# Package 'CTexploreR'

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**Title** Explores Cancer Testis Genes

**Version** 1.5.0

**Description** The CTexploreR package re-defines the list of Cancer Testis/Germline (CT) genes. It is based on publicly available RNAseq databases (GTEx, CCLE and TCGA) and summarises CT genes' main characteristics. Several visualisation functions allow to explore their expression in different types of tissues and cancer cells, or to inspect the methylation status of their promoters in normal tissues.

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# Contents



---

`all_genes` *All genes description table*

---

## Description

All genes description, imported from `CTdata`

## Usage

```
all_genes
```

### Format

A `tibble` object with 24488 rows and 47 columns.

- Rows correspond to CT genes
- Columns give CT genes characteristics

### Details

See `CTdata::all_genes` documentation for details

### Value

A tibble of all 24 488 genes with their characteristics

### Source

See `scripts/make_all_genes.R` in `CTdata` for details on how this list was created.

### Examples

```
all_genes
```

---

## `CCLE_expression` *Gene expression in CCLE Tumors*

---

### Description

Plots an expression heatmap of genes in CCLE tumor cell lines.

### Usage

```
CCLE_expression(
  genes = NULL,
  type = NULL,
  units = c("TPM", "log_TPM"),
  include_CTP = FALSE,
  values_only = FALSE
)
```

### Arguments

| | |
|---|---|
| `genes` | `character` naming the selected genes. The default value, `NULL`, takes all CT (specific) genes. |
| `type` | `character()` describing the tumor cell line(s) type to be plotted. Allowed cell lines are "Ovarian", "Leukemia", "Colorectal", "Skin", "Lung", "Bladder", "Kidney", "Breast", "Pancreatic", "Myeloma", "Brain", "Sarcoma", "Lymphoma", "Bone", "Neuroblastoma", "Gastric", "Uterine", "Head_and_Neck", "Bile_Duct" and "Esophageal". |
| `units` | `character(1)` with expression values unit. Can be "TPM" (default) or "log_TPM" (log(TPM + 1)) |

| | |
|---|---|
| include_CTP | logical(1) If TRUE, CTP genes are included. (FALSE by default). |
| values_only | logical(1). If TRUE, values are returned instead of the heatmap (FALSE by default). |

## Value

A heatmap of selected genes in CCLE cell lines from specified type. If values_only is TRUE, expression values are returned instead.

## Examples

```
## Not run:
CCLE_expression(
    genes = c("MAGEA1", "MAGEA3", "MAGEA4", "MAGEA6", "MAGEA10"),
    type = c("Skin", "Lung"), units = "log_TPM")

## End(Not run)
```

---

# check_names *Check spelling of entered variables*

---

## Description

Checks the spelling of a vector of entered variable(s) comparing it to a vector of valid names, and removes the ones that are absent from the vector of valid names.

## Usage

```
check_names(variable, valid_vector)
```

## Arguments

| | |
|---|---|
| variable | character() containing the names of variables to check. |
| valid_vector | character() with valid variable names. |

## Value

A character with valid variables.

## Examples

```
CTexploreR:::check_names(
    variable = c("Ovarian", "leukemia", "wrong_name"),
    valid_vector = c("ovarian", "leukemia")
)
```

## CT_correlated_genes *Gene correlations in CCLE cancer cell lines*

### Description

A function that uses expression data from CCLE cell lines and highlights genes correlated (or anti-correlated) with specified CT gene. Genes with a correlation coefficient above threshold are colored in red if they are CT genes or in blue, if not.

### Usage

```
CT_correlated_genes(gene, corr_thr = 0.5, values_only = FALSE)
```

### Arguments

| | |
|---|---|
| gene | CT gene selected |
| corr_thr | numeric(1) with default 0.5. Genes with an absolute correlation coefficient (Pearson) higher than this threshold will be highlighted. |
| values_only | logical(1), FALSE by default. If TRUE, the function will return the correlation coefficients with all genes instead of the plot. |

### Value

A plot where each dots represent the correlation coefficients (Pearson) between genes and the specified CT gene (entered as input). Genes with a correlation coefficient above threshold are colored in red if they are CT genes or in blue, if not. If values_only = TRUE, all correlations coefficients are returned instead.

### Examples

```
## Not run:
CT_correlated_genes(gene = "MAGEA3")

## End(Not run)
```

## CT_genes *CT genes description table*

### Description

Cancer-Testis (CT) genes description, imported from CTdata

### Usage

```
CT_genes
```

### Format

A `tibble` object with 280 rows and 47 columns.

- Rows correspond to CT genes
- Columns give CT genes characteristics

### Details

See `CTdata::CT_genes` documentation for details

### Value

A tibble of all 280 CT and CTP genes with their characteristics

### Source

See `scripts/make_CT_genes.R` in `CTdata` for details on how this list of curated CT genes was created.

### Examples

```
CT_genes
```

---

## `DAC_induction` *Gene expression in cells treated or not by a demethylating agent*

---

### Description

Plots a heatmap of normalised gene counts (log-transformed) in a selection of cells treated or not by 5-Aza-2'-Deoxycytidine (DAC), a demethylating agent.

### Usage

```
DAC_induction(
  genes = NULL,
  multimapping = TRUE,
  include_CTP = FALSE,
  values_only = FALSE
)
```

### Arguments

| | |
|---|---|
| `genes` | `character` naming the selected genes. The default value, `NULL`, takes all CT specific genes. |
| `multimapping` | `logical(1)` defining whether to use multi-mapped gene expression dataset `CTdata::DAC_treated_c` or `DAC_treated_cells`. Default is `TRUE`. |
| `include_CTP` | `logical(1)` If `TRUE`, CTP genes are included. (`FALSE` by default). |
| `values_only` | `logical(1)`. If `TRUE`, the function will return the gene normalised logcounts in all samples instead of the heatmap. Default is `FALSE`. |

## Details

RNAseq data from cells treated or not with 5-aza downloaded from SRA. (SRA references and information about cell lines and DAC treatment are stored the colData of `DAC_treated_cells`). Data was processed using a standard RNAseq pipeline. hisat2 was used to align reads to grch38 genome. featurecounts was used to assign reads to genes. Note that -M parameter was used or not to allow or not counting multi-mapping reads.

## Value

A heatmap of selected genes in cells treated or not by a demethylating agent. If `values_only` is `TRUE`, gene normalised logcounts are returned instead.

## Examples

```
DAC_induction(genes = c("MAGEA1", "MAGEA3", "MAGEA4", "MAGEA6", "CTAG1A"))
DAC_induction(genes = c("MAGEA1", "MAGEA3", "MAGEA4", "MAGEA6", "CTAG1A",
    multimapping = FALSE))
```

---

`embryos_mean_methylation`

*Promoter methylation of any gene in early embryos*

---

## Description

Plots a heatmap of mean promoter methylation levels of any genes in early embryos, using WGSB data from ("Single-cell DNA methylome sequencing of human preimplantation embryos". Zhu et al. Nat genetics 2018). Methylation levels in tissues correspond to the mean methylation of CpGs located in range of 1000 pb upstream and 500 pb downstream from gene TSS.

## Usage

```
embryos_mean_methylation(
  genes = NULL,
  stage = c("GV Oocyte", "MII Oocyte", "Sperm", "Zygote", "2-cell", "4-cell", "8-cell",
    "Morula", "Blastocyst", "Post-implantation"),
  include_CTP = FALSE,
  values_only = FALSE
)
```

## Arguments

| | |
|---|---|
| `genes` | `character` naming the selected genes. The default value, `NULL`, takes all CT (specific) genes. |
| `stage` | `character` defining the cell types to be plotted. Can be "GV Oocyte", "MII Oocyte", "Sperm", "Zygote", "2-cell", "4-cell", "8-cell", "Morula", "Blastocyst", "Post-implantation". |
| `include_CTP` | `logical(1)` If `TRUE`, CTP genes are included. (`FALSE` by default). |
| `values_only` | `logical(1)`, `FALSE` by default. If `TRUE`, the function will return the methylation values in all samples instead of the heatmap. |

## Value

Heatmap of mean promoter methylation of any gene in embryos. If `values_only = TRUE`, a RangedSummarizedExperiment with methylation values is returned instead.

## Examples

```
embryos_mean_methylation()
embryos_mean_methylation(c("MAGEA1", "MAGEA3", "MAGEA4", "MAGEC2", "MAGEB16"),
stage = c( "MII Oocyte", "Sperm", "Zygote", "2-cell", "4-cell", "8-cell",
"Morula"))
```

---

# embryo_expression *Gene expression in human embryos*

---

## Description

Plots a heatmap of genes expression in human early embryos, from "Petropoulos" scRNAseq dataset ("Single-Cell RNA-Seq Reveals Lineage and X Chromosome Dynamics in Human Preimplantation Embryos". Petropoulos et al., Cell 2016) or from "Zhu" scRNAseq dataset ("Single-cell DNA methylome sequencing of human preimplantation embryos". Zhu et al. Nat genetics 2018)

## Usage

```
embryo_expression(
  dataset = c("Petropoulos", "Zhu"),
  genes = NULL,
  include_CTP = FALSE,
  scale_lims = NULL,
  values_only = FALSE
)
```

## Arguments

| | |
|---|---|
| `dataset` | `character`. Indicates which scRNAseq dataset to use. Either Petropoulos or Zhu, no default. |
| `genes` | `character` naming the selected genes. The default value, `NULL`, takes all CT (specific) genes. |
| `include_CTP` | `logical(1)` If `TRUE`, CTP genes are included. (`FALSE` by default). |
| `scale_lims` | `vector of length 2` setting the lower and upper limits of the heatmap colorbar. By default, the lower limit is 0, and the upper limit corresponds to the third quartile of the logcounts values. |
| `values_only` | `logical(1)`. If `TRUE`, the function will return the SingleCellExperiment instead of the heatmap. Default is `FALSE`. |

## Value

A heatmap of selected CT genes expression in single cells from embryos. If `values_only = TRUE`, a SingleCellExperiment is returned instead.

## Examples

```
## Not run:
embryo_expression(dataset = "Petropoulos", include_CTP = FALSE)
embryo_expression(dataset = "Zhu", include_CTP = FALSE)

## End(Not run)
```

---

`fetal_germcells_expression`

*Gene expression in fetal germ cells*

---

## Description

Plots a heatmap of genes expression in fetal germ cells, using scRNAseq data from "Single-cell roadmap of human gonadal development" (Garcia-Alonso, Nature 2022)

## Usage

```
fetal_germcells_expression(
  genes = NULL,
  include_CTP = FALSE,
  ncells_max = 200,
  scale_lims = NULL,
  values_only = FALSE
)
```

## Arguments

| | |
|---|---|
| `genes` | `character` naming the selected genes. The default value, `NULL`, takes all CT (specific) genes. |
| `include_CTP` | `logical(1)` If `TRUE`, CTP genes are included. (`FALSE` by default). |
| `ncells_max` | `integer(1)` Sets the number of each cell type to represent on the heatmap (these cells will be randomly selected among each cell type) (set to 200 by default). If `NULL`, all cells are displayed. |
| `scale_lims` | `vector of length 2` setting the lower and upper limits of the heatmap colorbar. By default, the lower limit is 0, and the upper limit corresponds to the third quartile of the logcounts values. |
| `values_only` | `logical(1)`. If `TRUE`, the function will return the SingleCellExperiment instead of the heatmap. Default is `FALSE`. |

## Value

A heatmap of selected CT genes expression in single cells from fetal germ cells. If `values_only = TRUE`, a SingleCellExperiment is returned instead.

## Examples

```
## Not run:
fetal_germcells_expression(include_CTP = FALSE, ncells_max = 100)

## End(Not run)
```

## fetal_germcells_mean_methylation *Promoter methylation of any gene in fetal germ cells*

### Description

Plots a heatmap of mean promoter methylation levels of any genes in fetal germ cells, using WGSB data from "Dissecting the epigenomic dynamics of human fetal germ cell development at single-cell resolution" (Li et al. 2021). Methylation levels in tissues correspond to the mean methylation of CpGs located in range of 1000 pb upstream and 500 pb downstream from gene TSS.

### Usage

```
fetal_germcells_mean_methylation(
  genes = NULL,
  include_CTP = FALSE,
  values_only = FALSE
)
```

### Arguments

| | |
|---|---|
| genes | character naming the selected genes. The default value, NULL, takes all CT (specific) genes. |
| include_CTP | logical(1) If TRUE, CTP genes are included. (FALSE by default). |
| values_only | logical(1), FALSE by default. If TRUE, the function will return the methylation values in all samples instead of the heatmap. |

### Value

Heatmap of mean promoter methylation of any gene in normal tissues. If values_only = TRUE, a SummarizeExperiment with methylation values is returned instead.

### Examples

```
fetal_germcells_mean_methylation()
fetal_germcells_mean_methylation(c("MAGEA1", "MAGEA3", "MAGEA4", "MAGEC2"))
```

## GTEX_expression *Gene expression in normal tissues (GTEx)*

### Description

Plots an expression heatmap of genes in normal tissues (GTEx database).

### Usage

```
GTEX_expression(
  genes = NULL,
  units = c("TPM", "log_TPM"),
  include_CTP = FALSE,
  values_only = FALSE
)
```

### Arguments

| | |
|---|---|
| genes | character naming the selected genes. The default value, NULL, takes all CT (specific) genes. |
| units | character(1) with expression values unit. Can be "TPM" (default) or "log_TPM" (log(TPM + 1)). |
| include_CTP | logical(1) If TRUE, CTP genes are included. (FALSE by default). |
| values_only | logical(1). If TRUE, the function will return the expression values in all samples instead of the heatmap. Default is FALSE. |

### Value

A heatmap of selected genes expression in normal tissues. If values_only = TRUE, expression values are returned instead.

### Examples

```
GTEX_expression(units = "log_TPM")
GTEX_expression(genes = c("MAGEA1", "MAGEA3"), units = "log_TPM")
```

---

## hESC_expression *Gene expression in human embryonic stem cells*

---

### Description

Plots a heatmap of genes expression in human embryonic stem cells, using RNAseq data downloaded from Encode database.

### Usage

```
hESC_expression(
  genes = NULL,
  include_CTP = FALSE,
  units = c("TPM"),
  scale_lims = NULL,
  values_only = FALSE
)
```

### Arguments

| | |
|---|---|
| genes | character naming the selected genes. The default value, NULL, takes all CT (specific) genes. |
| include_CTP | logical(1) If TRUE, CTP genes are included. (FALSE by default). |
| units | character(1) with expression values unit. Can be "TPM" (default) or "log_TPM" (log(TPM + 1)). |
| scale_lims | vector of length 2 setting the lower and upper limits of the heatmap colorbar. By default, the lower limit is 0, and the upper limit corresponds to the third quartile of the logcounts values. |
| values_only | logical(1). If TRUE, the function will return the SingleCellExperiment instead of the heatmap. Default is FALSE. |

## Value

A heatmap of selected CT genes expression in single cells from human embryonic stem cells. If `values_only = TRUE`, a SummarizedExperiment is returned instead.

## Examples

```
## Not run:
hESC_expression(include_CTP = FALSE, units = "log_TPM",
                  values_only = FALSE)

## End(Not run)
```

---

# hESC_mean_methylation *Promoter methylation of any gene in hESC*

---

## Description

Plots a heatmap of mean promoter methylation levels of any genes in human embryonic cell lines. WGBS methylation data was downloaded from Encode. Methylation levels in tissues correspond to the mean methylation of CpGs located in range of 1000 pb upstream and 200 pb downstream from gene TSS.

## Usage

```
hESC_mean_methylation(
  genes = NULL,
  include_CTP = FALSE,
  values_only = FALSE,
  na.omit = TRUE
)
```

## Arguments

| | |
|---|---|
| genes | `character` naming the selected genes. The default value, `NULL`, takes all CT (specific) genes. |
| include_CTP | `logical(1)` If `TRUE`, CTP genes are included. (`FALSE` by default). |
| values_only | `logical(1)`, `FALSE` by default. If `TRUE`, the function will return the methylation values in all samples instead of the heatmap. |
| na.omit | `logical(1)` specifying if genes with missing methylation values in some tissues should be removed (`TRUE` by default). Note that no gene clustering will be done when methylation values are missing. |

## Value

Heatmap of mean promoter methylation of any gene in hESC. If `values_only = TRUE`, a SummarizedExperiment cobtaining methylation values is returned instead.

## Examples

```
## Not run:
hESC_mean_methylation()

## End(Not run)
```

---

`HPA_cell_type_expression` *Gene expression in different human cell types*

---

## Description

Plots a heatmap of genes expression in the different human cell types based on scRNAseq data obtained from the Human Protein Atlas (https://www.proteinatlas.org)

## Usage

```
HPA_cell_type_expression(
  genes = NULL,
  units = c("scaled", "TPM", "log_TPM"),
  include_CTP = FALSE,
  scale_lims = NULL,
  values_only = FALSE
)
```

## Arguments

| | |
|---|---|
| genes | `character` naming the selected genes. The default value, `NULL`, takes all CT (specific) genes. |
| units | `character(1)` with expression values unit. Can be `"TPM"`, `"log_TPM"` (log(TPM + 1)) or `"scaled"` (scaled TPM values). Default is `"scaled"`. |
| include_CTP | `logical(1)` If `TRUE`, CTP genes are included. (`FALSE` by default). |
| scale_lims | `vector of length 2` setting the lower and upper limits of the heatmap colorbar. |
| values_only | `logical(1)`. If `TRUE`, the function will return the SummarizedExperiment instead of the heatmap. Default is `FALSE`. |

## Value

A heatmap of selected CT genes expression in different human cell types. If `values_only = TRUE`, a SummarizedExperiment instead of the heatmap is returned instead.

## Examples

```
HPA_cell_type_expression(
    genes = NULL, units = "scaled", scale_lims = NULL,
    values_only = FALSE)
HPA_cell_type_expression(
    genes = c("MAGEA1", "MAGEA3", "MAGEA4"),
    units = "TPM", scale_lims = c(0, 50),
    values_only = FALSE)
```

`normal_tissues_mean_methylation` *Promoter methylation of any gene in normal tissues*

## Description

Plots a heatmap of mean promoter methylation levels of any genes in normal tissues. Methylation levels in tissues correspond to the mean methylation of CpGs located in range of 1000 pb upstream and 200 pb downstream from gene TSS.

## Usage

```
normal_tissues_mean_methylation(
  genes = NULL,
  include_CTP = FALSE,
  values_only = FALSE,
  na.omit = TRUE
)
```

## Arguments

| | |
|---|---|
| genes | `character` naming the selected genes. The default value, `NULL`, takes all CT (specific) genes. |
| include_CTP | `logical(1)` If `TRUE`, CTP genes are included. (`FALSE` by default). |
| values_only | `logical(1)`, `FALSE` by default. If `TRUE`, the function will return the methylation values in all samples instead of the heatmap. |
| na.omit | `logical(1)` specifying if genes with missing methylation values in some tissues should be removed (`TRUE` by default). Note that no gene clustering will be done when methylation values are missing. |

## Value

Heatmap of mean promoter methylation of any gene in normal tissues. If `values_only = TRUE`, methylation values are returned instead.

## Examples

```
normal_tissues_mean_methylation()
normal_tissues_mean_methylation(c("MAGEA1", "MAGEA2", "MAGEA3", "MAGEA4"))
normal_tissues_mean_methylation(c("MAGEA1", "MAGEA2", "MAGEA3", "MAGEA4"),
    na.omit = FALSE)
```

## normal_tissues_methylation

*Methylation of CpGs located in promoters in normal tissues*

### Description

Plots a heatmap of the methylation of CpGs located in a promoter, in normal tissues. X-axis corresponds to the CpGs position (related to TSS).

### Usage

```
normal_tissues_methylation(
  gene,
  nt_up = 1000,
  nt_down = 200,
  values_only = FALSE
)
```

### Arguments

| | |
|---|---|
| gene | Name of selected gene |
| nt_up | Number of nucleotides upstream the TSS to analyse (by default 1000, maximum value 5000) |
| nt_down | Number of nucleotides downstream the TSS to analyse (by default 200, maximum value 5000) |
| values_only | Boolean (FALSE by default). If set to TRUE, the function will return the methylation values of all cytosines in the promoter instead of the heatmap. |

### Value

Heatmap of the methylation of CpGs located in a promoter, in normal tissues. If values_only = TRUE, methylation values are returned instead.

### Examples

```
normal_tissues_methylation(gene = "TDRD1", 1000, 0)
```

## normal_tissue_expression_multimapping

*Expression values (TPM) of genes in normal tissues with or without multimapping*

### Description

Plots a heatmap of gene expression values in a set of normal tissues. Expression values (in TPM) have been evaluated by either counting or discarding multi-mapped reads. Indeed, many CT genes belong to gene families from which members have identical or nearly identical sequences. Some CT can only be detected in RNAseq data in which multimapping reads are not discarded.

## Usage

```
normal_tissue_expression_multimapping(
  genes = NULL,
  include_CTP = FALSE,
  multimapping = TRUE,
  units = c("TPM", "log_TPM"),
  values_only = FALSE
)
```

## Arguments

| | |
|---|---|
| genes | character naming the selected genes. The default value, NULL, takes all CT (specific) genes. |
| include_CTP | logical(1) If TRUE, CTP genes are included. (FALSE by default). |
| multimapping | logical(1) that specifies if returned expression values must take into account or not multi-mapped reads. TRUE by default. |
| units | character(1) with expression values unit. Can be "TPM" (default) or "log_TPM" (log(TPM + 1)). |
| values_only | logical(1). If TRUE, the function will return the expression values in all samples instead of the heatmap. Default is FALSE. |

## Details

RNAseq data from a set of normal tissues were downloaded from Encode. (see inst/scripts/make_CT_normal_tissues_mu for fastq references) Fastq files were processed using a standard RNAseq pipeline including FastQC for the quality control of the raw data, and trimmomatic to remove low quality reads and trim the adapter from the sequences. hisat2 was used to align reads to grch38 genome. featurecounts was used to assign reads to genes using Homo_sapiens.GRCh38.105.gtf.

Two different pipelines were run in order to remove or not multi-mapping reads. When multimapping was allowed, hisat2 was run with -k 20 parameter (reports up to 20 alignments per read), and featurecounts was run with -M parameter (multi-mapping reads are counted).

## Value

A heatmap of selected gene expression values in a set of normal tissues calculated by counting or discarding multi-mapped reads. If values_only = TRUE, gene expression values are returned instead.

## Examples

```
normal_tissue_expression_multimapping(
    genes = c("GAGE13", "CT45A6", "NXF2", "SSX2", "CTAG1A",
    "MAGEA3", "MAGEA6"), multimapping = FALSE)
normal_tissue_expression_multimapping(
    genes = c("GAGE13", "CT45A6", "NXF2", "SSX2", "CTAG1A",
    "MAGEA3", "MAGEA6"), multimapping = TRUE)
```

`oocytes_expression` *Gene expression in oocytes*

## Description

Plots a heatmap of genes expression in oocytes, using scRNAseq data from "Decoding dynamic epigenetic landscapes in human oocytes using single-cell multi-omics sequencing" (Yan et al. Cell Stem Cell 2021)

## Usage

```
oocytes_expression(
  genes = NULL,
  include_CTP = FALSE,
  ncells_max = 200,
  scale_lims = NULL,
  values_only = FALSE
)
```

## Arguments

| | |
|---|---|
| `genes` | `character` naming the selected genes. The default value, `NULL`, takes all CT (specific) genes. |
| `include_CTP` | `logical(1)` If `TRUE`, CTP genes are included. (`FALSE` by default). |
| `ncells_max` | `integer(1)` Sets the number of each cell type to represent on the heatmap (these cells will be randomly selected among each cell type) (set to 200 by default). If `NULL`, all cells are displayed. |
| `scale_lims` | `vector of length 2` setting the lower and upper limits of the heatmap colorbar. By default, the lower limit is 0, and the upper limit corresponds to the third quartile of the logcounts values. |
| `values_only` | `logical(1)`. If `TRUE`, the function will return the SingleCellExperiment instead of the heatmap. Default is `FALSE`. |

## Value

A heatmap of selected CT genes expression in single cells from human oocytes. If `values_only = TRUE`, a SingleCellExperiment is returned instead.

## Examples

```
## Not run:
oocytes_expression(include_CTP = FALSE, ncells_max = 100,
                   values_only = FALSE)

## End(Not run)
```

`prepare_TCGA_methylation_expression` *Prepare methylation and expression data of a gene in TCGA tumors*

## Description

Creates a Dataframe giving for each TCGA sample, the methylation level of a gene (mean methylation of probes located in its promoter) and the expression level of the gene (TPM value).

## Usage

```
prepare_TCGA_methylation_expression(
  tumor = "all",
  gene = NULL,
  nt_up = NULL,
  nt_down = NULL,
  include_normal_tissues = FALSE
)
```

## Arguments

| | |
|---|---|
| `tumor` | `character` defining the TCGA tumor type. Can be one of "SKCM", "LUAD", "LUSC", "COAD", "ESCA", "BRCA", "HNSC", or "all" (default). |
| `gene` | `character` selected CT gene. |
| `nt_up` | `numeric(1)` indicating the number of nucleotides upstream the TSS to define the promoter region (1000 by default) |
| `nt_down` | `numeric(1)` indicating the number of nucleotides downstream the TSS to define the promoter region (200 by default) |
| `include_normal_tissues` | `logical(1)`. If `TRUE`, the function will include normal peritumoral tissues in addition to tumoral samples. Default is `FALSE`. |

## Value

a Dataframe giving for each TCGA sample, the methylation level of a gene (mean methylation of probes located in its promoter) and the expression level of the gene (TPM value). The number of probes used to estimate the methylation level is also reported.

## Examples

```
## Not run:
  CTexploreR:::prepare_TCGA_methylation_expression("LUAD", gene = "TDRD1")

## End(Not run)
```

## set_fontsize *Determine font size*

### Description

Gives the fontsize to use for the heatmap based on the matrix's dimension.

### Usage

```
set_fontsize(matrix)
```

### Arguments

| | |
|---|---|
| matrix | matrix containing the data to visualise |

### Value

A logical number that is the fontsize to use

### Examples

```
CTexploreR:::set_fontsize(matrix(1:3, 9,8))
```

## subset_database *Subset databases*

### Description

Check the presence of the genes in the database then subsets the database to only keep these genes' data.

### Usage

```
subset_database(variable = NULL, data, include_CTP = FALSE)
```

### Arguments

| | |
|---|---|
| variable | character() containing the names genes to keep in the data. The default value, NULL, takes CT (specific) genes |
| data | Summarized Experiment or SingleCellExperiment object with valid variable names. |
| include_CTP | logical(1) If TRUE, CTP genes are included. (FALSE by default). |

### Value

A Summarized Experiment or SingleCellExperiment object with only the variables data

### Examples

```
CTexploreR:::subset_database(variable = "MAGEA1", data = CTdata::GTEX_data())
```

TCGA_expression *Gene expression in TCGA tumors*

## Description

Plots a heatmap of genes expression in TCGA samples (peritumoral and tumor samples when a specific tumor type is specified, or tumor samples only when tumor option is set to "all")

## Usage

```
TCGA_expression(
  tumor = "all",
  genes = NULL,
  include_CTP = FALSE,
  units = c("TPM", "log_TPM"),
  values_only = FALSE
)
```

## Arguments

| | |
|---|---|
| tumor | character defining the TCGA tumor type. Can be one of "SKCM", "LUAD", "LUSC", "COAD", "ESCA", "BRCA", "HNSC", or "all" (default). |
| genes | character naming the selected genes. The default value, NULL, takes all CT (specific) genes. |
| include_CTP | logical(1) If TRUE, CTP genes are included. (FALSE by default). |
| units | character(1) with expression values unit. Can be "TPM" (default) or "log_TPM" (log(TPM + 1)). |
| values_only | logical(1). If TRUE, the function will return the expression values in all samples instead of the heatmap. Default is FALSE. |

## Value

A heatmap of selected CT genes expression in TCGA samples. If values_only = TRUE, TPM expression data is returned instead.

## Examples

```
## Not run:
TCGA_expression(
    tumor = "LUAD", genes = c("MAGEA1", "MAGEA3"),
    units = "log_TPM")

## End(Not run)
```

`TCGA_methylation_expression_correlation` *Methylation-Expression correlation of any genes in TCGA samples*

## Description

Plots the correlation between methylation and expression values of a gene in TCGA samples.

## Usage

```
TCGA_methylation_expression_correlation(
  tumor = "all",
  gene = NULL,
  nt_up = 1000,
  nt_down = 200,
  min_probe_number = 3,
  include_normal_tissues = FALSE,
  values_only = FALSE
)
```

## Arguments

| | |
|---|---|
| `tumor` | `character` defining the TCGA tumor type. Can be one of "SKCM", "LUAD", "LUSC", "COAD", "ESCA", "BRCA", "HNSC", or "all" (default). |
| `gene` | `character` selected gene. |
| `nt_up` | `numeric(1)` indicating the number of nucleotides upstream the TSS to define the promoter region (1000 by default) |
| `nt_down` | `numeric(1)` indicating the number of nucleotides downstream the TSS to define the promoter region (200 by default) |
| `min_probe_number` | `numeric(1)` indicating the minimum number of probes (with methylation values) within the selected region to calculate its mean methylation level. Default is 3. |
| `include_normal_tissues` | `logical(1)`. If `TRUE`, the function will include normal peritumoral tissues in addition to tumoral samples. Default is `FALSE`. |
| `values_only` | `logical(1)`. If `TRUE`, the function will return the methylation and expression values in TCGA samples instead of the heatmap. Default is `FALSE`. |

## Details

The coefficient of correlation is set to `NA` if no probes are found in promoter regions or if less than 1% of tumors are positive (TPM >= 1) for the gene.

## Value

A scatter plot representing for each TCGA sample, gene expression and mean methylation values of probe(s) located in its promoter region (defined as 1000 nucleotides upstream TSS and 200 nucleotides downstream TSS by default). If `values_only = TRUE`, methylation and expression values are returned in a tibble instead.

## Examples

```
## Not run:
TCGA_methylation_expression_correlation("LUAD", gene = "TDRD1")

## End(Not run)
```

---

`testis_expression` *Gene expression in testis cells*

---

## Description

Plots a heatmap of genes expression in the different types of testis cells, using scRNAseq data from "The adult human testis transcriptional cell atlas" (Guo et al. 2018)

## Usage

```
testis_expression(
  cells = c("all", "germ_cells", "somatic_cells", "SSC", "Spermatogonia",
   "Early_spermatocyte", "Late_spermatocyte", "Round_spermatid", "Elongated_spermatid",
   "Sperm1", "Sperm2", "Macrophage", "Endothelial", "Myoid", "Sertoli", "Leydig"),
  genes = NULL,
  include_CTP = FALSE,
  scale_lims = NULL,
  values_only = FALSE
)
```

## Arguments

| | |
|---|---|
| `cells` | `character` defining the testis cell types to be plotted. Can be "germ_cells", "somatic_cells", "all" (default), or any or a combination of "SSC", "Spermatogonia", "Early_spermatocyte", "Late_spermatocyte", "Round_spermatid", "Elongated_spermatid", "Sperm1", "Sperm2", "Macrophage", "Endothelial", "Myoid", "Sertoli", "Leydig". |
| `genes` | `character` naming the selected genes. The default value, `NULL`, takes all CT (specific) genes. |
| `include_CTP` | `logical(1)` If `TRUE`, CTP genes are included. (`FALSE` by default). |
| `scale_lims` | `vector of length 2` setting the lower and upper limits of the heatmap colorbar. By default, the lower limit is 0, and the upper limit corresponds to the third quartile of the logcounts values. |
| `values_only` | `logical(1)`. If `TRUE`, the function will return the SingleCellExperiment instead of the heatmap. Default is `FALSE`. |

## Value

A heatmap of selected CT genes expression in single cells from adult testis. If `values_only = TRUE`, a SingleCellExperiment is returned instead.

## Examples

```
## Not run:
testis_expression(cells = "germ_cells",
                  genes = c("MAGEA1", "MAGEA3", "MAGEA4"))

## End(Not run)
```

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