

# Package ‘rccmisc’

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**Type** Package

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**Description** Functions either required by other Swedish Regional Cancer Center packages or standalone functions outside the scope of other packages.

**License** GPL-2

**Imports** dplyr

**Suggests** checkpoint, testthat, R.rsp, rvest, xml2

**BugReports** <https://bitbucket.com/cancercentrum/rccmisc/issues>

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as_numeric	<i>Test object for, or coerce to, numeric</i>
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### Description

as\_numeric is essentially a wrapper to as.numeric except that objects of class factor are first coerced to character and then to numeric. is\_numeric test if x is "somehow numeric" (see examples).

### Usage

```
as_numeric(x)
```

```
is_numeric(x)
```

### Arguments

x	object to be coerced or tested (and return a logical vector of the same length) or should it test the whole vector as one object and return a logical vector of length one. (TRUE by default).
---	--

### Examples

```
df <- data.frame(v = c("46513", "45"))
class(df$v) # factor

# Note that
as.numeric(df$v) # 2 1
# but
as_numeric(df$v) # 46513 45

is_numeric(1) # TRUE
is_numeric("1") # TRUE
is_numeric(as.factor(1)) # TRUE
is_numeric(as.factor("khh")) # FALSE
```

---

best_match	<i>Tries to correct misspelling of character string</i>
------------	---

---

### Description

This function uses fuzzy string matching to replace one possibly misspelled (or in other way not fully correct) character string with a correct version of the same string.

### Usage

```
best_match(x, key, no_match = NA, all = FALSE)
```

### Arguments

x	is a character string (or a character vector) that should be matched to the key
key	is a vector containing the correct spellings of the character strings.
no_match	Output value if there is no match. Default is NA. The input is returned unchanged if not matched and no_match = NULL.
all	is a boolean indicator to specify what happens if there is more than one match. Default is FALSE resulting in a warning message and that only the first match is used. If TRUE the returned vector will no longer have the same length as x.

### Value

The function returns a character vector of the same length as x if all = FALSE but with each element substituted to its best match in the key-vector. Strings that could not be matched are NA if (no\_match = TRUE) or unchanged if no\_match = FALSE. If all = TRUE, one input character string could result in more than one output character string. The output might therefore be longer than the input.

### See Also

[clean\\_text](#)

### Examples

```
best_match(c("Hej_apa!", "erik", "baban"), c("hej apa", "hej bepa", "kungen", "Erik"))
best_match(c("Hej_apa", "erik", "baban"),
  c("hej apa", "hej bepa", "kungen", "Erik"), no_match = FALSE)
```

---

change_col_name	<i>Change one column name of a data.frame</i>
-----------------	---

---

## Description

A data.frame can, by definition, have non unique column names. To change a column name to a new name that is already present in the data.frame might therefore lead to undesiered results. This function handles this problem by dropping the original column cousing the name clash.

## Usage

```
change_col_name(x, old_name, new_name, warning = FALSE)
```

## Arguments

x	data.frame with a column name to change
old_name	name (as character string) of column in x that should be changed.
new_name	new name (as character string) to use instead of old_name
warning	should a warning be given if a name clash occurs (FALSE by default)

## Value

The same data.frame but with one column named changed. (Note that the output might have one column less if dropped after name clash.)

## Examples

```
ab <- ba <- data.frame(a = letters[1:10], b = 1:10)

# One "traditional" way to change a column name
names(ab)[names(ab) == "a"] <- "b"
names(ab)
ab$b # Returns the first column with name "b"

# Using change_col_names instead:
change_col_name(ba, "a", "b")
```

---

clean_text	<i>Clean/standardize text</i>
------------	-------------------------------

---

**Description**

Removes punctuation and spaces from character string. Also makes it lower case.

**Usage**

```
clean_text(string)
```

**Arguments**

string            a character string to "clean"

**Value**

the cleaned character string (no punctuation, spaces or capital letters)

**See Also**

[best\\_match](#)

**Examples**

```
clean_text("HELLO_World!!!")
```

---

create_s3_method	<i>Template functions to generate basic S3 methods for new classes</i>
------------------	--

---

**Description**

create\_s3\_method creates a method that applies NextMethod but that also keeps additional attributes (such as class). create\_s3\_print creates a print method.

**Usage**

```
create_s3_method(generic = NULL, object = NULL)
```

```
create_s3_print(fun, ...)
```

**Arguments**

generic, object

as described for [NextMethod](#)

fun

Function to transform object before print (probably [as.character](#), [as.numeric](#) or similar).

...

additional arguments passed to print method

**Details**

Don't forget to also create for example a data.frame method by  
`as.data.frame.xxx <- as.data.frame.vector`

**Value**

S3-method.

**Examples**

```
a <- structure(1:10, class = c("b", "numeric"))
a[3] # Normal subsetting makes a loose its attributes
`.b` <- create_s3_method("[")
print.b <- create_s3_print(as.numeric)
a[3] # attributes preserved even if we can't see them
str(a[3])
```

---

cut.integer

*Convert integer vector to Factor*

---

**Description**

S3-method for cut applied to integer vectors where all outcome factors are integer intervals.

**Usage**

```
## S3 method for class 'integer'
cut(x, ...)
```

**Arguments**

```
x           integer vector
...         further arguments passed to or from other methods
```

**Value**

If `cut.default(x, ...)` returns only integer intervals, these are formatted in a more natural way and returned as an ordered factor. If non integer interval limits occur, the output of `cut.default(x, ...)` is returned as is.

**Examples**

```
cut.default(1:100, seq(0, 100, 20)) # Gives a quite unnatural output
cut(1:100, seq(0, 100, 20)) # Gives nicer and ordered output
cut(1:10, 3) # no integer intervals and therefor same as cut.default
```

---

exceed\_threshold      *Check if transformation/coercing of a vector is good enough*

---

### Description

This function is primarily aimed to check if the transformation of a vector was succesfull enough to return the transformed value instead of the original.

### Usage

```
exceed_threshold(original, transformed, threshold = 0.9, force = FALSE,
  ask = FALSE, var_name = "the input vector")
```

### Arguments

original	the original vector
transformed	the transformed vector with NA-values for non transformed values
threshold	is a numeric value in [0,1] specifying the proportion of cells in transformed that should be recognised as correctly coerced to accept the new class. This does not effect the function output (except when force = TRUE) but will have some diagnostic benefits.
force	Should a candidate vector (candidate according to threshold) be forced to its suggested class (with non-coercable elements set to NA). FALSE by default but if the function is called interactively, the user will also have the option to set force = TRUE on the fly.
ask	this argument gives you the chance to interactively inspect your data and specify if a column is a date or not, on the fly. This is FALSE by default for as.Dates.default but TRUE for as.Dates.dataframe. It only applies when the function is runed interactively and only when force == FALSE.
var_name	a name for the object to be used in messages (you could probably just leave this as default, NULL; it is mostly used for internal purposes!).

### Value

Either original or transformed.

### Examples

```
x <- c(rep("2012-01-01", 9), "foo")
exceed_threshold(x, as.Date(x))
exceed_threshold(x, as.Date(x), force = TRUE)
exceed_threshold(x, as.Date(x), ask = TRUE)
exceed_threshold(x, as.Date(x), threshold = 1)
exceed_threshold(x, as.Date(x), var_name = "bar", force = TRUE)

x <- c(1:9, "baz")
exceed_threshold(x, suppressWarnings(as.numeric(x)))
```

---

findvar *Find variables by name*

---

### Description

Function to search for a variable by its name. See the "Value" section for more details on the different functions.

### Usage

```
findvar_fun(df, ...)
```

```
findvar_in_df(pattern, df, ...)
```

```
findvar_anywhere(pattern, envir = .GlobalEnv, ...)
```

### Arguments

df	A data.frame from where the column names should be identified when returned function applied
...	Arguments passed to grep
pattern	A character string with name (or part of name) of the variables to find.
envir	environment holding data.frames where to search for the variables (the Global environment as default).

### Value

- `findvar_fun`: A function with argument `param` to search for `param` in `df`. See example!
- `findvar_in_df`: A vector with variable names from `df` matching the pattern.
- `findvar_anywhere`: Does not return anything but prints a message where variables matching the pattern can be found.

### Examples

```
find_cars <- findvar_fun(cars)
find_cars("sp")
```

```
findvar_in_df("sp", cars)
```

```
cars <- cars; iris <- iris
findvar_anywhere("petal")
```

---

is.inca	<i>Are we running on INCA?</i>
---------	--------------------------------

---

**Description**

Are we running on INCA?

**Usage**

```
is.inca()
```

**Value**

TRUE if we are running on INCA, FALSE otherwise

**Examples**

```
is.inca()
```

---

is.scalar_in	<i>Test if scalar is in intervall</i>
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---

**Description**

Test if scalar is in intervall

**Usage**

```
is.scalar_in(left, right)
```

```
is.scalar_in01(x)
```

**Arguments**

left, right      arguments passed to [between](#)

x                R object to be tested, most likely a numeric vector of length one (other formats are allowed but will always return FALSE).

**Value**

is.scalar\_in01 returns TRUE if x is an atomic vector of length one and  $0 \leq \text{as\_numeric}(x) \leq 1$ .  
is.scalar\_in return a function similar to is.scalar\_in01 but with specified boundaries.

**Examples**

```
is.scalar_in01(.5) # TRUE
is.scalar_in01(5) # FALSE
is.scalar_in01(seq(0,1,.1)) # FALSE

is_scalar_in09 <- is.scalar_in(0,9)
is_scalar_in09(5) # TRUE
```

---

is.wholenumber	<i>Test if a numeric vector consists of whole numbers</i>
----------------	---

---

**Description**

Function borrowed from the examle section for [integer](#).

**Usage**

```
is.wholenumber(x, tol = .Machine$double.eps^0.5)
```

**Arguments**

x	a numeric vector
tol	How much is x allowed to deviate from round(x) to be a whole number.

**Value**

Logical vector with same length as x.

**Examples**

```
is.wholenumber(1) # is TRUE
(x <- seq(1, 5, by = 0.5) )
is.wholenumber( x ) #--> TRUE FALSE TRUE ...
```

---

lownames	<i>Make all names in data.frame lower case</i>
----------	--

---

**Description**

Tests are also performed so that all column names will stay unique!

**Usage**

```
lownames(df)
```

**Arguments**

df                    A data.frame, possibly with some names with capital letters

**Value**

df is returned unchanged, except that capital letters in names are changed to lower case.

**Examples**

```
df <- data.frame>Hello = 1:10, World = 1:10)
lownames(df)
```

---

make\_r\_script                    *Dump skript together with all functions from package*

---

**Description**

Dump skript together with all functions from package

**Usage**

```
make_r_script(script = NULL, package, outfile = "./inca_r_script.R",
  all = TRUE)
```

**Arguments**

script                connection with script (file) to append tp function defenitions  
package               name of package (as character)  
outfile                filename for dump file  
all                    should all (even non exported) objects from the package be exported?

**Value**

nothing (function called for its side effects)

psum

*Parallel sum*

---

**Description**

This function is to `sum`, what `pmin` and `pmax` is to `min` and `max`.

**Usage**

```
psum(..., na.rm = FALSE)
```

**Arguments**

`...` numeric vectors  
`na.rm` a logical indicating whether missing values should be removed.

**Examples**

```
psum(1:10, 1:10, 1:10)
```

---

rccmisc

*Miscellaneous R functions for the Regional Cancer Centers*

---

**Description**

The content of the package is quite diversified. It contains various functions used for various purposes.

**Details**

Use `help(package="rccmisc")` to list all (exported) functions from the package.

**Author(s)**

Erik Bulow

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safe_ifelse	<i>A safe alternative to ifelse</i>
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---

### Description

This function is similar to `ifelse` with differences described in the details section.

### Usage

```
safe_ifelse(test, yes, no, na_as_false = TRUE, drop.levels = TRUE)
```

### Arguments

<code>test</code> , <code>yes</code> , <code>no</code>	arguments passed to <code>ifelse</code>
<code>na_as_false</code>	should NA values in <code>test</code> be handled as FALSE? TRUE (which is default) implies that <code>test &amp; !is.na(test)</code> must be fulfilled to return values from argument <code>yes</code>
<code>drop.levels</code>	This only applies when <code>yes</code> and <code>no</code> are factor variables. The result will then also be a factor. Unused levels (from <code>yes</code> and <code>no</code> combined) are dropped by default.

### Details

`safe_ifelse` differs from `ifelse` in the following ways:

- Both 'yes' and 'no' must be vectors of the same type or class. This ensures that the output will be of correct format.
- Factors can be combined without problem
- The argument `na.rm` makes it easier to handle cases when `cond = NA`

### Value

Vector of same length and class as `yes` and `no`.

### Examples

```
# Test must be TRUE to return 'yes'
safe_ifelse(NA, 1, 2) ## 2
ifelse(NA, 1, 2) ## NA

# Factors are problematic in ifelse
ifelse(TRUE, as.factor("hello"), 2) ## 1
## Not run:
safe_ifelse(TRUE, as.factor("hello"), 2) ## Error

## End(Not run)
safe_ifelse(TRUE, as.factor("hello"), as.factor(2)) ## hello
safe_ifelse(TRUE, as.factor("hello"), as.factor(2), drop.levels = FALSE)
```

---

specify_missing	<i>Specify missing values for a vector</i>
-----------------	--

---

**Description**

Change specified values to NA

**Usage**

```
specify_missing(x, ..., default_missing = c("", NA, "blanks"))
```

**Arguments**

x	vector
...	values that should be changed to NA if found in x
default_missing	a vector with additional default values to change to NA. These are treated the same as ... but are added by default if not removed. A special value "blank" can be used to indicate all empty strings (all characters matching [:blank:], see <a href="#">regex</a> ).

**Value**

x itself but with specified values set to NA.

**Examples**

```
x <- sample(100)
x[sample(100, 10)] <- 999
specify_missing(x, 999)
```

---

width	<i>Calculate the width of the range of x</i>
-------	--

---

**Description**

Calculate the width of the range of x

**Usage**

```
width(x)
```

**Arguments**

x	object to calculate range for
---	-------------------------------

**Value**

The width of the range of *x* as integer.

**Examples**

```
width(1:10)
width(c(6748, 234, 2456, 5678))
width(sample(345))
```

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