Folder where the data was downloaded. Default: GDCdata
summarizedExperiment
               Create a summarizedExperiment? Default TRUE (if possible)
remove.files.prepared
               Remove the files read? Default: FALSE This argument will be considered only
               if save argument is set to true
add.gistic2.mut
               If a list of genes (gene symbol) is given, columns with gistic2 results from
               GDAC firehose (hg19) and a column indicating if there is or not mutation in
               that gene (hg38) (TRUE or FALSE - use the MAF file for more information)
               will be added to the sample matrix in the summarized Experiment object.
mutant_variant_classification
               List of mutant_variant_classification that will be consider a sample mutant or
               not. Default: "Frame_Shift_Del", "Frame_Shift_Ins", "Missense_Mutation",
               "Nonsense_Mutation", "Splice_Site", "In_Frame_Del", "In_Frame_Ins", "Trans-
               lation_Start_Site", "Nonstop_Mutation"
```

### Value

A summarizedExperiment or a data.frame

### Author(s)

Tiago Chedraoui Silva

### Examples

```
## Not run:
query <- GDCquery(
  project = "TCGA-KIRP",
  data.category = "Simple Nucleotide Variation",
  data.type = "Masked Somatic Mutation"
)
GDCdownload(query, method = "api", directory = "maf")
maf <- GDCprepare(query, directory = "maf")

## End(Not run)
```

---

GDCprepare\_clinic      *Parsing clinical xml files*

---

## Description

This function receives the query argument and parses the clinical xml files based on the desired information

## Usage

```
GDCprepare_clinic(query, clinical.info, directory = "GDCdata")
```

## Arguments

query	Result from GDCquery, with data.category set to Clinical
clinical.info	Which information should be retrieved. Options Clinical: drug, admin, follow_up, radiation, patient, stage_event or new_tumor_event Options Biospecimen: protocol, admin, aliquot, analyte, bio_patient, sample, portion, slide
directory	Directory/Folder where the data was downloaded. Default: GDCdata

## Value

A data frame with the parsed values from the XML

## Examples

```
query <- GDCquery(
  project = "TCGA-COAD",
  data.category = "Clinical",
  data.format = "bcr xml",
  barcode = c("TCGA-RU-A8FL", "TCGA-AA-3972")
)
GDCdownload(query)
clinical <- GDCprepare_clinic(query, "patient")
clinical.drug <- GDCprepare_clinic(query, "drug")
clinical.radiation <- GDCprepare_clinic(query, "radiation")
clinical.admin <- GDCprepare_clinic(query, "admin")
## Not run:
query <- GDCquery(
  project = "TCGA-COAD",
  data.category = "Biospecimen",
  data.format = "bcr xml",
  data.type = "Biospecimen Supplement",
  barcode = c("TCGA-RU-A8FL", "TCGA-AA-3972")
)
GDCdownload(query)
clinical <- GDCprepare_clinic(query, "admin")
clinical.drug <- GDCprepare_clinic(query, "sample")
clinical.radiation <- GDCprepare_clinic(query, "portion")
clinical.admin <- GDCprepare_clinic(query, "slide")

## End(Not run)
```

GDCquery

*Query GDC data***Description**

Uses GDC API to search for search, it searches for both controlled and open-access data. For GDC data arguments project, data.category, data.type and workflow.type should be used Please, see the vignette for a table with the possibilities.

**Usage**

```
GDCquery(
  project,
  data.category,
  data.type,
  workflow.type,
  access,
  platform,
  barcode,
  data.format,
  experimental.strategy,
  sample.type
)
```

**Arguments**

project	A list of valid project (see list with <code>TCGAbiolinks::getGDCprojects()\$project_id</code> )
---------	--

- BEATAML1.0-COHORT
- BEATAML1.0-CRENOLANIB
- CGCI-BLGSP
- CPTAC-2
- CPTAC-3
- CTSP-DLBCL1
- FM-AD
- HCMI-CMDC
- MMRF-COMMPASS
- NCICCR-DLBCL
- OHSU-CNL
- ORGANOID-PANCREATIC
- TARGET-ALL-P1
- TARGET-ALL-P2
- TARGET-ALL-P3
- TARGET-AML
- TARGET-CCSK
- TARGET-NBL
- TARGET-OS
- TARGET-RT



- TARGET-WT
- TCGA-ACC
- TCGA-BLCA
- TCGA-BRCA
- TCGA-CESC
- TCGA-CHOL
- TCGA-COAD
- TCGA-DLBC
- TCGA-ESCA
- TCGA-GBM
- TCGA-HNSC
- TCGA-KICH
- TCGA-KIRC
- TCGA-KIRP
- TCGA-LAML
- TCGA-LGG
- TCGA-LIHC
- TCGA-LUAD
- TCGA-LUSC
- TCGA-MESO
- TCGA-OV
- TCGA-PAAD
- TCGA-PCPG
- TCGA-PRAD
- TCGA-READ
- TCGA-SARC
- TCGA-SKCM
- TCGA-STAD
- TCGA-TGCT
- TCGA-THCA
- TCGA-THYM
- TCGA-UCEC
- TCGA-UCS
- TCGA-UVM
- VAREPOP-APOLLO

`data.category` A valid project (see list with `TCGAbiolinks::getProjectSummary(project)`) For the complete list please check the vignette. List for harmonized database:

- Biospecimen
- Clinical
- Copy Number Variation
- DNA Methylation
- Sequencing Reads
- Simple Nucleotide Variation
- Transcriptome Profiling

`data.type` A data type to filter the files to download For the complete list please check the vignette.

`workflow.type` GDC workflow type  
`access` Filter by access type. Possible values: controlled, open  
`platform` Example:

CGH- 1x1M_G4447A	IlluminaGA_RNASeqV2
AgilentG4502A_07	IlluminaGA_mRNA_DGE
Human1MDuo	HumanMethylation450
HG-CGH-415K_G4124A	IlluminaGA_miRNASeq
HumanHap550	IlluminaHiSeq_miRNASeq
ABI	H-miRNA_8x15K
HG-CGH-244A	SOLiD_DNASeq
IlluminaDNAMethylation_OMA003_CPI	IlluminaGA_DNASeq_automated
IlluminaDNAMethylation_OMA002_CPI	HG-U133_Plus_2
HuEx- 1_0-st-v2	Mixed_DNASeq
H-miRNA_8x15Kv2	IlluminaGA_DNASeq_curated
MDA_RPPA_Core	IlluminaHiSeq_TotalRNASeqV2
HT_HG-U133A	IlluminaHiSeq_DNASeq_automated
diagnostic_images	microsat_i
IlluminaHiSeq_RNASeq	SOLiD_DNASeq_curated
IlluminaHiSeq_DNASeqC	Mixed_DNASeq_curated
IlluminaGA_RNASeq	IlluminaGA_DNASeq_Cont_automated
IlluminaGA_DNASeq	IlluminaHiSeq_WGBS
pathology_reports	IlluminaHiSeq_DNASeq_Cont_automated
Genome_Wide_SNP_6	bio
tissue_images	Mixed_DNASeq_automated
HumanMethylation27	Mixed_DNASeq_Cont_curated
IlluminaHiSeq_RNASeqV2	Mixed_DNASeq_Cont

`barcode` A list of barcodes to filter the files to download  
`data.format` Data format filter ("VCF", "TXT", "BAM", "SVS", "BCR XML", "BCR SSF XML", "TSV", "BCR Auxiliary XML", "BCR OMF XML", "BCR Biotab", "MAF", "BCR PPS XML", "XLSX")  
`experimental.strategy` Filter to experimental strategy. Harmonized: WXS, RNA-Seq, miRNA-Seq, Genotyping Array.  
`sample.type` A sample type to filter the files to download

**Value**

A data frame with the results and the parameters used

**Author(s)**

Tiago Chedraoui Silva

**Examples**

```

query <- GDCquery(
  project = "TCGA-ACC",
  data.category = "Copy Number Variation",
  data.type = "Copy Number Segment"
)

```

```

## Not run:
query <- GDCquery(
  project = "TARGET-AML",
  data.category = "Transcriptome Profiling",
  data.type = "miRNA Expression Quantification",
  workflow.type = "BCGSC miRNA Profiling",
  barcode = c("TARGET-20-PARUDL-03A-01R","TARGET-20-PASRRB-03A-01R")
)
query <- GDCquery(
  project = "TARGET-AML",
  data.category = "Transcriptome Profiling",
  data.type = "Gene Expression Quantification",
  workflow.type = "STAR - Counts",
  barcode = c("TARGET-20-PADZCG-04A-01R","TARGET-20-PARJCR-09A-01R")
)
query <- GDCquery(
  project = "TCGA-ACC",
  data.category = "Copy Number Variation",
  data.type = "Masked Copy Number Segment",
  sample.type = c("Primary Tumor")
)

## End(Not run)

```

---

GDCquery\_ATAC\_seq

*Retrieve open access ATAC-seq files from GDC server*


---

## Description

Retrieve open access ATAC-seq files from GDC server [https://gdc.cancer.gov/about-data/publications/ATACseq-AWG Manifest](https://gdc.cancer.gov/about-data/publications/ATACseq-AWG_Manifest) available at: [https://gdc.cancer.gov/files/public/file/ATACseq-AWG\\_Open\\_GDC-Manifest.txt](https://gdc.cancer.gov/files/public/file/ATACseq-AWG_Open_GDC-Manifest.txt)

## Usage

```
GDCquery_ATAC_seq(tumor = NULL, file.type = NULL)
```

## Arguments

tumor	a valid tumor
file.type	Write maf file into a csv document

## Value

A data frame with the maf file information

## Examples

```

query <- GDCquery_ATAC_seq(file.type = "txt")
## Not run:
  GDCdownload(query)

## End(Not run)
query <- GDCquery_ATAC_seq(tumor = "BRCA",file.type = "bigWigs")

```

```
## Not run:
  GDCdownload(query,method = "client")

## End(Not run)
```

---

GDCquery_clinic	<i>Get GDC clinical data</i>
-----------------	------------------------------

---

### Description

GDCquery\_clinic will download all clinical information from the API as the one with using the button from each project

### Usage

```
GDCquery_clinic(project, type = "clinical", save.csv = FALSE)
```

### Arguments

project	A valid project (see list with <code>getGDCprojects()\$project_id</code> )
---------	--

- BEATAML1.0-COHORT
- BEATAML1.0-CRENOLANIB
- CGCI-BLGSP
- CPTAC-2
- CPTAC-3
- CTSP-DLBCL1
- FM-AD
- HCMI-CMDC
- MMRF-COMMPASS
- NCICCR-DLBCL
- OHSU-CNL
- ORGANOID-PANCREATIC
- TARGET-ALL-P1
- TARGET-ALL-P2
- TARGET-ALL-P3
- TARGET-AML
- TARGET-CCSK
- TARGET-NBL
- TARGET-OS
- TARGET-RT
- TARGET-WT
- TCGA-ACC
- TCGA-BLCA
- TCGA-BRCA
- TCGA-CESC
- TCGA-CHOL
- TCGA-COAD

- TCGA-DLBC
- TCGA-ESCA
- TCGA-GBM
- TCGA-HNSC
- TCGA-KICH
- TCGA-KIRC
- TCGA-KIRP
- TCGA-LAML
- TCGA-LGG
- TCGA-LIHC
- TCGA-LUAD
- TCGA-LUSC
- TCGA-MESO
- TCGA-OV
- TCGA-PAAD
- TCGA-PCPG
- TCGA-PRAD
- TCGA-READ
- TCGA-SARC
- TCGA-SKCM
- TCGA-STAD
- TCGA-TGCT
- TCGA-THCA
- TCGA-THYM
- TCGA-UCEC
- TCGA-UCS
- TCGA-UVM
- VAREPOP-APOLLO

`type` A valid type. Options "clinical", "Biospecimen" (see list with `getGDCprojects()$project_id`]  
`save.csv` Write clinical information into a csv document

**Value**

A data frame with the clinical information

**Author(s)**

Tiago Chedraoui Silva

**Examples**

```
clinical <- GDCquery_clinic(  
  project = "TCGA-ACC",  
  type = "clinical",  
  save.csv = FALSE  
)  
clinical <- GDCquery_clinic(  
  project = "TCGA-ACC",
```

```

    type = "biospecimen",
    save.csv = FALSE
  )
## Not run:
clinical_cptac_3 <- GDCquery_clinic(
  project = "CPTAC-3",
  type = "clinical"
)
clinical_cptac_2 <- GDCquery_clinic(
  project = "CPTAC-2",
  type = "clinical"
)
clinical_HCMI_CMDC <- GDCquery_clinic(
  project = "HCMI-CMDC",
  type = "clinical"
)
clinical_GCI_HTMCP_CC <- GDCquery_clinic(
  project = "CGCI-STMCP-CC",
  type = "clinical"
)
clinical <- GDCquery_clinic(
  project = "NCICCR-DLBCL",
  type = "clinical"
)
clinical <- GDCquery_clinic(
  project = "ORGANOID-PANCREATIC",
  type = "clinical"
)

## End(Not run)

```

---

geneInfo

*geneInfo for normalization of RNAseq data*

---

### Description

geneInfo for normalization of RNAseq data

### Format

A data frame with 20531 rows and 2 variables

---

geneInfoHT

*geneInfoHT for normalization of HTseq data*

---

### Description

Code to generate the data in examples

### Format

A data frame with 23486 rows and 2 variables

**Examples**

```

## Not run:
library(EDASeq)
library(biomaRt)
#get ensembl gene IDs for hg38
ensembl <- useMart("ensembl", dataset = "hsapiens_gene_ensembl")
biomart_getID <- getBM(attributes = c("ensembl_gene_id"), mart = ensembl)
#get gene length and GC content for all IDs

step <- 500
geneInfoHT <- plyr::adply(seq(1,length(biomart_getID$ensembl_gene_id),step),.margins = 1,.fun = function(x){
  begin <- x
  end <- x + step
  if(end > length(biomart_getID$ensembl_gene_id)) end <- length(biomart_getID$ensembl_gene_id)
  file <- paste0("geneInfoHT_from_",begin,"_to_",end,".rda")
  if(!file.exists(file)){
    df <- getGeneLengthAndGCCContent(biomart_getID$ensembl_gene_id[begin:end] , org="hsa", mode = c("biomart"))
    save(df,file = file)
  } else {
    df <- get(load(file))
  }
  df
},.progress = "time")
saveRDS(getdata, file = "getGLGC_download.RDS")a
save(getdata, file = "getGLGC_download.rda")
#Save output as data frame with correct header names
geneInfoHT <- data.frame(
  geneLength = getdata[,1] ,
  gcContent = getdata[,2]
)
#Save final table
save(geneInfoHT, file = "data/geneInfoHT.rda")

## End(Not run)

```

---

GenesCutID

*GenesCutID*


---

**Description**

GenesCutID

**Usage**

GenesCutID(GeneList)

**Arguments**

GeneList      GeneList

**Value**

list of gene symbol without IDs

---

GeneSplitRegulon	<i>GeneSplitRegulon</i>
------------------	-------------------------

---

**Description**

GeneSplitRegulon

**Usage**

```
GeneSplitRegulon(Genelist, Sep)
```

**Arguments**

Genelist	Genelist
Sep	Sep

**Value**

GeneSplitRegulon

---

get.GRCh.bioMart	<i>Get hg19 gene annotation or hg38 (gencode v36)</i>
------------------	---

---

**Description**

Get hg19 (from biomart) or hg38 (gencode v36) gene annotation

**Usage**

```
get.GRCh.bioMart(genome = c("hg19", "hg38"), as.granges = FALSE)
```

**Arguments**

genome	hg38 or hg19
as.granges	Output as GRanges or data.frame



---

getAdjacencyBiogrid     *Get a matrix of interactions of genes from biogrid*

---

### Description

Using biogrid database, it will create a matrix of gene interactions. If columns A and row B has value 1, it means the gene A and gene B interacts.

### Usage

```
getAdjacencyBiogrid(tmp.biogrid, names.genes = NULL)
```

### Arguments

tmp.biogrid	Biogrid table
names.genes	List of genes to filter from output. Default: consider all genes

### Value

A matrix with 1 for genes that interacts, 0 for no interaction.

### Examples

```
names.genes.de <- c("PLCB1", "MCL1", "PRDX4", "TTF2", "TACC3", "PARP4", "LSM1")
tmp.biogrid <- data.frame("Official.Symbol.Interactor.A" = names.genes.de,
                        "Official.Symbol.Interactor.B" = rev(names.genes.de))
net.biogrid.de <- getAdjacencyBiogrid(tmp.biogrid, names.genes.de)
## Not run:
file <- paste0("http://thebiogrid.org/downloads/archives/",
              "Release%20Archive/BIOGRID-3.4.133/BIOGRID-ALL-3.4.133.tab2.zip")
downloader::download(file, basename(file))
unzip(basename(file), junkpaths = TRUE)
tmp.biogrid <- read.csv(gsub("zip", "txt", basename(file)),
                      header = TRUE, sep = "\t", stringsAsFactors = FALSE)
names.genes.de <- c("PLCB1", "MCL1", "PRDX4", "TTF2", "TACC3", "PARP4", "LSM1")
net.biogrid.de <- getAdjacencyBiogrid(tmp.biogrid, names.genes.de)

## End(Not run)
```

---

getDataCategorySummary

*Create a Summary table for each sample in a project saying if it contains or not files for a certain data category*

---

### Description

Create a Summary table for each sample in a project saying if it contains or not files for a certain data category

**Usage**

```
getDataCategorySummary(project)
```

**Arguments**

project            A GDC project

**Value**

A data frame

**Author(s)**

Tiago Chedraoui Silva

**Examples**

```
summary <- getDataCategorySummary("TCGA-ACC")
```

---

getGDCInfo

*Check GDC server status*

---

**Description**

Check GDC server status using the api <https://api.gdc.cancer.gov/status>

**Usage**

```
getGDCInfo()
```

**Value**

Return true all status

**Examples**

```
info <- getGDCInfo()
```

---

getGDCprojects	<i>Retrieve all GDC projects</i>
----------------	----------------------------------

---

**Description**

getGDCprojects uses the following api to get projects <https://api.gdc.cancer.gov/projects>

**Usage**

```
getGDCprojects()
```

**Value**

A data frame with last GDC projects

**Examples**

```
projects <- getGDCprojects()
```

---

getGistic	<i>Download GISTIC data from firehose</i>
-----------	---

---

**Description**

Download GISTIC data from firehose from [http://gdac.broadinstitute.org/runs/analyses\\_\\_latest/data/](http://gdac.broadinstitute.org/runs/analyses__latest/data/)

**Usage**

```
getGistic(disease, type = "thresholded")
```

**Arguments**

disease	TCGA disease. Option available in <a href="http://gdac.broadinstitute.org/runs/analyses__latest/data/">http://gdac.broadinstitute.org/runs/analyses__latest/data/</a>
type	Results type: thresholded or data

---

getLinkedOmicsData     *Retrieve linkedOmics data*

---

### Description

Retrieve linkedOmics data from <http://linkedomics.org/>

### Usage

```
getLinkedOmicsData(project, dataset)
```

### Arguments

project     A linkedOmics project:

- TCGA-ACC
- TCGA-BLCA
- TCGA-BRCA
- TCGA-CESC
- TCGA-CHOL
- TCGA-COADREAD
- TCGA-DLBC
- TCGA-ESCA
- TCGA-GBM
- TCGA-GBMLGG
- TCGA-HNSC
- TCGA-KICH
- TCGA-KIPAN
- TCGA-KIRC
- TCGA-KIRP
- TCGA-LAML
- TCGA-LGG
- TCGA-LIHC
- TCGA-LUAD
- TCGA-LUSC
- TCGA-MESO
- TCGA-OV
- TCGA-PAAD
- TCGA-PCPG
- TCGA-PRAD
- TCGA-SARC
- TCGA-SKCM
- TCGA-STAD
- TCGA-STES
- TCGA-TGCT
- TCGA-THCA
- TCGA-THYM

- TCGA-UCEC
  - TCGA-UCS
  - TCGA-UVM
  - CPTAC-COAD
- dataset
- A dataset from the list below
- Annotated mutation
  - Clinical
  - Glycoproteome (Gene level)
  - Glycoproteome (Site level)
  - Methylation (CpG-site level, HM27)
  - Methylation (CpG-site level, HM450K)
  - Methylation (Gene level, HM27)
  - Methylation (Gene level, HM450K)
  - miRNA (GA, Gene level)
  - miRNA (GA, Isoform level)
  - miRNA (GA, miRgene level)
  - miRNA (Gene level)
  - miRNA (HiSeq, Gene level)
  - miRNA (HiSeq, miRgene level)
  - miRNA (isoform level)
  - miRNA (miRgene level)
  - Mutation (Gene level)
  - Mutation (Site level)
  - Mutation raw file (Somatic and MSIndel)
  - Phosphoproteome (Gene level)
  - Phosphoproteome (Site level)
  - Phosphoproteomics (Normal)
  - Phosphoproteomics (Tumor)
  - Proteome (Gene level)
  - Proteome (Gene Level)
  - Proteome (JHU, Gene level)
  - Proteome (PNNL, Gene level, Normal TMT Unshared Log Ratio)
  - Proteome (PNNL, Gene level, Tumor TMT Unshared Log Ratio)
  - Proteome (PNNL, Gene level)
  - Proteome (VU, Gene level, Label-free Unshared Counts)
  - RNAseq (GA, Gene level)
  - RNAseq (HiSeq, Gene level)
  - RPPA (Analyte level)
  - RPPA (Analyte Level)
  - RPPA (Gene level)
  - RPPA (Gene Level)
  - SCNV (Focal level, log-ratio)
  - SCNV (Focal level, Thresholded)
  - SCNV (Gene level, log ratio)
  - SCNV (Gene level, log-ratio)
  - SCNV (Gene level, Thresholded)
  - SCNV (Segment level)

**Value**

A matrix with the data

**Examples**

```
## Not run:
TCGA_COAD_protein <- getLinkedOmicsData(
  project = "TCGA-COADREAD",
  dataset = "Proteome (Gene level)"
)
TCGA_COAD_RNASeq_hiseq <- getLinkedOmicsData(
  project = "TCGA-COADREAD",
  dataset = "RNAseq (HiSeq, Gene level)"
)
TCGA_COAD_RNASeq_ga <- getLinkedOmicsData(
  project = "TCGA-COADREAD",
  dataset = "RNAseq (GA, Gene level)"
)
TCGA_COAD_RPPA <- getLinkedOmicsData(
  project = "TCGA-COADREAD",
  dataset = "RPPA (Gene level)"
)

## End(Not run)
```

---

getManifest	<i>Get a Manifest from GDCquery output that can be used with GDC-client</i>
-------------	---

---

**Description**

Get a Manifest from GDCquery output that can be used with GDC-client

**Usage**

```
getManifest(query, save = FALSE)
```

**Arguments**

query	A query for GDCquery function
save	Write Manifest to a txt file (tab separated)

**Examples**

```
query <- GDCquery(
  project = "TARGET-AML",
  data.category = "Transcriptome Profiling",
  data.type = "Gene Expression Quantification",
  workflow.type = "STAR - Counts",
  barcode = c("TARGET-20-PADZCG-04A-01R", "TARGET-20-PARJCR-09A-01R")
)
getManifest(query)
```

---

`getMC3MAF`*Retrieve open access mc3 MAF file from GDC server*

---

**Description**

Download data from <https://gdc.cancer.gov/about-data/publications/mc3-2017> <https://gdc-docs.nci.nih.gov/Data/Release>

**Usage**

```
getMC3MAF()
```

**Value**

A data frame with the MAF file information from <https://gdc.cancer.gov/about-data/publications/mc3-2017>

**Examples**

```
## Not run:  
maf <- getMC3MAF()  
  
## End(Not run)
```

---

`getNbCases`*Get Number of cases in GDC for a project*

---

**Description**

Get Number of cases in GDC for a project

**Usage**

```
getNbCases(project, data.category)
```

**Arguments**

```
project      A GDC project  
data.category A GDC project data category
```

**Author(s)**

Tiago Chedraoui Silva

**Examples**

```
## Not run:  
getNbCases("TCGA-ACC", "Clinical")  
getNbCases("CPTAC-2", "Clinical")  
  
## End(Not run)
```

---

getNbFiles                      *Get Number of files in GDC for a project*

---

**Description**

Get Number of files in GDC for a project

**Usage**

```
getNbFiles(project, data.category)
```

**Arguments**

```
project                      A GDC project
data.category                A GDC project data category
```

**Author(s)**

Tiago Chedraoui Silva

**Examples**

```
## Not run:
getNbFiles("TCGA-ACC", "Clinical")
getNbFiles("CPTAC-2", "Clinical")

## End(Not run)
```

---

getProjectSummary              *Get Project Summary from GDC*

---

**Description**

Get Project Summary from GDC

**Usage**

```
getProjectSummary(project)
```

**Arguments**

```
project                      A GDC project
```

**Author(s)**

Tiago Chedraoui Silva



**Examples**

```
getProjectSummary("TCGA-ACC")
## Not run:
getProjectSummary("CPTAC-2")

## End(Not run)
```

---

getResults	<i>Get the results table from query</i>
------------	---

---

**Description**

Get the results table from query, it can select columns with cols argument and return a number of rows using rows argument.

**Usage**

```
getResults(query, rows, cols)
```

**Arguments**

query	A object from GDCquery
rows	Rows identifiers (row numbers)
cols	Columns identifiers (col names)

**Value**

Table with query results

**Examples**

```
query <- GDCquery(
  project = "TCGA-GBM",
  data.category = "Transcriptome Profiling",
  data.type = "Gene Expression Quantification",
  workflow.type = "STAR - Counts",
  barcode = c("TCGA-14-0736-02A-01R-2005-01", "TCGA-06-0211-02A-02R-2005-01")
)
results <- getResults(query)
```

---

getSampleFilesSummary *Retrieve summary of files per sample in a project*

---

### Description

Retrieve the number of files under each data\_category + data\_type + experimental\_strategy + platform Almost like <https://portal.gdc.cancer.gov/exploration>

### Usage

```
getSampleFilesSummary(project, files.access = NA)
```

### Arguments

project            A GDC project  
files.access      Filter by file access ("open" or "controlled"). Default: no filter

### Value

A data frame with the maf file information

### Author(s)

Tiago Chedraoui Silva

### Examples

```
summary <- getSampleFilesSummary("TCGA-UCS")
## Not run:
summary <- getSampleFilesSummary(c("TCGA-OV", "TCGA-ACC"))

## End(Not run)
```

---

getTSS            *getTSS to fetch GENCODE gene annotation (transcripts level) from Bioconductor package biomaRt If upstream and downstream are specified in TSS list, promoter regions of GENCODE gene will be generated.*

---

### Description

getTSS to fetch GENCODE gene annotation (transcripts level) from Bioconductor package biomaRt If upstream and downstream are specified in TSS list, promoter regions of GENCODE gene will be generated.

### Usage

```
getTSS(
  genome = c("hg38", "hg19"),
  TSS = list(upstream = NULL, downstream = NULL)
)
```

**Arguments**

genome	Which genome build will be used: hg38 (default) or hg19.
TSS	A list. Contains upstream and downstream like TSS=list(upstream, downstream). When upstream and downstream is specified, coordinates of promoter regions with gene annotation will be generated.

**Value**

GENCODE gene annotation if TSS is not specified. Coordinates of GENCODE gene promoter regions if TSS is specified.

**Examples**

```
# get GENCODE gene annotation (transcripts level)
## Not run:
  getTSS <- getTSS()
  getTSS <- getTSS(genome.build = "hg38", TSS=list(upstream=1000, downstream=1000))

## End(Not run)
```

---

get\_IDs

---

*Extract information from TCGA barcodes.*


---

**Description**

get\_IDs allows user to extract metadata from barcodes. The dataframe returned has columns for 'project', 'tss', 'participant', 'sample', "portion", "plate", and "center"

**Usage**

```
get_IDs(data)
```

**Arguments**

data	numeric matrix, each row represents a gene, each column represents a sample
------	---

**Value**

data frame with columns 'project', 'tss', 'participant', 'sample', "portion", "plate", "center", "condition"

**Description**

Biplot for Principal Components using ggplot2

**Usage**

```
ggbiplot(
  pcoobj,
  choices = 1:2,
  scale = 1,
  pc.biplot = TRUE,
  obs.scale = 1 - scale,
  var.scale = scale,
  groups = NULL,
  ellipse = FALSE,
  ellipse.prob = 0.68,
  labels = NULL,
  labels.size = 3,
  alpha = 1,
  var.axes = TRUE,
  circle = FALSE,
  circle.prob = 0.69,
  varname.size = 3,
  varname.adjust = 1.5,
  varname.abbrev = FALSE
)
```

**Arguments**

pcoobj	an object returned by prcomp() or princomp()
choices	which PCs to plot
scale	covariance biplot (scale = 1), form biplot (scale = 0). When scale = 1, the inner product between the variables approximates the covariance and the distance between the points approximates the Mahalanobis distance.
pc.biplot	for compatibility with biplot.princomp()
obs.scale	scale factor to apply to observations
var.scale	scale factor to apply to variables
groups	optional factor variable indicating the groups that the observations belong to. If provided the points will be colored according to groups
ellipse	draw a normal data ellipse for each group?
ellipse.prob	size of the ellipse in Normal probability
labels	optional vector of labels for the observations
labels.size	size of the text used for the labels
alpha	alpha transparency value for the points (0 = transparent, 1 = opaque)

<code>var.axes</code>	draw arrows for the variables?
<code>circle</code>	draw a correlation circle? (only applies when <code>prcomp</code> was called with <code>scale = TRUE</code> and when <code>var.scale = 1</code> )
<code>circle.prob</code>	definition of <code>circle.prob</code>
<code>varname.size</code>	size of the text for variable names
<code>varname.adjust</code>	adjustment factor the placement of the variable names, $\geq 1$ means farther from the arrow
<code>varname.abbrev</code>	whether or not to abbreviate the variable names

**Value**

A `ggplot2` plot

**Author(s)**

Vincent Q. Vu.

---

<code>gliomaClassifier</code>	<i>Glioma classifier</i>
-------------------------------	--------------------------

---

**Description**

Classify DNA methylation gliomas using data from <https://doi.org/10.1016/j.cell.2015.12.028>

**Usage**

```
gliomaClassifier(data)
```

**Arguments**

<code>data</code>	DNA methylation matrix or Summarized Experiments with samples on columns and probes on the rows
-------------------	---

**Value**

A list of 3 data frames: 1) Sample final classification 2) Each model final classification 3) Each class probability of classification

**Author(s)**

Tiago Chedraoui Silva, Tathiane Malta, Houtan Noushmehr

**Examples**

```
## Not run:
query <- GDCquery(
  project= "TCGA-GBM",
  data.category = "DNA methylation",
  barcode = c("TCGA-06-0122", "TCGA-14-1456"),
  platform = "Illumina Human Methylation 27",
  legacy = TRUE
)
GDCdownload(query)
data.hg19 <- GDCprepare(query)
classification <- gliomaClassifier(data.hg19)

# Comparing results
TCGAquery_subtype("GBM") %>%
dplyr::filter(patient %in% c("TCGA-06-0122", "TCGA-14-1456")) %>%
dplyr::select("patient", "Supervised.DNA.Methylation.Cluster")

## End(Not run)
```

---

isServeOK	<i>Check GDC server status is OK</i>
-----------	--------------------------------------

---

**Description**

Check GDC server status using the api <https://api.gdc.cancer.gov/status>

**Usage**

```
isServeOK()
```

**Value**

Return true if status is ok

**Examples**

```
status <- isServeOK()
```

---

matchedMetExp	<i>Get GDC primary tumors samples with both DNA methylation (HM450K) and Gene expression data</i>
---------------	---

---

**Description**

For a given TCGA project it gets the primary tumors samples (barcode) with both DNA methylation and Gene expression data from GDC database

**Usage**

```
matchedMetExp(project, n = NULL)
```

**Arguments**

project            A GDC project  
 n                    Number of samples to return. If NULL return all (default)

**Value**

A vector of barcodes

**Examples**

```
# Get ACC samples with both DNA methylation (HM450K) and gene expression aligned to hg19
samples <- matchedMetExp("TCGA-UCS")
```

---

MESO\_PCBC\_stemSig      *A numeric vector with SC-derived mesoderm (MESO) signature trained on PCBC's dataset*

---

**Description**

A numeric vector with SC-derived mesoderm (MESO) signature trained on PCBC's dataset

**Format**

A numeric vector with 12956 genes

---

met.gbm.27k            *A DNA methylation RangedSummarizedExperiment for 8 samples (only first 20 probes) aligned against hg19*

---

**Description**

A DNA methylation RangedSummarizedExperiment for 8 samples (only first 20 probes) aligned against hg19

**Format**

A RangedSummarizedExperiment: 20 probes, 8 samples

---

msi\_results            *MSI data for two samples*

---

**Description**

MSI data for two samples

**Format**

A data frame: 2 rows, 4 columns

---

pancan2018

*A data frame with all TCGA molecular subtypes*

---

### Description

A data frame with all TCGA molecular subtypes

### Format

A data frame with 7,734 lines and 10 columns

---

PanCancerAtlas\_subtypes

*Retrieve table with TCGA molecular subtypes*

---

### Description

PanCancerAtlas\_subtypes is a curated table with molecular subtypes for 24 TCGA cancer types

### Usage

```
PanCancerAtlas_subtypes()
```

### Value

a data.frame with barcode and molecular subtypes for 24 cancer types

### Examples

```
molecular.subtypes <- PanCancerAtlas_subtypes()
```

---

SC\_PCBC\_stemSig

*A numeric vector with stem cell-like signature trained on PCBC's dataset*

---

### Description

A numeric vector with stem cell-like signature trained on PCBC's dataset

### Format

A numeric vector with 12956 genes



---

splitAPICall	<i>internal function to break a huge API call into smaller ones so it respects the max character limit of a string</i>
--------------	--

---

**Description**

internal function to break a huge API call into smaller ones so it respects the max character limit of a string

**Usage**

```
splitAPICall(FUN, step = 20, items)
```

**Arguments**

FUN	function that calls the API
step	How many items to be evaluated per API call
items	vector of items to be using within the function (list of barcodes, aliquot ids, etc)

**Author(s)**

Tiago Chedraoui Silva

---

TabSubtypesCol_merged	<i>TCGA samples with their Pam50 subtypes</i>
-----------------------	---

---

**Description**

A dataset containing the Sample Ids from TCGA and PAM50 subtyping attributes of 4768 tumor patients

**Usage**

```
TabSubtypesCol_merged
```

**Format**

A data frame with 4768 rows and 3 variables:

**samples** Sample ID from TCGA barcodes, character string

**subtype** Pam50 classification, character string

**color** color, character string ...

---

tabSurvKMcompleteDEGs *tabSurvKMcompleteDEGs*

---

### Description

tabSurvKMcompleteDEGs

### Format

A data frame with 200 rows and 7 variables

---

TCGAanalyze\_analyseGRN

*Generate network*

---

### Description

TCGAanalyze\_analyseGRN perform gene regulatory network.

### Usage

TCGAanalyze\_analyseGRN(TFs, normCounts, kNum)

### Arguments

TFs	a vector of genes.
normCounts	is a matrix of gene expression with genes in rows and samples in columns.
kNum	the number of nearest neighbors to consider to estimate the mutual information. Must be less than the number of columns of normCounts.

### Value

an adjacent matrix

---

TCGAanalyze\_Clustering

*Hierarchical cluster analysis*

---

### Description

Hierarchical cluster analysis using several methods such as ward.D", "ward.D2", "single", "complete", "average" (= UPGMA), "mcquitty" (= WPGMA), "median" (= WPGMC) or "centroid" (= UPGMC).

### Usage

TCGAanalyze\_Clustering(tabDF, method, methodHC = "ward.D2")

**Arguments**

tabDF	is a dataframe or numeric matrix, each row represents a gene, each column represents a sample come from TCGAPrepare.
method	is method to be used for generic cluster such as 'hclust' or 'consensus'
methodHC	is method to be used for Hierarchical cluster.

**Value**

object of class hclust if method selected is 'hclust'. If method selected is 'Consensus' returns a list of length maxK (maximum cluster number to evaluate.). Each element is a list containing consensus-Matrix (numerical matrix), consensusTree (hclust), consensusClass (consensus class assignments). ConsensusClusterPlus also produces images.

---

TCGAanalyze\_DEA

*Differential expression analysis (DEA) using edgeR or limma package.*


---

**Description**

TCGAanalyze\_DEA allows user to perform Differentially expression analysis (DEA), using edgeR package or limma to identify differentially expressed genes (DEGs). It is possible to do a two-class analysis.

TCGAanalyze\_DEA performs DEA using following functions from edgeR:

1. edgeR::DGEList converts the count matrix into an edgeR object.
2. edgeR::estimateCommonDisp each gene gets assigned the same dispersion estimate.
3. edgeR::exactTest performs pair-wise tests for differential expression between two groups.
4. edgeR::topTags takes the output from exactTest(), adjusts the raw p-values using the False Discovery Rate (FDR) correction, and returns the top differentially expressed genes.

TCGAanalyze\_DEA performs DEA using following functions from limma:

1. limma::makeContrasts construct matrix of custom contrasts.
2. limma::lmFit Fit linear model for each gene given a series of arrays.
3. limma::contrasts.fit Given a linear model fit to microarray data, compute estimated coefficients and standard errors for a given set of contrasts.
4. limma::eBayes Given a microarray linear model fit, compute moderated t-statistics, moderated F-statistic, and log-odds of differential expression by empirical Bayes moderation of the standard errors towards a common value.
5. limma::topTable Extract a table of the top-ranked genes from a linear model fit.

**Usage**

```
TCGAanalyze_DEA(
  mat1,
  mat2,
  metadata = TRUE,
  Cond1type,
  Cond2type,
  pipeline = "edgeR",
```

```

method = "exactTest",
fdr.cut = 1,
logFC.cut = 0,
batch.factors = NULL,
ClinicalDF = data.frame(),
paired = FALSE,
log.trans = FALSE,
voom = FALSE,
trend = FALSE,
MAT = data.frame(),
contrast.formula = "",
Condtypes = c()
)

```

### Arguments

mat1	numeric matrix, each row represents a gene, each column represents a sample with Cond1type
mat2	numeric matrix, each row represents a gene, each column represents a sample with Cond2type
metadata	Add metadata
Cond1type	a string containing the class label of the samples in mat1 (e.g., control group)
Cond2type	a string containing the class label of the samples in mat2 (e.g., case group)
pipeline	a string to specify which package to use ("limma" or "edgeR")
method	is 'glmLRT' (1) or 'exactTest' (2) used for edgeR (1) Fit a negative binomial generalized log-linear model to the read counts for each gene (2) Compute gene-wise exact tests for differences in the means between two groups of negative-binomially distributed counts.
fdr.cut	is a threshold to filter DEGs according their p-value corrected
logFC.cut	is a threshold to filter DEGs according their logFC
batch.factors	a vector containing strings to specify options for batch correction. Options are "Plate", "TSS", "Year", "Portion", "Center", and "Patients"
ClinicalDF	a dataframe returned by GDCquery_clinic() to be used to extract year data
paired	boolean to account for paired or non-paired samples. Set to TRUE for paired case
log.trans	boolean to perform log cpm transformation. Set to TRUE for log transformation
voom	boolean to perform voom transformation for limma-voom pipeline. Set to TRUE for voom transformation
trend	boolean to perform limma-trend pipeline. Set to TRUE to go through limma-trend
MAT	matrix containing expression set as all samples in columns and genes as rows. Do not provide if mat1 and mat2 are used
contrast.formula	string input to determine coefficients and to design contrasts in a customized way
Condtypes	vector of grouping for samples in MAT

**Value**

table with DEGs containing for each gene logFC, logCPM, pValue, and FDR, also for each contrast

**Examples**

```
dataNorm <- TCGAbiolinks::TCGAanalyze_Normalization(dataBRCA, geneInfo)
dataFilt <- TCGAanalyze_Filtering(tabDF = dataBRCA, method = "quantile", qnt.cut = 0.25)
samplesNT <- TCGAquery_SampleTypes(colnames(dataFilt), typesample = c("NT"))
samplesTP <- TCGAquery_SampleTypes(colnames(dataFilt), typesample = c("TP"))
dataDEGs <- TCGAanalyze_DEA(
  mat1 = dataFilt[,samplesNT],
  mat2 = dataFilt[,samplesTP],
  Cond1type = "Normal",
  Cond2type = "Tumor"
)
```

---

TCGAanalyze\_DEA\_Affy *Differentially expression analysis (DEA) using limma package.*

---

**Description**

Differentially expression analysis (DEA) using limma package.

**Usage**

```
TCGAanalyze_DEA_Affy(AffySet, FC.cut = 0.01)
```

**Arguments**

AffySet	A matrix-like data object containing log-ratios or log-expression values for a series of arrays, with rows corresponding to genes and columns to samples
FC.cut	write

**Value**

List of list with tables in 2 by 2 comparison of the top-ranked genes from a linear model fitted by DEA's limma

**Examples**

```
## Not run:
to add example

## End(Not run)
```

**Description**

This function will search for differentially methylated CpG sites, which are regarded as possible functional regions involved in gene transcriptional regulation.

In order to find these regions we use the beta-values (methylation values ranging from 0.0 to 1.0) to compare two groups.

Firstly, it calculates the difference between the mean methylation of each group for each probes. Secondly, it calculates the p-value using the wilcoxon test using the Benjamini-Hochberg adjustment method. The default parameters will require a minimum absolute beta values delta of 0.2 and a false discovery rate (FDR)-adjusted Wilcoxon rank-sum P-value of < 0.01 for the difference.

After these analysis, we save a volcano plot (x-axis:diff mean methylation, y-axis: significance) that will help the user identify the differentially methylated CpG sites and return the object with the calculus in the rowRanges.

If the calculus already exists in the object it will not recalculated. You should set overwrite parameter to TRUE to force it, or remove the columns with the results from the object.

**Usage**

```
TCGAanalyze_DMC(
  data,
  groupCol = NULL,
  group1 = NULL,
  group2 = NULL,
  alternative = "two.sided",
  diffmean.cut = 0.2,
  paired = FALSE,
  adj.method = "BH",
  plot.filename = "methylation_volcano.pdf",
  ylab = expression(paste(-Log[10], " (FDR corrected P-values)")),
  xlab = expression(paste("DNA Methylation difference (", beta, "-values)")),
  title = NULL,
  legend = "Legend",
  color = c("black", "red", "darkgreen"),
  label = NULL,
  xlim = NULL,
  ylim = NULL,
  p.cut = 0.01,
  probe.names = FALSE,
  cores = 1,
  save = TRUE,
  save.directory = ".",
  filename = NULL
)
```

**Arguments**

data                      SummarizedExperiment obtained from the TCGAPrepare

groupCol	Columns with the groups inside the SummarizedExperiment object. (This will be obtained by the function colData(data))
group1	In case our object has more than 2 groups, you should set the name of the group
group2	In case our object has more than 2 groups, you should set the name of the group
alternative	wilcoxon test alternative
diffmean.cut	diffmean threshold. Default: 0.2
paired	Wilcoxon paired parameter. Default: FALSE
adj.method	Adjusted method for the p-value calculation
plot.filename	Filename. Default: volcano.pdf, volcano.svg, volcano.png. If set to FALSE, there will be no plot.
ylab	y axis text
xlab	x axis text
title	main title. If not specified it will be "Volcano plot (group1 vs group2)
legend	Legend title
color	vector of colors to be used in graph
label	vector of labels to be used in the figure. Example: c("Not Significant", "Hypermethylated in group1", "Hypomethylated in group1")
xlim	x limits to cut image
ylim	y limits to cut image
p.cut	p values threshold. Default: 0.01
probe.names	is probe.names
cores	Number of cores to be used in the non-parametric test Default = groupCol.group1.group2.rda
save	Save object with results? Default: TRUE
save.directory	Directory to save the files. Default: working directory
filename	Name of the file to save the object.

## Value

Volcano plot saved and the given data with the results (diffmean.group1.group2,p.value.group1.group2, p.value.adj.group1.group2,status.group1.group2) in the rowRanges where group1 and group2 are the names of the groups

## Examples

```
nrows <- 200; ncols <- 20
counts <- matrix(
  runif(nrows * ncols, 1, 1e4), nrows,
  dimnames = list(paste0("cg",1:200),paste0("S",1:20))
)
rowRanges <- GenomicRanges::GRanges(
  rep(c("chr1", "chr2"), c(50, 150)),
  IRanges::IRanges(floor(runif(200, 1e5, 1e6)), width = 100),
  strand = sample(c("+", "-"), 200, TRUE),
  feature_id = sprintf("ID%03d", 1:200)
)
names(rowRanges) <- paste0("cg",1:200)
colData <- S4Vectors::DataFrame(
  Treatment = rep(c("ChIP", "Input"), 5),
```

```

    row.names = paste0("S",1:20),
    group = rep(c("group1","group2"),c(10,10))
  )
data <- SummarizedExperiment::SummarizedExperiment(
  assays=S4Vectors::SimpleList(counts=counts),
  rowRanges = rowRanges,
  colData = colData
)
SummarizedExperiment::colData(data)$group <- c(rep("group 1",ncol(data)/2),
  rep("group 2",ncol(data)/2))
hypo.hyper <- TCGAanalyze_DMC(data, p.cut = 0.85,"group","group 1","group 2")
SummarizedExperiment::colData(data)$group2 <- c(rep("group_1",ncol(data)/2),
  rep("group_2",ncol(data)/2))
hypo.hyper <- TCGAanalyze_DMC(
  data = data,
  p.cut = 0.85,
  groupCol = "group2",
  group1 = "group_1",
  group2 = "group_2"
)

```

---

TCGAanalyze\_EA

*Enrichment analysis of a gene-set with GO [BP,MF,CC] and pathways.*


---

## Description

The rationale behind an enrichment analysis (gene-set, pathway etc) is to compute statistics of whether the overlap between the focus list (signature) and the gene-set is significant. ie the confidence that overlap between the list is not due to chance. The Gene Ontology project describes genes (gene products) using terms from three structured vocabularies: biological process, cellular component and molecular function. The Gene Ontology Enrichment component, also referred to as the "GO Terms" component, allows the genes in any such "changed-gene" list to be characterized using the Gene Ontology terms annotated to them. It asks, whether for any particular GO term, the fraction of genes assigned to it in the "changed-gene" list is higher than expected by chance (is over-represented), relative to the fraction of genes assigned to that term in the reference set. In statistical terms it performs the analysis tests the null hypothesis that, for any particular ontology term, there is no difference in the proportion of genes annotated to it in the reference list and the proportion annotated to it in the test list. We adopted a Fisher Exact Test to perform the EA.

## Usage

```

TCGAanalyze_EA(
  GeneName,
  RegulonList,
  TableEnrichment,
  EAGenes,
  GOtype,
  FDRThresh = 0.01,
  GeneSymbolsTable = FALSE
)

```



**Arguments**

GeneName	is the name of gene signatures list
RegulonList	is a gene signature (list of genes) in which perform EA.
TableEnrichment	is a table related to annotations of gene symbols such as GO[BP,MF,CC] and Pathways. It was created from DAVID gene ontology on-line.
EAGenes	is a table with informations about genes such as ID, Gene, Description, Location and Family.
GOtype	is type of gene ontology Biological process (BP), Molecular Function (MF), Cellular componet (CC)
FDRThresh	pvalue corrected (FDR) as threshold to selected significant BP, MF,CC, or pathways. (default FDR < 0.01)
GeneSymbolsTable	if it is TRUE will return a table with GeneSymbols in common GO or pathways.

**Value**

Table with enriched GO or pathways by selected gene signature.

**Examples**

```
## Not run:
EAGenes <- get("EAGenes")
RegulonList <- rownames(dataDEGsFiltLevel)
ResBP <- TCGAanalyze_EA(
  GeneName="DEA genes Normal Vs Tumor",
  RegulonList = RegulonList,
  TableEnrichment = DAVID_BP_matrix,
  EAGenes = EAGenes,
  GOtype = "DavidBP"
)

## End(Not run)
```

---

TCGAanalyze\_EAcomplete

*Enrichment analysis for Gene Ontology (GO) [BP,MF,CC] and Pathways*

---

**Description**

Researchers, in order to better understand the underlying biological processes, often want to retrieve a functional profile of a set of genes that might have an important role. This can be done by performing an enrichment analysis.

We will perform an enrichment analysis on gene sets using the TCGAanalyze\_EAcomplete function. Given a set of genes that are up-regulated under certain conditions, an enrichment analysis will find identify classes of genes or proteins that are # over-represented using annotations for that gene set.

**Usage**

```
TCGAanalyze_EAcomplete(TFname, RegulonList)
```

**Arguments**

TFname is the name of the list of genes or TF's regulon.  
RegulonList List of genes such as TF's regulon or DEGs where to find enrichment.

**Value**

Enrichment analysis GO[BP,MF,CC] and Pathways complete table enriched by genelist.

**Examples**

```
Genelist <- c("FN1","COL1A1")
ansEA <- TCGAanalyze_EAcomplete(TFname="DEA genes Normal Vs Tumor",Genelist)
## Not run:
Genelist <- rownames(dataDEGsFiltLevel)
system.time(ansEA <- TCGAanalyze_EAcomplete(TFname="DEA genes Normal Vs Tumor",Genelist))

## End(Not run)
```

---

TCGAanalyze\_Filtering *Filtering mRNA transcripts and miRNA selecting a threshold.*

---

**Description**

TCGAanalyze\_Filtering allows user to filter mRNA transcripts and miRNA, samples, higher than the threshold defined quantile mean across all samples.

**Usage**

```
TCGAanalyze_Filtering(
  tabDF,
  method,
  qnt.cut = 0.25,
  var.func = IQR,
  var.cutoff = 0.75,
  eta = 0.05,
  foldChange = 1
)
```

**Arguments**

tabDF is a dataframe or numeric matrix, each row represents a gene, each column represents a sample come from TCGAPrepare  
method is method of filtering such as 'quantile', 'varFilter', 'filter1', 'filter2'  
qnt.cut is threshold selected as mean for filtering  
var.func is function used as the per-feature filtering statistic. See genefilter documentation

var.cutoff is a numeric value. See genefilter documentation  
 eta is a parameter for filter1. default eta = 0.05.  
 foldChange is a parameter for filter2. default foldChange = 1.

**Value**

A filtered dataframe or numeric matrix where each row represents a gene, each column represents a sample

**Examples**

```
dataNorm <- TCGAbiolinks::TCGAanalyze_Normalization(dataBRCA, geneInfo)
dataNorm <- TCGAanalyze_Normalization(tabDF = dataBRCA,
geneInfo = geneInfo,
method = "geneLength")
dataFilt <- TCGAanalyze_Filtering(tabDF = dataNorm, method = "quantile", qnt.cut = 0.25)
```

---

TCGAanalyze\_LevelTab *Adding information related to DEGs genes from DEA as mean values in two conditions.*

---

**Description**

TCGAanalyze\_LevelTab allows user to add information related to DEGs genes from Differentially expression analysis (DEA) such as mean values and in two conditions.

**Usage**

```
TCGAanalyze_LevelTab(
  FC_FDR_table_mRNA,
  typeCond1,
  typeCond2,
  TableCond1,
  TableCond2,
  typeOrder = TRUE
)
```

**Arguments**

FC\_FDR\_table\_mRNA Output of dataDEGs filter by  $\text{abs}(\text{LogFC}) \geq 1$

typeCond1 a string containing the class label of the samples in TableCond1 (e.g., control group)

typeCond2 a string containing the class label of the samples in TableCond2 (e.g., case group)

TableCond1 numeric matrix, each row represents a gene, each column represents a sample with Cond1type

TableCond2 numeric matrix, each row represents a gene, each column represents a sample with Cond2type

typeOrder typeOrder

**Value**

table with DEGs, log Fold Change (FC), false discovery rate (FDR), the gene expression level for samples in Cond1type, and Cond2type, and Delta value (the difference of gene expression between the two conditions multiplied logFC)

**Examples**

```

dataNorm <- TCGAbiolinks::TCGAanalyze_Normalization(dataBRCA, geneInfo)
dataFilt <- TCGAanalyze_Filtering(tabDF = dataBRCA, method = "quantile", qnt.cut = 0.25)
samplesNT <- TCGAquery_SampleTypes(colnames(dataFilt), typesample = c("NT"))
samplesTP <- TCGAquery_SampleTypes(colnames(dataFilt), typesample = c("TP"))
dataDEGs <- TCGAanalyze_DEA(
  dataFilt[,samplesNT],
  dataFilt[,samplesTP],
  Cond1type = "Normal",
  Cond2type = "Tumor"
)
dataDEGsFilt <- dataDEGs[abs(dataDEGs$logFC) >= 1,]
dataTP <- dataFilt[,samplesTP]
dataTN <- dataFilt[,samplesNT]
dataDEGsFiltLevel <- TCGAanalyze_LevelTab(
  FC_FDR_table_mRNA = dataDEGsFilt,
  typeCond1 = "Tumor",
  typeCond2 = "Normal",
  TableCond1 = dataTP,
  TableCond2 = dataTN
)

```

---

TCGAanalyze\_networkInference

*infer gene regulatory networks*

---

**Description**

TCGAanalyze\_networkInference taking expression data as input, this will return an adjacency matrix of interactions

**Usage**

```
TCGAanalyze_networkInference(data, optionMethod = "clr")
```

**Arguments**

data                    expression data, genes in columns, samples in rows  
optionMethod          inference method, chose from aracne, c3net, clr and mrnet

**Value**

an adjacent matrix

---

 TCGAanalyze\_Normalization

*normalization mRNA transcripts and miRNA using EDASeq package.*


---

## Description

TCGAanalyze\_Normalization allows user to normalize mRNA transcripts and miRNA, using EDASeq package.

Normalization for RNA-Seq Numerical and graphical summaries of RNA-Seq read data. Within-lane normalization procedures to adjust for GC-content effect (or other gene-level effects) on read counts: loess robust local regression, global-scaling, and full-quantile normalization (Risso et al., 2011). Between-lane normalization procedures to adjust for distributional differences between lanes (e.g., sequencing depth): global-scaling and full-quantile normalization (Bullard et al., 2010).

For instance returns all mRNA or miRNA with mean across all samples, higher than the threshold defined quantile mean across all samples.

TCGAanalyze\_Normalization performs normalization using following functions from EDASeq

1. EDASeq::newSeqExpressionSet
2. EDASeq::withinLaneNormalization
3. EDASeq::betweenLaneNormalization
4. EDASeq::counts

## Usage

```
TCGAanalyze_Normalization(tabDF, geneInfo, method = "geneLength")
```

## Arguments

tabDF	Rnaseq numeric matrix, each row represents a gene, each column represents a sample
geneInfo	Information matrix of 20531 genes about geneLength and gcContent. Two objects are provided: TCGAbiolinks::geneInfoHT,TCGAbiolinks::geneInfo
method	is method of normalization such as 'gcContent' or 'geneLength'

## Value

Rnaseq matrix normalized with counts slot holds the count data as a matrix of non-negative integer count values, one row for each observational unit (gene or the like), and one column for each sample.

## Examples

```
dataNorm <- TCGAbiolinks::TCGAanalyze_Normalization(dataBRCA, geneInfo)
```

---

TCGAanalyze\_Pathview *Generate pathview graph*

---

### Description

TCGAanalyze\_Pathview pathway based data integration and visualization.

### Usage

```
TCGAanalyze_Pathview(dataDEGs, pathwayKEGG = "hsa05200")
```

### Arguments

dataDEGs	dataDEGs
pathwayKEGG	pathwayKEGG

### Value

an adjacent matrix

### Examples

```
## Not run:
dataDEGs <- data.frame(mRNA = c("TP53","TP63","TP73"), logFC = c(1,2,3))
TCGAanalyze_Pathview(dataDEGs)

## End(Not run)
```

---

TCGAanalyze\_Preprocessing

*Array Array Intensity correlation (AAIC) and correlation boxplot to define outlier*

---

### Description

TCGAanalyze\_Preprocessing perform Array Array Intensity correlation (AAIC). It defines a square symmetric matrix of spearman correlation among samples. According this matrix and boxplot of correlation samples by samples it is possible to find samples with low correlation that can be identified as possible outliers.

### Usage

```
TCGAanalyze_Preprocessing(
  object,
  cor.cut = 0,
  datatype = names(assays(object))[1],
  filename = NULL,
  width = 1000,
  height = 1000
)
```

**Arguments**

object	gene expression of class RangedSummarizedExperiment from TCGAprepare
cor.cut	is a threshold to filter samples according their spearman correlation in samples by samples. default cor.cut is 0
datatype	is a string from RangedSummarizedExperiment assay
filename	Filename of the image file
width	Image width
height	Image height

**Value**

Plot with array array intensity correlation and boxplot of correlation samples by samples

---

TCGAanalyze\_Stemness *Generate Stemness Score based on RNASeq (mRNAsi stemness index)*  
*Malta et al., Cell, 2018*

---

**Description**

TCGAanalyze\_Stemness generate the mRNAsi score

**Usage**

```
TCGAanalyze_Stemness(stemSig, dataGE, colname.score = "stemness_score")
```

**Arguments**

stemSig	is a vector of the stemness Signature generated using gelnets package. Please check the data from <a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5902191/">https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5902191/</a> <ul style="list-style-type: none"> <li>• <a href="#">SC_PCBC_stemSig</a> - Stemness Score</li> <li>• <a href="#">DE_PCBC_stemSig</a> - endoderm score</li> <li>• <a href="#">EB_PCBC_stemSig</a> - embryoid bodies score</li> <li>• <a href="#">ECTO_PCBC_stemSig</a> - ectoderm score</li> <li>• <a href="#">MESO_PCBC_stemSig</a> - mesoderm score</li> </ul>
dataGE	is a matrix of Gene expression (genes in rows, samples in cols) from TCGAprepare
colname.score	Column name of the output. Default "stemness_score"

**Value**

table with samples and selected score

**Examples**

```

# Selecting TCGA breast cancer (10 samples) for example stored in dataBRCA
dataNorm <- TCGAanalyze_Normalization(
  tabDF = dataBRCA,
  geneInfo = geneInfo
)

# quantile filter of genes
dataFilt <- TCGAanalyze_Filtering(
  tabDF = dataNorm,
  method = "quantile",
  qnt.cut = 0.25
)

Stemness_score <- TCGAanalyze_Stemness(
  stemSig = SC_PCBC_stemSig,
  dataGE = dataFilt,
  colname.score = "SC_PCBC_stem_score"
)

ECTO_score <- TCGAanalyze_Stemness(
  stemSig = ECTO_PCBC_stemSig,
  dataGE = dataFilt,
  colname.score = "ECTO_PCBC_stem_score"
)

MESO_score <- TCGAanalyze_Stemness(
  stemSig = MESO_PCBC_stemSig,
  dataGE = dataFilt,
  colname.score = "MESO_PCBC_stem_score"
)

```

---

TCGAanalyze\_survival *Creates survival analysis*

---

**Description**

Creates a survival plot from TCGA patient clinical data using survival library. It uses the fields `days_to_death` and `vital`, plus a columns for groups.

**Usage**

```

TCGAanalyze_survival(
  data,
  clusterCol = NULL,
  legend = "Legend",
  labels = NULL,
  risk.table = TRUE,
  xlim = NULL,
  main = "Kaplan-Meier Overall Survival Curves",
  ylab = "Probability of survival",
  xlab = "Time since diagnosis (days)",
  filename = "survival.pdf",
  color = NULL,
  height = 8,
  width = 12,

```



```

    dpi = 300,
    pvalue = TRUE,
    conf.int = TRUE,
    ...
  )

```

### Arguments

data	TCGA Clinical patient with the information days_to_death
clusterCol	Column with groups to plot. This is a mandatory field, the caption will be based in this column
legend	Legend title of the figure
labels	labels of the plot
risk.table	show or not the risk table
xlim	x axis limits e.g. xlim = c(0, 1000). Present narrower X axis, but not affect survival estimates.
main	main title of the plot
ylab	y axis text of the plot
xlab	x axis text of the plot
filename	The name of the pdf file.
color	Define the colors/Pallete for lines.
height	Image height
width	Image width
dpi	Figure quality
pvalue	show p-value of log-rank test
conf.int	show confidence intervals for point estimates of survival curves.
...	Further arguments passed to <a href="#">ggsurvplot</a> .

### Value

Survival plot

### Examples

```

# clin <- GDCquery_clinic("TCGA-BRCA","clinical")
clin <- data.frame(
  vital_status = c("alive","alive","alive","dead","alive",
                  "alive","dead","alive","dead","alive"),
  days_to_death = c(NA,NA,NA,172,NA,NA,3472,NA,786,NA),
  days_to_last_follow_up = c(3011,965,718,NA,1914,423,NA,5,656,1417),
  gender = c(rep("male",5),rep("female",5))
)
TCGAanalyze_survival(clin, clusterCol="gender")
TCGAanalyze_survival(clin, clusterCol="gender", xlim = 1000)
TCGAanalyze_survival(clin,
  clusterCol="gender",
  risk.table = FALSE,
  conf.int = FALSE,
  color = c("pink","blue"))

```

```
TCGAanalyze_survival(clin,
                      clusterCol="gender",
                      risk.table = FALSE,
                      xlim = c(100,1000),
                      conf.int = FALSE,
                      color = c("Dark2"))
```

---

TCGAanalyze\_SurvivalKM

*survival analysis (SA) univariate with Kaplan-Meier (KM) method.*

---

### Description

TCGAanalyze\_SurvivalKM perform an univariate Kaplan-Meier (KM) survival analysis (SA). It performed Kaplan-Meier survival univariate using complete follow up with all days taking one gene a time from Genelist of gene symbols. For each gene according its level of mean expression in cancer samples, defining two thresholds for quantile expression of that gene in all samples (default ThreshTop=0.67,ThreshDown=0.33) it is possible to define a threshold of intensity of gene expression to divide the samples in 3 groups (High, intermediate, low). TCGAanalyze\_SurvivalKM performs SA between High and low groups using following functions from survival package

1. survival::Surv
2. survival::survdiff
3. survival::survfit

### Usage

```
TCGAanalyze_SurvivalKM(
  clinical_patient,
  dataGE,
  Genelist,
  Survresult = FALSE,
  ThreshTop = 0.67,
  ThreshDown = 0.33,
  p.cut = 0.05,
  group1,
  group2
)
```

### Arguments

clinical_patient	is a data.frame using function 'clinic' with information related to barcode / samples such as bcr_patient_barcode, days_to_death , days_to_last_follow_up , vital_status, etc
dataGE	is a matrix of Gene expression (genes in rows, samples in cols) from TCGAprepare
Genelist	is a list of gene symbols where perform survival KM.
Survresult	is a parameter (default = FALSE) if is TRUE will show KM plot and results.
ThreshTop	is a quantile threshold to identify samples with high expression of a gene

ThreshDown	is a quantile threshold to identify samples with low expression of a gene
p.cut	p.values threshold. Default: 0.05
group1	a string containing the barcode list of the samples in in control group
group2	a string containing the barcode list of the samples in in disease group

### Value

table with survival genes pvalues from KM.

### Examples

```
# Selecting only 20 genes for example
dataBRCAcomplete <- log2(dataBRCA[1:20,] + 1)

# clinical_patient_Cancer <- GDCquery_clinic("TCGA-BRCA", "clinical")
clinical_patient_Cancer <- data.frame(
  bcr_patient_barcode = substr(colnames(dataBRCAcomplete),1,12),
  vital_status = c(rep("alive",3),"dead",rep("alive",2),rep(c("dead","alive"),2)),
  days_to_death = c(NA,NA,NA,172,NA,NA,3472,NA,786,NA),
  days_to_last_follow_up = c(3011,965,718,NA,1914,423,NA,5,656,1417)
)

group1 <- TCGAquery_SampleTypes(colnames(dataBRCAcomplete), typesample = c("NT"))
group2 <- TCGAquery_SampleTypes(colnames(dataBRCAcomplete), typesample = c("TP"))

tabSurvKM <- TCGAanalyze_SurvivalKM(
  clinical_patient = clinical_patient_Cancer,
  dataGE = dataBRCAcomplete,
  Genelist = rownames(dataBRCAcomplete),
  Survresult = FALSE,
  p.cut = 0.4,
  ThreshTop = 0.67,
  ThreshDown = 0.33,
  group1 = group1, # Control group
  group2 = group2
) # Disease group

# If the groups are not specified group1 == group2 and all samples are used
## Not run:
tabSurvKM <- TCGAanalyze_SurvivalKM(
  clinical_patient_Cancer,
  dataBRCAcomplete,
  Genelist = rownames(dataBRCAcomplete),
  Survresult = TRUE,
  p.cut = 0.2,
  ThreshTop = 0.67,
  ThreshDown = 0.33
)

## End(Not run)
```

---

TCGAbatch\_Correction *Batch correction using ComBat and Voom transformation using limma package.*

---

## Description

TCGAbatch\_correction allows user to perform a Voom correction on gene expression data and have it ready for DEA. One can also use ComBat for batch correction for exploratory analysis. If batch.factor or adjustment argument is "Year" please provide clinical data. If no batch factor is provided, the data will be voom corrected only

TCGAanalyze\_DEA performs DEA using following functions from sva and limma:

1. limma::voom Transform RNA-Seq Data Ready for Linear Modelling.
2. sva::ComBat Adjust for batch effects using an empirical Bayes framework.

## Usage

```
TCGAbatch_Correction(
  tabDF,
  batch.factor = NULL,
  adjustment = NULL,
  ClinicalDF = data.frame(),
  UnpublishedData = FALSE,
  AnnotationDF = data.frame()
)
```

## Arguments

tabDF	numeric matrix, each row represents a gene, each column represents a sample
batch.factor	a string containing the batch factor to use for correction. Options are "Plate", "TSS", "Year", "Portion", "Center"
adjustment	vector containing strings for factors to adjust for using ComBat. Options are "Plate", "TSS", "Year", "Portion", "Center"
ClinicalDF	a dataframe returned by GDCquery_clinic() to be used to extract year data
UnpublishedData	if TRUE perform a batch correction after adding new data
AnnotationDF	a dataframe with column Batch indicating different batches of the samples in the tabDF

## Value

data frame with ComBat batch correction applied

---

TCGAprepare\_Affy      *Prepare CEL files into an AffyBatch.*

---

**Description**

Prepare CEL files into an AffyBatch.

**Usage**

TCGAprepare\_Affy(ClinData, PathFolder, TabCel)

**Arguments**

ClinData	write
PathFolder	write
TabCel	write

**Value**

Normalized Expression data from Affy eSets

**Examples**

```
## Not run:
to add example

## End(Not run)
```

---

TCGAquery\_MatchedCoupledSampleTypes  
*Retrieve multiple tissue types from the same patients.*

---

**Description**

TCGAquery\_MatchedCoupledSampleTypes

**Usage**

TCGAquery\_MatchedCoupledSampleTypes(barcode, typesample)

**Arguments**

barcode	barcode
typesample	typesample

**Value**

a list of samples / barcode filtered by type sample selected

**Examples**

```
TCGAquery_MatchedCoupledSampleTypes(c("TCGA-B0-4698-01Z-00-DX1",
                                       "TCGA-B0-4698-02Z-00-DX1"),
                                       c("TP", "TR"))
barcode <- c("TARGET-20-PANSBH-02A-02D", "TARGET-20-PANSBH-01A-02D",
            "TCGA-B0-4698-01Z-00-DX1", "TCGA-CZ-4863-02Z-00-DX1",
            "TARGET-20-PANSZZ-02A-02D", "TARGET-20-PANSZZ-11A-02D",
            "TCGA-B0-4699-01Z-00-DX1", "TCGA-B0-4699-02Z-00-DX1"
            )
TCGAquery_MatchedCoupledSampleTypes(barcode, c("TR", "TP"))
```

---

TCGAquery\_recount2      *Query gene counts of TCGA and GTEx data from the Recount2 project*

---

**Description**

TCGArecount2\_query queries and downloads data produced by the Recount2 project. User can specify which project and which tissue to query

**Usage**

```
TCGAquery_recount2(project, tissue = c())
```

**Arguments**

project	is a string denoting which project the user wants. Options are "tcga" and "gtex"
tissue	a vector of tissue(s) to download. Options are "adipose tissue", "adrenal gland", "bladder", "blood", "blood vessel", "bone marrow", "brain", "breast", "cervix uteri", "colon", "esophagus", "fallopian tube", "heart", "kidney", "liver", "lung", "muscle", "nerve", "ovary", "pancreas", "pituitary", "prostate", "salivary gland", "skin", "small intestine", "spleen", "stomach", "testis", "thyroid", "uterus", "vagina"

**Value**

List with \$subtypes attribute as a dataframe with barcodes, samples, subtypes, and colors. The \$filtered attribute is returned as filtered samples with no subtype info

**Examples**

```
## Not run:
brain.rec<-TCGAquery_recount2(project = "gtex", tissue = "brain")

## End(Not run)
```

---

TCGAquery\_SampleTypes *Retrieve multiple tissue types not from the same patients.*

---

### Description

TCGAquery\_SampleTypes for a given list of samples and types, return the union of samples that are from these type.

### Usage

```
TCGAquery_SampleTypes(barcode, typesample)
```

### Arguments

barcode is a list of samples as TCGA barcodes  
 typesample a character vector indicating tissue type to query. Example:

TP	PRIMARY SOLID TUMOR
TR	RECURRENT SOLID TUMOR
TB	Primary Blood Derived Cancer-Peripheral Blood
TRBM	Recurrent Blood Derived Cancer-Bone Marrow
TAP	Additional-New Primary
TM	Metastatic
TAM	Additional Metastatic
THOC	Human Tumor Original Cells
TBM	Primary Blood Derived Cancer-Bone Marrow
NB	Blood Derived Normal
NT	Solid Tissue Normal
NBC	Buccal Cell Normal
NEBV	EBV Immortalized Normal
NBM	Bone Marrow Normal

### Value

a list of samples / barcode filtered by type sample selected

### Examples

```
# selection of normal samples "NT"
barcode <- c("TCGA-B0-4698-01Z-00-DX1", "TCGA-CZ-4863-02Z-00-DX1")
# Returns the second barcode
TCGAquery_SampleTypes(barcode, "TR")
# Returns both barcode
TCGAquery_SampleTypes(barcode, c("TR", "TP"))
barcode <- c("TARGET-20-PANSBH-14A-02D", "TARGET-20-PANSBH-01A-02D",
            "TCGA-B0-4698-01Z-00-DX1", "TCGA-CZ-4863-02Z-00-DX1")
TCGAquery_SampleTypes(barcode, c("TR", "TP"))
```

---

TCGAquery\_subtype      *Retrieve molecular subtypes for a given tumor*

---

**Description**

TCGAquery\_subtype Retrieve molecular subtypes for a given tumor

**Usage**

```
TCGAquery_subtype(tumor)
```

**Arguments**

tumor                    is a cancer Examples:

```
                          lgg    gbm    luad    stad    brca
                          coad   read
```

**Value**

a data.frame with barcode and molecular subtypes

**Examples**

```
dataSubt <- TCGAquery_subtype(tumor = "lgg")
```

---

TCGAtumor\_purity      *Filters TCGA barcodes according to purity parameters*

---

**Description**

TCGAtumor\_purity Filters TCGA samples using 5 estimates from 5 methods as thresholds.

**Usage**

```
TCGAtumor_purity(barcodes, estimate, absolute, lump, ihc, cpe)
```

**Arguments**

barcodes	is a vector of TCGA barcodes
estimate	uses gene expression profiles of 141 immune genes and 141 stromal genes
absolute	which uses somatic copy-number data (estimations were available for only 11 cancer types)
lump	(leukocytes unmethylation for purity), which averages 44 non-methylated immune-specific CpG sites
ihc	as estimated by image analysis of haematoxylin and eosin stain slides produced by the Nationwide Childrens Hospital Biospecimen Core Resource
cpe	CPE is a derived consensus measurement as the median purity level after normalizing levels from all methods to give them equal means and s.ds



**Value**

List with \$pure\_barcodes attribute as a vector of pure samples and \$filtered attribute as filtered samples with no purity info

**Examples**

```
dataTableSubt <- TCGAtumor_purity("TCGA-60-2721-01A-01R-0851-07",
  estimate = 0.6,
  absolute = 0.6,
  ihc = 0.8,
  lump = 0.8,
  cpe = 0.7)
```

---

TCGAvsualize\_BarPlot *Barplot of subtypes and clinical info in groups of gene expression clustered.*

---

**Description**

Barplot of subtypes and clinical info in groups of gene expression clustered.

**Usage**

```
TCGAvsualize_BarPlot(
  DFfilt,
  DFclin,
  DFsubt,
  data_Hc2,
  Subtype,
  cbPalette,
  filename,
  width,
  height,
  dpi
)
```

**Arguments**

DFfilt	write
DFclin	write
DFsubt	write
data_Hc2	write
Subtype	write
cbPalette	Define the colors of the bar.
filename	The name of the pdf file
width	Image width
height	Image height
dpi	Image dpi

**Value**

barplot image in pdf or png file

---

TCGAvisualize\_EAbarplot

*barPlot for a complete Enrichment Analysis*

---

**Description**

The figure shows canonical pathways significantly overrepresented (enriched) by the DEGs (differentially expressed genes). The most statistically significant canonical pathways identified in DEGs list are listed according to their p value corrected FDR (-Log) (colored bars) and the ratio of list genes found in each pathway over the total number of genes in that pathway (Ratio, red line).

**Usage**

```
TCGAvisualize_EAbarplot(
  tf,
  GOMFTab,
  GOBPTab,
  GOCCTab,
  PathTab,
  nBar,
  nRGTAB,
  filename = "TCGAvisualize_EAbarplot_Output.pdf",
  text.size = 1,
  mfrow = c(2, 2),
  xlim = NULL,
  fig.width = 30,
  fig.height = 15,
  color = c("orange", "cyan", "green", "yellow")
)
```

**Arguments**

tf	is a list of gene symbols
GOMFTab	is results from TCGAanalyze_EAcomplete related to Molecular Function (MF)
GOBPTab	is results from TCGAanalyze_EAcomplete related to Biological Process (BP)
GOCCTab	is results from TCGAanalyze_EAcomplete related to Cellular Component (CC)
PathTab	is results from TCGAanalyze_EAcomplete related to Pathways EA
nBar	is the number of bar histogram selected to show (default = 10)
nRGTAB	is the gene signature list with gene symbols.
filename	Name for the pdf. If null it will return the plot.
text.size	Text size
mfrow	Vector with number of rows/columns of the plot. Default 2 rows/2 columns "c(2,2)"
xlim	Upper limit of the x-axis.
fig.width	Default 30
fig.height	Default 15
color	A vector of colors for each barplot. Deafult: c("orange", "cyan", "green", "yellow")

**Value**

Complete barPlot from Enrichment Analysis showing significant (default FDR < 0.01) BP,CC,MF and pathways enriched by list of genes.

**Examples**

```
Genelist <- c("FN1","COL1A1")
ansEA <- TCGAanalyze_EAcomplete(TFname="DEA genes Normal Vs Tumor",Genelist)
TCGAvisualize_EAbarplot(tf = rownames(ansEA$ResBP),
  GOBPTab = ansEA$ResBP,
  GOCCTab = ansEA$ResCC,
  GOMFTab = ansEA$ResMF,
  PathTab = ansEA$ResPat,
  nRGTab = Genelist,
  nBar = 10,
  filename="a.pdf")
## Not run:
Genelist <- rownames(dataDEGsFiltLevel)
system.time(ansEA <- TCGAanalyze_EAcomplete(TFname="DEA genes Normal Vs Tumor",Genelist))
# Enrichment Analysis EA (TCGAvisualize)
# Gene Ontology (GO) and Pathway enrichment barPlot
TCGAvisualize_EAbarplot(tf = rownames(ansEA$ResBP),
  GOBPTab = ansEA$ResBP,
  GOCCTab = ansEA$ResCC,
  GOMFTab = ansEA$ResMF,
  PathTab = ansEA$ResPat,
  nRGTab = Genelist,
  nBar = 10)

## End(Not run)
```

---

TCGAvisualize\_Heatmap *Heatmap with more sensible behavior using heatmap.plus*

---

**Description**

Heatmap with more sensible behavior using heatmap.plus

**Usage**

```
TCGAvisualize_Heatmap(
  data,
  col.metadata,
  row.metadata,
  col.colors = NULL,
  row.colors = NULL,
  show_column_names = FALSE,
  show_row_names = FALSE,
  cluster_rows = FALSE,
  cluster_columns = FALSE,
  sortCol,
  extremes = NULL,
  rownames.size = 12,
```

```

title = NULL,
color.levels = NULL,
values.label = NULL,
filename = "heatmap.pdf",
width = 10,
height = 10,
type = "expression",
scale = "none",
heatmap.legend.color.bar = "continuous"
)

```

### Arguments

<code>data</code>	The object to with the heatmap data (expression, methylation)
<code>col.metadata</code>	Metadata for the columns (samples). It should have on of the following columns: barcode (28 characters) column to match with the samples. It will also work with "bcr_patient_barcode"(12 chars),"patient"(12 chars),"sample"(16 chars) columns but as one patient might have more than one sample, this coul lead to errors in the annotation. The code will throw a warning in case two samples are from the same patient.
<code>row.metadata</code>	Metadata for the rows genes (expression) or probes (methylation)
<code>col.colors</code>	A list of names colors
<code>row.colors</code>	A list of named colors
<code>show_column_names</code>	Show column names names? Default: FALSE
<code>show_row_names</code>	Show row names? Default: FALSE
<code>cluster_rows</code>	Cluster rows ? Default: FALSE
<code>cluster_columns</code>	Cluster columns ? Default: FALSE
<code>sortCol</code>	Name of the column to be used to sort the columns
<code>extremes</code>	Extremes of colors (vector of 3 values)
<code>rownames.size</code>	Rownames size
<code>title</code>	Title of the plot
<code>color.levels</code>	A vector with the colors (low level, middle level, high level)
<code>values.label</code>	Text of the levels in the heatmap
<code>filename</code>	Filename to save the heatmap. Default: heatmap.png
<code>width</code>	figure width
<code>height</code>	figure height
<code>type</code>	Select the colors of the heatmap values. Possible values are "expression" (default), "methylation"
<code>scale</code>	Use z-score to make the heatmap? If we want to show differences between genes, it is good to make Z-score by samples (force each sample to have zero mean and standard deviation=1). If we want to show differences between samples, it is good to make Z-score by genes (force each gene to have zero mean and standard deviation=1). Possibilities: "row", "col". Default "none"
<code>heatmap.legend.color.bar</code>	Heatmap legends values type. Options: "continuous", "discrete"

**Value**

Heatmap plotted in the device

**Examples**

```
row.mdat <- matrix(c("FALSE", "FALSE",
                    "TRUE", "TRUE",
                    "FALSE", "FALSE",
                    "TRUE", "FALSE",
                    "FALSE", "TRUE"
                    ),
                  nrow = 5, ncol = 2, byrow = TRUE,
                  dimnames = list(
                    c("probe1", "probe2", "probe3", "probe4", "probe5"),
                    c("duplicated", "Enhancer region")))
dat <- matrix(c(0.3, 0.2, 0.3, 1, 1, 0.1, 1, 1, 0, 0.8, 1, 0.7, 0.7, 0.3, 1),
             nrow = 5, ncol = 3, byrow = TRUE,
             dimnames = list(
               c("probe1", "probe2", "probe3", "probe4", "probe5"),
               c("TCGA-DU-6410",
                 "TCGA-DU-A5TS",
                 "TCGA-HT-7688")))

mdat <- data.frame(patient=c("TCGA-DU-6410", "TCGA-DU-A5TS", "TCGA-HT-7688"),
                  Sex=c("Male", "Female", "Male"),
                  COCcluster=c("coc1", "coc1", "coc1"),
                  IDHtype=c("IDHwt", "IDHmut-cod", "IDHmut-noncod"))

TCGAvisualize_Heatmap(dat,
  col.metadata = mdat,
  row.metadata = row.mdat,
  row.colors = list(duplicated = c("FALSE" = "pink",
                                   "TRUE" = "green"),
                    "Enhancer region" = c("FALSE" = "purple",
                                           "TRUE" = "grey")),
  col.colors = list(Sex = c("Male" = "blue", "Female" = "red"),
                    COCcluster=c("coc1" = "grey"),
                    IDHtype=c("IDHwt" = "cyan",
                               "IDHmut-cod" = "tomato",
                               "IDHmut-noncod" = "gold")),
  type = "methylation",
  show_row_names=TRUE)
```

---

TCGAvisualize\_meanMethylation

*Mean methylation boxplot*

---

**Description**

Creates a mean methylation boxplot for groups (groupCol), subgroups will be highlighted as shapes if the subgroupCol was set.

Observation: Data is a summarizedExperiment.

**Usage**

```
TCGAvvisualize_meanMethylation(
  data,
  groupCol = NULL,
  subgroupCol = NULL,
  shapes = NULL,
  print.pvalue = FALSE,
  plot.jitter = TRUE,
  jitter.size = 3,
  filename = "groupMeanMet.pdf",
  ylab = expression(paste("Mean DNA methylation (", beta, "-values)")),
  xlab = NULL,
  title = "Mean DNA methylation",
  labels = NULL,
  group.legend = NULL,
  subgroup.legend = NULL,
  color = NULL,
  y.limits = NULL,
  sort,
  order,
  legend.position = "top",
  legend.title.position = "top",
  legend.ncols = 3,
  add.axis.x.text = TRUE,
  width = 10,
  height = 10,
  dpi = 600,
  axis.text.x.angle = 90
)
```

**Arguments**

<code>data</code>	SummarizedExperiment object obtained from TCGAPrepate
<code>groupCol</code>	Columns in <code>colData(data)</code> that defines the groups. If no columns defined a columns called "Patients" will be used
<code>subgroupCol</code>	Columns in <code>colData(data)</code> that defines the subgroups.
<code>shapes</code>	Shape vector of the subgroups. It must have the size of the levels of the subgroups. Example: <code>shapes = c(21,23)</code> if for two levels
<code>print.pvalue</code>	Print p-value for two groups
<code>plot.jitter</code>	Plot jitter? Default TRUE
<code>jitter.size</code>	Plot jitter size? Default 3
<code>filename</code>	The name of the pdf that will be saved
<code>ylab</code>	y axis text in the plot
<code>xlab</code>	x axis text in the plot
<code>title</code>	main title in the plot
<code>labels</code>	Labels of the groups
<code>group.legend</code>	Name of the group legend. DEFAULT: <code>groupCol</code>
<code>subgroup.legend</code>	Name of the subgroup legend. DEFAULT: <code>subgroupCol</code>

color	vector of colors to be used in graph
y.limits	Change lower/upper y-axis limit
sort	Sort boxplot by mean or median. Possible values: mean.asc, mean.desc, median.asc, median.desc
order	Order of the boxplots
legend.position	Legend position ("top", "right", "left", "bottom")
legend.title.position	Legend title position ("top", "right", "left", "bottom")
legend.ncols	Number of columns of the legend
add.axis.x.text	Add text to x-axis? Default: FALSE
width	Plot width default:10
height	Plot height default:10
dpi	Pdf dpi default:600
axis.text.x.angle	Angle of text in the x axis

## Value

Save the pdf survival plot

## Examples

```
nrows <- 200; ncols <- 21
counts <- matrix(runif(nrows * ncols, 0, 1), nrows)
rowRanges <- GenomicRanges::GRanges(rep(c("chr1", "chr2"), c(50, 150)),
  IRanges::IRanges(floor(runif(200, 1e5, 1e6)), width=100),
  strand=sample(c("+", "-"), 200, TRUE),
  feature_id=sprintf("ID%03d", 1:200))
colData <- S4Vectors::DataFrame(Treatment=rep(c("ChIP", "Input", "Other"), 7),
  row.names=LETTERS[1:21],
  group=rep(c("group1", "group2", "group3"), c(7,7,7)),
  subgroup=rep(c("subgroup1", "subgroup2", "subgroup3"), 7))
data <- SummarizedExperiment::SummarizedExperiment(
  assays=S4Vectors::SimpleList(counts=counts),
  rowRanges=rowRanges,
  colData=colData)
TCGAvsualize_meanMethylation(data, groupCol = "group")
# change lower/upper y-axis limit
TCGAvsualize_meanMethylation(data, groupCol = "group", y.limits = c(0,1))
# change lower y-axis limit
TCGAvsualize_meanMethylation(data, groupCol = "group", y.limits = 0)
TCGAvsualize_meanMethylation(data, groupCol = "group", subgroupCol="subgroup")
TCGAvsualize_meanMethylation(data, groupCol = "group")
TCGAvsualize_meanMethylation(data, groupCol = "group", sort="mean.desc", filename="meandesc.pdf")
TCGAvsualize_meanMethylation(data, groupCol = "group", sort="mean.asc", filename="meanasc.pdf")
TCGAvsualize_meanMethylation(data, groupCol = "group", sort="median.asc", filename="medianasc.pdf")
TCGAvsualize_meanMethylation(data, groupCol = "group", sort="median.desc", filename="mediandesc.pdf")
```

---

 TCGAvsualize\_oncoprint

*Creating a oncoprint*


---

## Description

Creating a oncoprint

## Usage

```
TCGAvsualize_oncoprint(
  mut,
  genes,
  filename,
  color,
  annotation.position = "bottom",
  annotation,
  height,
  width = 10,
  rm.empty.columns = FALSE,
  show.column.names = FALSE,
  show.row.barplot = TRUE,
  label.title = "Mutation",
  column.names.size = 8,
  label.font.size = 16,
  rows.font.size = 16,
  dist.col = 0.5,
  dist.row = 0.5,
  information = "Variant_Type",
  row.order = TRUE,
  col.order = TRUE,
  heatmap.legend.side = "bottom",
  annotation.legend.side = "bottom"
)
```

## Arguments

mut	A dataframe from the mutation annotation file (see TCGAquery_maf from TC- GAbiolinks)
genes	Gene list
filename	name of the pdf
color	named vector for the plot
annotation.position	Position of the annotation "bottom" or "top"
annotation	Matrix or data frame with the annotation. Should have a column bcr_patient_barcode with the same ID of the mutation object
height	pdf height
width	pdf width



```

rm.empty.columns      If there is no alteration in that sample, whether remove it on the oncoprint
show.column.names     Show column names? Default: FALSE
show.row.barplot      Show barplot annotation on rows?
label.title           Title of the label
column.names.size     Size of the fonts of the columns names
label.font.size       Size of the fonts
rows.font.size        Size of the fonts
dist.col              distance between columns in the plot
dist.row              distance between rows in the plot
information            Which column to use as information from MAF. Options: 1) "Variant_Classification"
                      (The information will be "Frame_Shift_Del", "Frame_Shift_Ins", "In_Frame_Del",
                      "In_Frame_Ins", "Missense_Mutation", "Nonsense_Mutation", "Nonstop_Mutation",
                      "RNA", "Silent", "Splice_Site", "Targeted_Region", "Translation_Start_Site")
                      2) "Variant_Type" (The information will be INS,DEL,SNP)
row.order              Order the genes (rows) Default:TRUE. Genes with more mutations will be in
                      the first rows
col.order              Order columns. Default:TRUE.
heatmap.legend.side   Position of the heatmap legend
annotation.legend.side Position of the annotation legend

```

**Value**

A oncoprint plot

**Examples**

```

## Not run:
library(dplyr)
query <- GDCquery(
  project = "TCGA-CHOL",
  data.category = "Simple Nucleotide Variation",
  access = "open",
  legacy = FALSE,
  data.type = "Masked Somatic Mutation",
  workflow.type = "Aliquot Ensemble Somatic Variant Merging and Masking"
)
GDCdownload(query)
mut <- GDCprepare(query)
TCGAvsualize_oncoprint(mut = mut, genes = mut$Hugo_Symbol[1:10], rm.empty.columns = TRUE)
TCGAvsualize_oncoprint(
  mut = mut, genes = mut$Hugo_Symbol[1:10],
  filename = "onco.pdf",
  color = c("background"="#CCCCCC", "DEL"="purple", "INS"="yellow", "SNP"="brown")
)
clin <- GDCquery_clinic("TCGA-ACC", "clinical")

```

```

clin <- clin[,c("bcr_patient_barcode","disease","gender","tumor_stage","race","vital_status")]
TCGAvisualize_oncoprint(
  mut = mut, genes = mut$Hugo_Symbol[1:20],
  filename = "onco.pdf",
  annotation = clin,
  color=c("background"="#CCCCCC","DEL"="purple","INS"="yellow","SNP"="brown"),
  rows.font.size=10,
  heatmap.legend.side = "right",
  dist.col = 0,
  label.font.size = 10
)

## End(Not run)

```

---

TCGAvisualize\_PCA      *Principal components analysis (PCA) plot*

---

### Description

TCGAvisualize\_PCA performs a principal components analysis (PCA) on the given data matrix and returns the results as an object of class `prcomp`, and shows results in PCA level.

### Usage

```
TCGAvisualize_PCA(dataFilet, dataDEGsFiltLevel, ntopgenes, group1, group2)
```

### Arguments

<code>dataFilet</code>	A filtered dataframe or numeric matrix where each row represents a gene, each column represents a sample from function <code>TCGAanalyze_Filtering</code>
<code>dataDEGsFiltLevel</code>	table with DEGs, log Fold Change (FC), false discovery rate (FDR), the gene expression level, etc, from function <code>TCGAanalyze_LevelTab</code> .
<code>ntopgenes</code>	number of DEGs genes to plot in PCA
<code>group1</code>	a string containing the barcode list of the samples in in control group
<code>group2</code>	a string containing the barcode list of the samples in in disease group the name of the group

### Value

principal components analysis (PCA) plot of PC1 and PC2

### Examples

```

# normalization of genes
dataNorm <- TCGAanalyze_Normalization(tabDF = dataBRCA, geneInfo = geneInfo,
method = "geneLength")
# quantile filter of genes
dataFilt <- TCGAanalyze_Filtering(tabDF = dataBRCA, method = "quantile", qnt.cut = 0.25)
# Principal Component Analysis plot for ntop selected DEGs
# selection of normal samples "NT"
group1 <- TCGAquery_SampleTypes(colnames(dataFilt), typesample = c("NT"))

```

```
# selection of normal samples "TP"
group2 <- TCGAquery_SampleTypes(colnames(dataFilt), typesample = c("TP"))
pca <- TCGAvisualize_PCA(dataFilt,dataDEGsFiltLevel, ntopgenes = 200, group1, group2)
```

---

TCGAvisualize\_starburst

*Create starburst plot*

---

## Description

Create Starburst plot for comparison of DNA methylation and gene expression. The log<sub>10</sub> (FDR-corrected P value) is plotted for beta value for DNA methylation (x axis) and gene expression (y axis) for each gene.

The black dashed line shows the FDR-adjusted P value of 0.01.

You can set names to TRUE to get the names of the significant genes.

Candidate biologically significant genes will be circled in the plot.

Candidate biologically significant are the genes that respect the expression (logFC.cut), DNA methylation (diffmean.cut) and significance thresholds (exp.p.cut, met.p.cut)

## Usage

```
TCGAvisualize_starburst(
  met,
  exp,
  group1 = NULL,
  group2 = NULL,
  exp.p.cut = 0.01,
  met.p.cut = 0.01,
  diffmean.cut = 0,
  logFC.cut = 0,
  met.platform = c("Illumina Human Methylation 450", "Illumina Human Methylation 27",
    "Illumina Methylation Epic"),
  genome,
  names = FALSE,
  names.fill = TRUE,
  filename = "starburst.png",
  return.plot = FALSE,
  ylab = expression(atop("Gene Expression", paste(-Log[10],
    "(FDR corrected P values)"))),
  xlab = expression(atop("DNA Methylation", paste(-Log[10],
    "(FDR corrected P values)"))),
  title = "Starburst Plot",
  legend = "DNA Methylation/Expression Relation",
  color = NULL,
  label = c("Not Significant", "Up regulated & Hypo methylated",
    "Down regulated & Hypo methylated", "hypo methylated", "hyper methylated",
    "Up regulated", "Down regulated", "Up regulated & Hyper methylated",
    "Down regulated & Hyper methylated"),
  xlim = NULL,
  ylim = NULL,
```

```

    height = 10,
    width = 20,
    dpi = 600
)

```

### Arguments

<code>met</code>	A SummarizedExperiment with methylation data obtained from the TCGAPrepare or Data frame from DMR_results file. Expected colData columns: <code>diffmean</code> , <code>p.value.adj</code> and <code>p.value</code> . Execute <code>volcanoPlot</code> function in order to obtain these values for the object.
<code>exp</code>	Object obtained by <code>DEArnaSEQ</code> function
<code>group1</code>	The name of the group 1. Obs: Column <code>p.value.adj.group1.group2</code> should exist
<code>group2</code>	The name of the group 2. Obs: Column <code>p.value.adj.group1.group2</code> should exist
<code>exp.p.cut</code>	expression p value cut-off
<code>met.p.cut</code>	methylation p value cut-off
<code>diffmean.cut</code>	If set, the probes with <code>diffmean</code> higher than methylation cut-off will be highlighted in the plot. And the data frame return will be subseted.
<code>logFC.cut</code>	If set, the probes with expression fold change higher than methylation cut-off will be highlighted in the plot. And the data frame return will be subseted.
<code>met.platform</code>	DNA methylation platform "Illumina Human Methylation 450", "Illumina Human Methylation 27", "Illumina Methylation Epic"
<code>genome</code>	Genome of reference ("hg38" or "hg19") used to identify nearest probes TSS
<code>names</code>	Add the names of the significant genes? Default: FALSE
<code>names.fill</code>	Names should be filled in a color box? Default: TRUE
<code>filename</code>	The filename of the file (it can be pdf, svg, png, etc)
<code>return.plot</code>	If true only plot object will be returned (pdf will not be created)
<code>ylab</code>	y axis text
<code>xlab</code>	x axis text
<code>title</code>	main title
<code>legend</code>	legend title
<code>color</code>	vector of colors to be used in graph
<code>label</code>	vector of labels to be used in graph
<code>xlim</code>	x limits to cut image
<code>ylim</code>	y limits to cut image
<code>height</code>	Figure height
<code>width</code>	Figure width
<code>dpi</code>	Figure dpi

### Details

Input: data with gene expression/methylation expression Output: starburst plot

### Value

Save a starburst plot

**Examples**

```

## Not run:
library(SummarizedExperiment)
met <- TCGAbiolinks::getMetPlatInfo(
  genome = "hg38",
  platform = "Illumina Human Methylation 27"
)
values(met) <- NULL
met$probeID <- names(met)
nrows <- length(met); ncols <- 20
counts <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
colData <- S4Vectors::DataFrame(
  Treatment = rep(c("ChIP", "Input"), 5),
  row.names = LETTERS[1:20],
  group = rep(c("group1", "group2"), c(10, 10))
)
met <- SummarizedExperiment::SummarizedExperiment(
  assays = S4Vectors::SimpleList(counts=counts),
  rowRanges = met,
  colData = colData
)
rowRanges(met)$diffmean.g1.g2 <- c(runif(nrows, -0.1, 0.1))
rowRanges(met)$diffmean.g2.g1 <- -1*(rowRanges(met)$diffmean.g1.g2)
rowRanges(met)$p.value.g1.g2 <- c(runif(nrows, 0, 1))
rowRanges(met)$p.value.adj.g1.g2 <- c(runif(nrows, 0, 1))
exp <- TCGAbiolinks::get.GRCh.bioMart("hg38")
exp$logFC <- runif(nrow(exp), -5, 5)
exp$FDR <- runif(nrow(exp), 0.01, 1)

result <- TCGAvisualize_starburst(
  met,
  exp,
  exp.p.cut = 0.05,
  met.p.cut = 0.05,
  logFC.cut = 2,
  group1 = "g1",
  group2 = "g2",
  genome = "hg38",
  met.platform = "27k",
  diffmean.cut = 0.0,
  names = TRUE
)

## End(Not run)

```

---

TCGAvisualize\_SurvivalCoxNET

*Survival analysis with univariate Cox regression package (dnet)*


---

**Description**

TCGAvisualize\_SurvivalCoxNET can help an user to identify a group of survival genes that are significant from univariate Kaplan Meier Analysis and also for Cox Regression. It shows in the end a network build with community of genes with similar range of pvalues from Cox regression (same

color) and that interaction among those genes is already validated in literatures using the STRING database (version 9.1). TCGAvisualize\_SurvivalCoxNET perform survival analysis with univariate Cox regression and package (dnet) using following functions wrapping from these packages:

1. survival::coxph
2. igraph::subgraph.edges
3. igraph::layout.fruchterman.reingold
4. igraph::spinglass.community
5. igraph::communities
6. dnet::dRDataLoader
7. dnet::dNetInduce
8. dnet::dNetPipeline
9. dnet::visNet
10. dnet::dCommSignif

### Usage

```
TCGAvisualize_SurvivalCoxNET(
  clinical_patient,
  dataGE,
  Genelist,
  org.Hs.string,
  scoreConfidence = 700,
  titlePlot = "TCGAvisualize_SurvivalCoxNET Example"
)
```

### Arguments

<code>clinical_patient</code>	is a data.frame using function 'clinic' with information related to barcode / samples such as <code>bcr_patient_barcode</code> , <code>days_to_death</code> , <code>days_to_last_followup</code> , <code>vital_status</code> , etc
<code>dataGE</code>	is a matrix of Gene expression (genes in rows, samples in cols) from TCGAprepare
<code>Genelist</code>	is a list of gene symbols where perform survival KM.
<code>org.Hs.string</code>	an igraph object that contains a functional protein association network in human. The network is extracted from the STRING database (version 10).
<code>scoreConfidence</code>	restrict to those edges with high confidence (eg. <code>score&gt;=700</code> )
<code>titlePlot</code>	is the title to show in the final plot.

### Details

TCGAvisualize\_SurvivalCoxNET allow user to perform the complete workflow using coxph and dnet package related to survival analysis with an identification of gene-active networks from high-throughput omics data using gene expression and clinical data.

1. Cox regression survival analysis to obtain hazard ratio (HR) and p-values
2. fit a Cox proportional hazards model and ANOVA (Chisq test)

3. Network communities
4. An igraph object that contains a functional protein association network in human. The network is extracted from the STRING database (version 9.1). Only those associations with medium confidence (score $\geq$ 400) are retained.
5. restrict to those edges with high confidence (score $\geq$ 700)
6. extract network that only contains genes in pvals
7. Identification of gene-active network
8. visualisation of the gene-active network itself
9. the layout of the network visualisation (fixed in different visuals)
10. color nodes according to communities (identified via a spin-glass model and simulated annealing)
11. node sizes according to degrees
12. highlight different communities
13. visualize the subnetwork

### Value

net IGRAPH with related Cox survival genes in community (same pval and color) and with interactions from STRING database.

---

TCGAVisualize\_volcano *Creates a volcano plot for DNA methylation or gene expression*

---

### Description

Creates a volcano plot from the gene expression and DNA methylation analysis.

### Usage

```
TCGAVisualize_volcano(
  x,
  y,
  filename = "volcano.pdf",
  ylab = expression(paste(-Log[10], " (FDR corrected P-values)")),
  xlab = NULL,
  title = "Volcano plot",
  legend = NULL,
  label = NULL,
  xlim = NULL,
  ylim = NULL,
  color = c("black", "red", "green"),
  names = NULL,
  names.fill = TRUE,
  show.names = "significant",
  x.cut = 0,
  y.cut = 0.01,
  height = 5,
  width = 10,
```

```

highlight = NULL,
highlight.color = "orange",
names.size = 4,
dpi = 300
)

```

### Arguments

x	x-axis data (i.e. Diff mean beta-values or Log2FC).
y	FDR adjusted p-value (q-value). This data will be transformed to -log10 values.
filename	File name: volcano.pdf, volcano.svg, volcano.png. If NULL returns the ggplot object.
ylab	y axis text. Default: -Log10 FDR corrected P-values
xlab	x axis text. Default: No text. Examples of input: expression(paste(Log[2], "FoldChange"))
title	main title. If not specified it will be "Volcano plot (group1 vs group2)
legend	Legend title
label	vector of labels to be used in the figure. Example: c("Not Significant", "Hypermethylated in group1", "Hypomethylated in group1")#'
xlim	x limits to cut image (i.e. c(-4,4))
ylim	y limits to cut image (i.e. c(-1,10))
color	vector of colors to be used in graph
names	Names to be plotted if significant. Should be the same size of x and y
names.fill	Names should be filled in a color box? Default: TRUE
show.names	What names will be showed? Possibilities: "both", "significant", "highlighted"
x.cut	x-axis threshold. Default: 0.0 If you give only one number (e.g. 0.2) the cut-offs will be -0.2 and 0.2. Or you can give different cut-offs as a vector (e.g. c(-0.3,0.4))
y.cut	q-values threshold (i.e. 0.01, 10^-10)
height	Figure height
width	Figure width
highlight	List of genes/probes to be highlighted. It should be in the names argument.
highlight.color	Color of the points highlighted
names.size	Size of the names text
dpi	Figure dpi

### Details

Creates a volcano plot from the gene expression and DNA methylation analysis. Please see the vignette for more information

### Value

Saves the volcano plot in the current folder



**Examples**

```

log2_foldchange <- runif(200, -2, 2)
fdr <- runif(200, 0.01, 1)
TCGAVisualize_volcano(
  x = log2_foldchange,
  y = fdr,
  x.cut = 1.5,
  y.cut = 0.01,
  title = "Title example",
  xlab = expression(paste(Log[2], "FoldChange"))
)
## Not run:
beta_diff <- runif(200, -1, 1)
fdr <- runif(200, 0.01, 1)
TCGAVisualize_volcano(
  x = beta_diff,
  y = fdr,
  x.cut = 1.5,
  y.cut = 0.01,
  title = "Title example",
  xlab = expression(paste("DNA Methylation difference (", beta, "-values)"))
)
TCGAVisualize_volcano(
  x,
  y,
  filename = NULL,
  y.cut = 10000000,
  x.cut=0.8,
  names = rep("AAAA",length(x)),
  legend = "Status",
  names.fill = FALSE
)
TCGAVisualize_volcano(
  x,
  y,
  filename = NULL,
  y.cut = 10000000,
  x.cut = 0.8,
  names = as.character(1:length(x)),
  legend = "Status",
  names.fill = TRUE, highlight = c("1","2"),
  show = "both"
)
TCGAVisualize_volcano(
  x,
  y,
  filename = NULL,
  y.cut = 10000000,
  x.cut = c(-0.3,0.8),
  names = as.character(1:length(x)),
  legend = "Status",
  names.fill = TRUE,
  highlight = c("1","2"),
  show = "both"
)

```

```
## End(Not run)
while (!(is.null(dev.list()["RStudioGD"]))) {dev.off()}
```

---

TCGA\_MolecularSubtype *Retrieve molecular subtypes for given TCGA barcodes*

---

### Description

TCGA\_MolecularSubtype Retrieve molecular subtypes from TCGA consortium for a given set of barcodes

### Usage

```
TCGA_MolecularSubtype(barcodes)
```

### Arguments

barcodes is a vector of TCGA barcodes

### Value

List with \$subtypes attribute as a dataframe with barcodes, samples, subtypes, and colors. The \$filtered attribute is returned as filtered samples with no subtype info

### Examples

```
TCGA_MolecularSubtype("TCGA-60-2721-01A-01R-0851-07")
```

---

Tumor.purity *TCGA samples with their Tumor Purity measures*

---

### Description

A dataset containing the Sample Ids from TCGA tumor purity measured according to 4 estimates attributes of 9364 tumor patients

### Usage

```
Tumor.purity
```

**Format**

A data frame with 9364 rows and 7 variables:

**Sample.ID** Sample ID from TCGA barcodes, character string

**Cancer.type** Cancer type, character string

**ESTIMATE** uses gene expression profiles of 141 immune genes and 141 stromal genes, 0-1 value

**ABSOLUTE** uses somatic copy-number data (estimations were available for only 11 cancer types), 0-1 value

**LUMP** (leukocytes unmethylation for purity), which averages 44 non-methylated immune-specific CpG sites, 0-1value

**IHC** as estimated by image analysis of haematoxylin and eosin stain slides produced by the Nationwide Childrens Hospital Biospecimen Core Resource, 0-1 value

**CPE** derived consensus measurement as the median purity level after normalizing levels from all methods to give them equal means and s.ds, 0-1 value ...

**Source**

<https://images.nature.com/original/nature-assets/ncomms/2015/151204/ncomms9971/extref/ncomms9971-s2.xlsx>

---

UseRaw_afterFilter	<i>Use raw count from the DataPrep object which genes are removed by normalization and filtering steps.</i>
--------------------	---

---

**Description**

function to keep raw counts after filtering and/or normalizing.

**Usage**

```
UseRaw_afterFilter(DataPrep, DataFilt)
```

**Arguments**

DataPrep	DataPrep object returned by TCGAanalyze_Preprocessing()
DataFilt	Filtered data frame containing samples in columns and genes in rows after normalization and/or filtering steps

**Value**

Filtered return object similar to DataPrep with genes removed after normalization and filtering process.

**Examples**

```
## Not run:
  dataPrep_raw <- UseRaw_afterFilter(dataPrep, dataFilt)

## End(Not run)
```

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