

# Package ‘yulab.utils’

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**Title** Supporting Functions for Packages Maintained by 'YuLab-SMU'

**Version** 0.1.8

**Description** Miscellaneous functions commonly used by 'YuLab-SMU'.

**Imports** cli, digest, fs, rlang, tools, utils

**Suggests** htr2, jsonlite, openssl, rappdirs

**ByteCompile** true

**License** Artistic-2.0

**URL** <https://yulab-smu.top/>

**BugReports** <https://github.com/YuLab-SMU/yulab.utils/issues>

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check_pkg	<i>check_pkg</i>
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### Description

Check whether the input packages are installed

### Usage

```
check_pkg(pkg, reason = NULL, ...)
```

### Arguments

pkg	package names
reason	the reason to check the pkg. If NULL, it will set the reason to the parent call.
...	additional parameters that passed to <code>rlang::check_installed()</code>

### Details

This function check whether the input packages are installed. If not, it asks the user whether to install the missing packages.

### Value

see also [check\\_installed](#)

**Author(s)**

Guangchuang Yu

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combinations	<i>combinations</i>
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**Description**

all possible combinations of n sets

**Usage**

combinations(n)

**Arguments**

n                    number of sets

**Value**

a list of all combinations

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CRANpkg	<i>print md text of package with link to homepage (CRAN or Bioconductor)</i>
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**Description**

print md text of package with link to homepage (CRAN or Bioconductor)

**Usage**

CRANpkg(pkg)

Biocpkg(pkg)

**Arguments**

pkg                    package name

**Value**

md text string

**Author(s)**

Guangchuang Yu

exec                    *exec*

---

**Description**

run system command

**Usage**

```
exec(command)
```

**Arguments**

command                system command to run

**Value**

An exec instance that stores system command outputs

**Author(s)**

Guangchuang Yu

---

get\_dependencies        *get\_dependencies*

---

**Description**

get reverse dependencies

**Usage**

```
get_dependencies(pkg, repo = c("CRAN", "BioC"))
```

**Arguments**

pkg                    package name  
repo                    'CRAN' and/or 'BioC'

**Value**

reverse dependencies

**Author(s)**

Guangchuang Yu

---

*get\_fun\_from\_pkg*      *get\_fun\_from\_pkg*

---

**Description**

load function from package

**Usage**

`get_fun_from_pkg(pkg, fun)`

**Arguments**

<code>pkg</code>	package
<code>fun</code>	function

**Value**

function

**Author(s)**

Guangchuang Yu

**Examples**

`get_fun_from_pkg('utils', 'zip')`

---

*Githubpkg*      *print md text of package with link to github repo*

---

**Description**

print md text of package with link to github repo

**Usage**

`Githubpkg(user, pkg)`

**Arguments**

<code>user</code>	github user
<code>pkg</code>	package name

**Value**

md text string

**Author(s)**

Guangchuang Yu

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has_internet	<i>has_internet</i>
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**Description**

test for internet connection via reading lines from a URL

**Usage**

```
has_internet(site = "https://www.baidu.com/")
```

**Arguments**

site	URL to test connection
------	------------------------

**Value**

logical value

**Author(s)**

Guangchuang Yu

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initial_cache	<i>cache intermediate data</i>
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**Description**

Yulab provides a set of utilities to cache intermediate data, including initialize the cached item, update cached item and remove the cached item, etc.

**Usage**

```
initial_cache()

get_cache()

rm_cache()

initial_cache_item(item)

get_cache_item(item)

rm_cache_item(item)

update_cache_item(item, elements)

get_cache_element(item, elements)
```

**Arguments**

item	the name of the cached item
elements	elements to be cached in the item

**Value**

return the cache environment, item or selected elements, depends on the functions.

**Examples**

```
## Not run:
slow_fib <- function(x) {
  if (x < 2) return(1)
  slow_fib(x-2) + slow_fib(x-1)
}

fast_fib <- function(x) {
  if (x < 2) return(1)
  res <- get_cache_element('fibonacci', as.character(x))
  if (!is.null(res)) {
    return(res)
  }
  res <- fast_fib(x-2) + fast_fib(x-1)
  e <- list()
  e[[as.character(x)]] <- res
  update_cache_item('fibonacci', e)
  return(res)
}

system.time(slow_fib(30))
system.time(fast_fib(30))
```

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

---

install_zip	<i>install_zip</i>
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---

### Description

install R package from zip file of source codes

### Usage

```
install_zip(file, args = "--no-build-vignettes")
```

### Arguments

file	zip file
args	argument to build package

### Value

No return value, called for install R package from zip file of source codes

### Author(s)

Guangchuang Yu

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install_zip_gh	<i>install_zip_gh</i>
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---

### Description

install github package

### Usage

```
install_zip_gh(repo, ref = "HEAD", args = "--no-build-vignettes")
```

### Arguments

repo	github repo
ref	github branch, default is HEAD, which means the default branch of the GitHub repo
args	argument to build package



**Details**

it download the zip file first and use `install_zip` to install it

**Value**

No return value, called for installing github package

**Author(s)**

Guangchuang Yu

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<code>is.installed</code>	<i>is.installed</i>
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---

**Description**

Check whether the input packages are installed

**Usage**

```
is.installed(packages)
```

**Arguments**

packages      package names

**Details**

This function check whether the input packages are installed

**Value**

logical vector

**Author(s)**

Guangchuang Yu

**Examples**

```
is.installed(c("dplyr", "ggplot2"))
```

---

ls2df	<i>Convert a list of vector (e.g, gene IDs) to a data.frame object</i>
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---

**Description**

Convert a list of vector to a data.frame object.

**Usage**

```
ls2df(inputList)
```

**Arguments**

inputList      A list of vector

**Value**

a data.frame object.

---

mat2df	<i>mat2df</i>
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**Description**

convert a matrix to a tidy data frame (from wide to long format as described in the tidyverse concept)

**Usage**

```
mat2df(x)
```

**Arguments**

x                      the input matrix

**Value**

a data.frame in long format with the 'value' column stores the original values and 'row' and 'col' columns stored in row and column index as in x

**Author(s)**

Guangchuang Yu

**Examples**

```
x <- matrix(1:15, nrow = 3)
mat2df(x)
```

---

mat2list	<i>mat2list</i>
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---

**Description**

convert a matrix to a list

**Usage**

```
mat2list(x)
```

**Arguments**

x                    the input matrix

**Value**

a list that contains matrix columns as its elements

**Examples**

```
x <- matrix(1:15, nrow = 3)
mat2list(x)
```

---

mypkg	<i>mypkg</i>
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---

**Description**

print md text of link to a package

**Usage**

```
mypkg(pkg, url)
```

**Arguments**

pkg                    package name  
url                    package url

**Value**

md text string

**Author(s)**

Guangchuang Yu

---

```
o
```

---

**Description**

open selected directory or file

**Usage**

```
o(file = ".")
```

**Arguments**

file                   to be open; open working directory by default

**Value**

No return value, called for opening specific directory or file

**Author(s)**

Guangchuang Yu

**Examples**

```
## Not run:
## to open current working directory
o()

## End(Not run)
```

---

```
packageTitle           packageTitle
```

---

**Description**

Extract package title

**Usage**

```
packageTitle(pkg, repo = "CRAN")
```

**Arguments**

pkg                   package name  
repo                   'CRAN' and/or 'BioC'

**Value**

reverse dependencies

**Author(s)**

Guangchuang Yu

---

*pload*                      *pload*

---

**Description**

loading a package

**Usage**

```
pload(package, action = "auto")
```

**Arguments**

package	package name
action	function used to install package. If 'action = "auto"', it will try to use 'Bioc-Manager::install()' if it is available.

**Details**

The function use 'library()' to load the package. If the package is not installed, the function will try to install it before loading it.

**Value**

the selected package loaded to the R session

**Author(s)**

Guangchuang Yu

rbindlist                      *rbindlist*

---

**Description**

rbind a list

**Usage**

```
rbindlist(x)
```

**Arguments**

x                      a list that have similar elements that can be rbind to a data.frame

**Value**

data.frame

**Author(s)**

Guangchuang Yu

---

read.cb                      *read.cb*

---

**Description**

read clipboard

**Usage**

```
read.cb(reader = read.table, ...)
```

**Arguments**

reader                      function to read the clipboard  
...                      parameters for the reader

**Value**

clipboard content, output type depends on the output of the reader

**Author(s)**

Guangchuang Yu

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scale_range	<i>scale-range</i>
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**Description**

normalized data by range

**Usage**

```
scale_range(data)
```

**Arguments**

data            the input data.

**Value**

normalized data

**Author(s)**

Guangchuang Yu

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scihub_dl	<i>download publication via scihub</i>
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**Description**

using scihub to download publication using doi

**Usage**

```
scihub_dl(doi, scihub = "sci-hub.tw", download = TRUE)
```

**Arguments**

doi            doi  
scihub        scihub website  
download      whether download the pdf file

**Value**

pdf url

**Author(s)**

Guangchuang Yu

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set_PCRE	<i>switch regular expression style (PCRE vs TRE)</i>
----------	--

---

### Description

The `set_regexpr_style()` allows user to specify which style to be used, while the `auto_set_regexpr_style()` automatically set the style depending on the operating system (TRE for Windows and PCRE for other OSs (Linux and Mac)).

### Usage

`set_PCRE()`

`set_TRE()`

`use_perl()`

`set_regexpr_style(style)`

`auto_set_regexpr_style()`

### Arguments

`style`            one of 'PCRE' or 'TRE'

### Details

`set_PCRE()` force to use PCRE style while `set_TRE()` force to use TRE.

Note that all these functions are not change the behavior of `gsub()` and `regexpr()`. The functions are just set a global option to store the user's choice of whether using `perl = TRUE`.

Users can access the option via `use_perl()` and pass the return value to `gsub()` or `regexpr()` to specify the style in use.

### Value

logical value of whether use perl

### Author(s)

Guangchuang Yu

### References

<https://stackoverflow.com/questions/47240375/regular-expressions-in-base-r-perl-true-vs-the-default>



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show_in_excel	<i>show_in_excel</i>
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**Description**

Open data frame in Excel. It can be used in pipe.

**Usage**

```
show_in_excel(.data)
```

**Arguments**

.data            a data frame to be open

**Value**

original .data

**Author(s)**

Guangchuang Yu

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str_detect	<i>str_detect</i>
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---

**Description**

Detect the presence/absence of a match

**Usage**

```
str_detect(string, pattern, negate = FALSE)
```

**Arguments**

string            input string  
pattern           pattern to look for  
negate            if TRUE, inverts the resulting boolean vector

**Value**

logical vector

**Author(s)**

Guangchuang Yu

---

str_extract	<i>str_extract</i>
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---

**Description**

Extract a substring using a pattern

**Usage**

```
str_extract(string, pattern)
```

**Arguments**

string	input string
pattern	a regular expression to describe the pattern to extracted from the 'string'

**Value**

substring

**Author(s)**

Guangchuang Yu

---

str_starts	<i>str_starts</i>
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---

**Description**

Detect the presence or absence of a pattern at the beginning or end of a string or string vector.

**Usage**

```
str_starts(string, pattern, negate = FALSE)
```

```
str_ends(string, pattern, negate = FALSE)
```

**Arguments**

string	input string
pattern	pattern with which the string starts or ends
negate	if TRUE, return non-matching elements

**Value**

a logical vector

**Author(s)**

Guangchuang Yu

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<i>str_wrap</i>	<i>str_wrap</i>
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---

**Description**

wrapping long string to multiple lines

**Usage**

```
str_wrap(string, width = getOption("width"))
```

**Arguments**

<i>string</i>	input string
<i>width</i>	the maximum number of characters before wrapping to a new line

**Value**

update strings with new line character inserted

**Author(s)**

Guangchuang Yu

---

<i>yread_tsv</i>	<i>yread</i>
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---

**Description**

read file with caching

**Usage**

```
yread_tsv(  
  file,  
  reader = utils::read.delim,  
  params = list(),  
  cache_dir = tempdir()  
)  
  
yread(file, reader = readLines, params = list(), cache_dir = NULL)
```

**Arguments**

file	a file or url
reader	a function to read the 'file_url'
params	a list of parameters that passed to the 'reader'
cache_dir	a folder to store cache files. If set to NULL will disable cache.

**Details**

This function read a file (local or url) and cache the content.

**Value**

the output of using the 'reader' to read the 'file\_url' with parameters specified by the 'params'

**Author(s)**

Yonghe Xia and Guangchuang Yu

---

yulab\_msg

*yulab\_msg*

---

**Description**

Messages for R package developed by YuLab

**Usage**

```
yulab_msg(pkgname = NULL, n = 1)
```

**Arguments**

pkgname	package name
n	number of citation messages

**Value**

package message

**Author(s)**

Guangchuang Yu

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