

# Package ‘TCGAretriever’

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**Type** Package

**Title** Retrieve Genomic and Clinical Data from CBioPortal Including TCGA Data

**Version** 1.10.3

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**Depends** R (>= 3.5.0)

**Imports** httr, reshape2, jsonlite

**Suggests** stats, utils, knitr, rmarkdown, ggplot2, dplyr

**VignetteBuilder** knitr

**Description** The Cancer Genome Atlas (TCGA) is a program aimed at improving our understanding of Cancer Biology. Several TCGA Datasets are available online. 'TCGAretriever' helps accessing and downloading TCGA data hosted on 'cBioPortal' via its Web Interface (see <<https://www.cbioportal.org/>> for more information).

**License** GPL-3

**LazyData** true

**URL** [https://www.data-pulse.com/dev\\_site/TCGAretriever/](https://www.data-pulse.com/dev_site/TCGAretriever/)

**Encoding** UTF-8

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blcaOutputExamples      *TCGAREtriever Examples*

---

## Description

A list of objects including examples of the output returned by different ‘TCGAREtriever’ functions. The objects were obtained from the “blca\_tcga” study (bladder cancer).

## Usage

```
data(blcaOutputExamples)
```

## Format

A list including 7 elements.

**exmpl\_1** data.frame (dimensions: 10 by 13). Sample output of the ‘get\_cancer\_studies()’ function.

**exmpl\_2** data.frame (dimensions: 10 by 5). Sample output of the ‘get\_cancer\_types()’ function.

**exmpl\_3** data.frame (dimensions: 9 by 5). Sample output of the ‘get\_case\_lists()’ function.

**exmpl\_4** list including 9 elements. Sample output of the ‘expand\_cases()’ function.

**exmpl\_5** data.frame (dimensions: 10 by 94). Sample output of the ‘get\_clinical\_data()’ function.

**exmpl\_6** data.frame (dimensions: 9 by 8). Sample output of the ‘get\_genetic\_profiles()’ function.

**exmpl\_7** data.frame (dimensions: 10 by 3). Sample output of the ‘get\_gene\_identifiers()’ function.

**exmpl\_8** data.frame (dimensions: 2 by 10). Sample output of the ‘get\_molecular\_data()’ function.

**exmpl\_9** data.frame (dimensions: 6 by 27). Sample output of the ‘get\_mutation\_data()’ function.

## Details

The object was built using the following lines of code. `blcaOutputExamples <- list( exmpl_1 = head(get_cancer_studies(), 10), exmpl_2 = head(get_cancer_types(), 10), exmpl_3 = head(get_case_lists("blca_tcga"), 10), exmpl_4 = expand_cases("blca_tcga"), exmpl_5 = head(get_clinical_data("blca_tcga"), 10), exmpl_6 = head(get_genetic_profiles("blca_tcga"), 10), exmpl_7 = head(get_gene_identifiers("blca_tcga"), 10), exmpl_8 = get_molecular_data(case_list_id = 'blca_tcga_3way_complete', gprofile_id = 'blca_tcga_rna_seq_v2_mrna', glist = c("TP53", "E2F1"))[, 1:10], exmpl_9 = head(get_mutation_data(case_list_id = 'blca_tcga_sequenced', gprofile_id = 'blca_tcga_mutations', glist = c('TP53', 'PTEN'))))`

**Examples**

```
data(blcaOutputExamples)
blcaOutputExamples$exmpl_1
```

---

check\_TCGAretriever\_connection

*Check Connection to the cBioPortal Server*

---

**Description**

Performs a connection check to determine if the remote cBioPortal data server is reachable and responsive.

**Usage**

```
check_TCGAretriever_connection()
```

**Details**

This function attempts to fetch cancer studies within a strict 2-second time limit. If the function returns 'FALSE', it may indicate:

- The server is currently down for maintenance.
- The user's internet connection is inactive or blocked by a firewall.
- The connection speed is too slow to support reliable data retrieval for larger datasets.

**Value**

logical; 'TRUE' if the system can connect and retrieve data within the time limit, 'FALSE' otherwise.

**Author(s)**

Damiano Fantini, <damiano.fantini@gmail.com>

**References**

[https://www.data-pulse.com/dev\\_site/TCGAretriever/](https://www.data-pulse.com/dev_site/TCGAretriever/)

**Examples**

```
## Not run:
check_TCGAretriever_connection()

## End(Not run)
```

---

`expand_cases`*Samples Included in a List of Samples.*

---

**Description**

Each study includes one or more "case lists". Each case list is a collection of samples that were analyzed using one or more platforms/assays. It is possible to obtain a list of all sample identifiers for each case list of interest.

**Usage**

```
expand_cases(csid, dryrun = FALSE)
```

**Arguments**

<code>csid</code>	String corresponding to a TCGA Cancer Study identifier.
<code>dryrun</code>	Logical. If TRUE, all other arguments (if any) are ignored and a representative example is returned as output. No Internet connection is required for executing the operation when 'dryrun' is TRUE.

**Value**

list containing as many elements as TCGA case lists available for a given TCGA Study. Each element is named after a case list identifier. Also, each element is a character vector including all sample identifiers (case ids) corresponding to the corresponding case list identifier.

**Author(s)**

Damiano Fantini, <damiano.fantini@gmail.com>

**References**

[https://www.data-pulse.com/dev\\_site/TCGAretriever/](https://www.data-pulse.com/dev_site/TCGAretriever/)

**Examples**

```
# Set `dryrun = FALSE` (default option) in production!  
x <- expand_cases("blca_tcga", dryrun = TRUE)  
lapply(x, utils::head)
```

---

fetch\_all\_tcgadata      *Fetch All Molecular Data for a Cancer Profile of Interest.*

---

## Description

Recursively query cbioportal to retrieve data corresponding to all available genes. Data are returned as a 'data.frame' that can be easily manipulated for downstream analyses.

## Usage

```
fetch_all_tcgadata(case_list_id, gprofile_id, mutations = FALSE)
```

## Arguments

case\_list\_id      string corresponding to the identifier of the TCGA Case List of interest  
gprofile\_id      string corresponding to the identifier of the TCGA Profile of interest  
mutations      logical. If TRUE, extended mutation data are fetched instead of the standard TCGA data

## Value

A data.frame is returned, including the desired TCGA data. Typically, rows are genes and columns are cases. If "extended mutation" data are retrieved (mutations = TRUE), rows correspond to individual mutations while columns are populated with mutation features

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

[https://www.data-pulse.com/dev\\_site/TCGAretriever/](https://www.data-pulse.com/dev_site/TCGAretriever/)

## Examples

```
# The examples below require an active Internet connection.
# Note: execution may take several minutes.
## Not run:
# Download all brca_pub mutation data (complete samples)
all_brca_MUT <- fetch_all_tcgadata(case_list_id = "brca_tcga_pub_complete",
                                  gprofile_id = "brca_tcga_pub_mutations",
                                  mutations = TRUE)

# Download all brca_pub RNA expression data (complete samples)
all_brca_RNA <- fetch_all_tcgadata(case_list_id = "brca_tcga_pub_complete",
                                   gprofile_id = "brca_tcga_pub_mrna",
                                   mutations = FALSE)
```

```
## End(Not run)
```

---

get\_cancer\_studies      *Retrieve the List of Cancer Studies Available at cbiportal.*

---

### Description

Retrieve information about the studies or datasets available at cbiportal.org. Information include a 'studyId', description, references, and more.

### Usage

```
get_cancer_studies(dryrun = FALSE)
```

### Arguments

dryrun                      Logical. If TRUE, all other arguments (if any) are ignored and a representative example is returned as output. No Internet connection is required for executing the operation when 'dryrun' is TRUE.

### Value

Data Frame including cancer study information.

### Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

### References

[https://www.data-pulse.com/dev\\_site/TCGAretriever/](https://www.data-pulse.com/dev_site/TCGAretriever/)

### Examples

```
# Set `dryrun = FALSE` (default option) in production!  
all_studies <- get_cancer_studies(dryrun = TRUE)  
utils::head(all_studies)
```

---

get_cancer_types	<i>Retrieve Cancer Types.</i>
------------------	-------------------------------

---

**Description**

Retrieve information about cancer types and corresponding abbreviations from cbiportal.org. Information include identifiers, names, and parental cancer type.

**Usage**

```
get_cancer_types(dryrun = FALSE)
```

**Arguments**

dryrun	Logical. If TRUE, all other arguments (if any) are ignored and a representative example is returned as output. No Internet connection is required for executing the operation when 'dryrun' is TRUE.
--------	--

**Value**

A data.frame including cancer type information.

**Author(s)**

Damiano Fantini, <damiano.fantini@gmail.com>

**References**

[https://www.data-pulse.com/dev\\_site/TCGAretriever/](https://www.data-pulse.com/dev_site/TCGAretriever/)

**Examples**

```
# Set `dryrun = FALSE` (default option) in production!  
all_canc <- get_cancer_types(dryrun = TRUE)  
utils::head(all_canc)
```

---

get\_case\_lists      *Retrieve Case List Available for a Specific Cancer Study.*

---

### Description

Each study includes one or more "case lists". Each case list is a collection of samples that were analyzed using one or more platforms/assays. It is possible to obtain a list of case list identifiers from cbiportal.org for a cancer study of interest. Identifier, name, description and category are returned for each entry.

### Usage

```
get_case_lists(csid, dryrun = FALSE)
```

### Arguments

csid	String corresponding to the Identifier of the Study of Interest
dryrun	Logical. If TRUE, all other arguments (if any) are ignored and a representative example is returned as output. No Internet connection is required for executing the operation when 'dryrun' is TRUE.

### Value

Data Frame including Case List information.

### Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

### References

[https://www.data-pulse.com/dev\\_site/TCGAretriever/](https://www.data-pulse.com/dev_site/TCGAretriever/)

### Examples

```
# Set `dryrun = FALSE` (default option) in production!  
blca_case_lists <- get_case_lists("blca_tcga", dryrun = TRUE)  
blca_case_lists
```

---

get\_clinical\_data      *Retrieve Clinical Information for a Cancer Study.*

---

### Description

Retrieve Clinical Information about the samples included in a cancer study of interest. For each sample/case, information about the corresponding cancer patient are returned. These may include sex, age, therapeutic regimen, tumor stage, survival status, as well as other information.

### Usage

```
get_clinical_data(csid, case_list_id = NULL, dryrun = FALSE)
```

### Arguments

csid	String corresponding to a TCGA Cancer Study identifier.
case_list_id	String corresponding to the case_list identifier of interest. This Can be NULL.
dryrun	Logical. If TRUE, all other arguments (if any) are ignored and a representative example is returned as output. No Internet connection is required for executing the operation when 'dryrun' is TRUE.

### Value

data.frame including clinical information of a list of samples/cases of interest.

### Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

### References

[https://www.data-pulse.com/dev\\_site/TCGAretriever/](https://www.data-pulse.com/dev_site/TCGAretriever/)

### Examples

```
# Set `dryrun = FALSE` (default option) in production!  
clinic_data <- get_clinical_data("blca_tcga", dryrun = TRUE)  
utils::head(clinic_data[, 1:7])
```

---

get\_genetic\_profiles *Retrieve Genetic Profiles for a TCGA Study of Interest*

---

### Description

Retrieve Information about all genetic profiles associated with a cancer study of interest. Each cancer study includes one or more types of molecular analyses. The corresponding assays or platforms are referred to as genetic profiles. A genetic profile identifier is required to download molecular data.

### Usage

```
get_genetic_profiles(csid = NULL, dryrun = FALSE)
```

### Arguments

csid	String corresponding to the cancer study id of interest
dryrun	Logical. If TRUE, all other arguments (if any) are ignored and a representative example is returned as output. No Internet connection is required for executing the operation when 'dryrun' is TRUE.

### Value

data.frame including information about genetic profiles.

### Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

### References

[https://www.data-pulse.com/dev\\_site/TCGAretriever/](https://www.data-pulse.com/dev_site/TCGAretriever/)

### Examples

```
# Set `dryrun = FALSE` (default option) in production!  
get_genetic_profiles("blca_tcga", dryrun = TRUE)
```

---

get\_gene\_identifiers *Retrieve All Gene Identifiers*

---

## Description

Obtain all valid gene identifiers, including ENTREZ gene identifiers and HUGO gene symbols. Genes are classified according to the gene type (\*e.g.\*, 'protein-coding', 'pseudogene', 'miRNA', ...). Note that miRNA and phosphoprotein genes are associated with a negative entrezGeneId.

## Usage

```
get_gene_identifiers(dryrun = FALSE)
```

## Arguments

dryrun	Logical. If TRUE, all other arguments (if any) are ignored and a representative example is returned as output. No Internet connection is required for executing the operation when 'dryrun' is TRUE.
--------	--

## Value

Data Frame including gene identifiers.

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

## References

[https://www.data-pulse.com/dev\\_site/TCGAretriever/](https://www.data-pulse.com/dev_site/TCGAretriever/)

## Examples

```
# Set `dryrun = FALSE` (default option) in production!  
x <- get_gene_identifiers(dryrun = TRUE)
```

---

get_molecular_data	<i>Retrieve Molecular Data corresponding to a Genetic Profile of Interest.</i>
--------------------	--

---

### Description

Retrieve Data corresponding to a Genetic Profile of interest from a cancer study of interest. This function is the workhorse of the TCGAretreiver package and can be used to fetch data concerning several genes at once. For retrieving mutation data, please use the 'get\_mutation\_data()' function. For large queries (more than 500 genes), please use the 'fetch\_all\_tcgadata()' function.

### Usage

```
get_molecular_data(  
  case_list_id,  
  gprofile_id,  
  glist = c("TP53", "E2F1"),  
  dryrun = FALSE  
)
```

### Arguments

case_list_id	String corresponding to the Identifier of a list of cases.
gprofile_id	String corresponding to the Identifier of a genetic Profile of interest.
glist	Vector including one or more gene identifiers (ENTREZID or OFFICIAL_SYMBOL). ENTREZID gene identifiers should be passed as numeric.
dryrun	Logical. If TRUE, all other arguments (if any) are ignored and a representative example is returned as output. No Internet connection is required for executing the operation when 'dryrun' is TRUE.

### Value

data.frame including the molecular data of interest. Rows are genes, columns are samples.

### Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

### References

[https://www.data-pulse.com/dev\\_site/TCGAretreiver/](https://www.data-pulse.com/dev_site/TCGAretreiver/)

## Examples

```
# Set `dryrun = FALSE` (default option) in production!  
x <- get_molecular_data(case_list_id = 'blca_tcga_3way_complete',  
                        gprofile_id = 'blca_tcga_rna_seq_v2_mrna',  
                        glist = c("TP53", "E2F1"), dryrun = TRUE)  
  
x[, 1:10]
```

---

get_mutation_data	<i>Retrieve Mutation Data corresponding to a Genetic Profile of Interest.</i>
-------------------	---

---

## Description

Retrieve DNA Sequence Variations (Mutations) identified by exome sequencing projects. This function is the workhorse of the TCGAretreiver package for mutation data and can be used to fetch data concerning several genes at once. For retrieving non-mutation data, please use the 'get\_molecular\_data()' function. For large queries (more than 500 genes), please use the 'fetch\_all\_tcgadata()' function.

## Usage

```
get_mutation_data(  
  case_list_id,  
  gprofile_id,  
  glist = c("TP53", "E2F1"),  
  dryrun = FALSE  
)
```

## Arguments

case_list_id	String corresponding to the Identifier of a list of cases.
gprofile_id	String corresponding to the Identifier of a genetic Profile of interest.
glist	Vector including one or more gene identifiers (ENTREZID or OFFICIAL_SYMOL). ENTREZID gene identifiers should be passed as numeric.
dryrun	Logical. If TRUE, all other arguments (if any) are ignored and a representative example is returned as output. No Internet connection is required for executing the operation when 'dryrun' is TRUE.

## Value

data Frame including one row per mutation

## Author(s)

Damiano Fantini, <damiano.fantini@gmail.com>

**References**

[https://www.data-pulse.com/dev\\_site/TCGAretriever/](https://www.data-pulse.com/dev_site/TCGAretriever/)

**Examples**

```
# Set `dryrun = FALSE` (default option) in production!
x <- get_mutation_data(case_list_id = 'blca_tcga_sequenced',
                      gprofile_id = 'blca_tcga_mutations',
                      glist = c('TP53', 'PTEN'), dryrun = TRUE)
utils::head(x[, c(4, 7, 23, 15, 16, 17, 24, 18, 21)])
```

---

make\_groups

*Split Numeric Vectors in Groups.*

---

**Description**

Assign each element of a numeric vector to a group. Grouping is based on ranks: numeric values are sorted and then split in 2 or more groups. Values may be sorted in an increasing or decreasing fashion. The vector is returned in the original order. Labels may be assigned to each group.

**Usage**

```
make_groups(num_vector, groups, group_labels = NULL, desc = FALSE)
```

**Arguments**

num_vector	numeric vector. It includes the values to be assigned to the different groups
groups	integer. The number of groups that will be generated
group_labels	character vector. Labels for each group. Note that the length of group_labels has to be equal to the number of groups
desc	logical. If TRUE, the sorting is applied in a decreasing fashion

**Value**

data.frame including the vector provided as argument in the original order ("value") and the grouping vector ("rank"). If labels are provided as an argument, group labels are also included in the data.frame ("labels").

**Author(s)**

Damiano Fantini, <damiano.fantini@gmail.com>

**References**

[https://www.data-pulse.com/dev\\_site/TCGAretriever/](https://www.data-pulse.com/dev_site/TCGAretriever/)

**Examples**

```
exprs_geneX <- c(19.1,18.4,22.4,15.5,20.2,17.4,9.4,12.4,31.2,33.2,18.4,22.1)
groups_num <- 3
groups_labels <- c("high", "med", "low")
make_groups(exprs_geneX, groups_num, groups_labels, desc = TRUE)
```

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