

# Package ‘corrr’

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**Type** Package

**Version** 0.4.2

**Title** Correlations in R

**Description** A tool for exploring correlations.

It makes it possible to easily perform routine tasks when exploring correlation matrices such as ignoring the diagonal, focusing on the correlations of certain variables against others, or rearranging and visualizing the matrix in terms of the strength of the correlations.

**Depends** R (>= 3.3.0)

**Imports** dplyr (>= 0.8), ggplot2 (>= 2.2.0), seriation (>= 1.2-0), purrr (>= 0.2.2), tibble (>= 2.0), ggrepel (>= 0.6.5), methods (>= 3.4.3), rlang (>= 0.4.0)

**Suggests** testthat (>= 2.1.0), knitr (>= 1.13), rmarkdown (>= 0.9.6), dbplyr (>= 1.2.1), DBI, RSQLite, sparklyr (>= 0.9), covr

**VignetteBuilder** knitr

**Encoding** UTF-8

**LazyData** yes

**License** MIT + file LICENSE

**URL** <https://github.com/tidymodels/corrr>

**BugReports** <https://github.com/tidymodels/corrr/issues>

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**NeedsCompilation** no

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**R topics documented:**

as_cordf . . . . .	2
as_matrix . . . . .	3
correlate . . . . .	3
dice . . . . .	5
fashion . . . . .	5
first_col . . . . .	6
focus . . . . .	7
focus_if . . . . .	8
network_plot . . . . .	8
pair_n . . . . .	9
rearrange . . . . .	10
retract . . . . .	11
rplot . . . . .	11
shave . . . . .	12
stretch . . . . .	13

<b>Index</b>	<b>14</b>
--------------	-----------

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as_cordf	<i>Coerce lists and matrices to correlation data frames</i>
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**Description**

A wrapper function to coerce objects in a valid format (such as correlation matrices created using the base function, `cor`) into a correlation data frame.

**Usage**

```
as_cordf(x, diagonal = NA)
```

**Arguments**

x	A list, data frame or matrix that can be coerced into a correlation data frame.
diagonal	Value (typically numeric or NA) to set the diagonal to.

**Value**

A correlation data frame

**Examples**

```
x <- cor(mtcars)
as_cordf(x)
as_cordf(x, diagonal = 1)
```

---

as_matrix	<i>Convert a correlation data frame to matrix format</i>
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---

**Description**

Convert a correlation data frame to original matrix format.

**Usage**

```
as_matrix(x, diagonal)
```

**Arguments**

`x` A correlation data frame. See [correlate](#) or [as\\_cordf](#).  
`diagonal` Value (typically numeric or NA) to set the diagonal to.

**Value**

Correlation matrix

**Examples**

```
x <- correlate(mtcars)
as_matrix(x)
```

---

correlate	<i>Correlation Data Frame</i>
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**Description**

An implementation of `stats::cor()`, which returns a correlation data frame rather than a matrix. See details below. Additional adjustment include the use of pairwise deletion by default.

**Usage**

```
correlate(
  x,
  y = NULL,
  use = "pairwise.complete.obs",
  method = "pearson",
  diagonal = NA,
  quiet = FALSE
)
```

**Arguments**

x	a numeric vector, matrix or data frame.
y	NULL (default) or a vector, matrix or data frame with compatible dimensions to x. The default is equivalent to $y = x$ (but more efficient).
use	an optional character string giving a method for computing covariances in the presence of missing values. This must be (an abbreviation of) one of the strings "everything", "all.obs", "complete.obs", "na.or.complete", or "pairwise.complete.obs".
method	a character string indicating which correlation coefficient (or covariance) is to be computed. One of "pearson" (default), "kendall", or "spearman": can be abbreviated.
diagonal	Value (typically numeric or NA) to set the diagonal to.
quiet	Set as TRUE to suppress message about 'method' and 'use' parameters.

**Details**

This function returns a correlation matrix as a correlation data frame in the following format:

A tibble (see [tibble](#))

- An additional class, "cor\_df"
- A "rowname" column
- Standardized variances (the matrix diagonal) set to missing values by default (NA) so they can be ignored in calculations.

**Value**

A correlation data frame (cor\_df)

**Examples**

```
## Not run:
correlate(iris)

## End(Not run)

correlate(iris[-5])

correlate(mtcars)

## Not run:

# Also supports DB backend and collects results into memory

library(sparklyr)
sc <- spark_connect(master = "local")
mtcars_tbl <- copy_to(sc, mtcars)
mtcars_tbl %>%
  correlate(use = "pairwise.complete.obs", method = "spearman")
spark_disconnect(sc)
```

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

---

dice	<i>Returns a correlation table with the selected fields only</i>
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---

### Description

Returns a correlation table with the selected fields only

### Usage

```
dice(x, ...)
```

### Arguments

x	A correlation table, class cor_df
...	A list of variables in the correlation table

### Examples

```
dice(correlate(mtcars), mpg, wt, am)
```

---

fashion	<i>Fashion a correlation data frame for printing.</i>
---------	---

---

### Description

For the purpose of printing, convert a correlation data frame into a noquote matrix with the correlations cleanly formatted (leading zeros removed; spaced for signs) and the diagonal (or any NA) left blank.

### Usage

```
fashion(x, decimals = 2, leading_zeros = FALSE, na_print = "")
```

### Arguments

x	Scalar, vector, matrix or data frame.
decimals	Number of decimal places to display for numbers.
leading_zeros	Should leading zeros be displayed for decimals (e.g., 0.1)? If FALSE, they will be removed.
na_print	Character string indicating NA values in printed output

**Value**

noquote. Also a data frame if x is a matrix or data frame.

**Examples**

```
# Examples with correlate()
library(dplyr)
mtcars %>% correlate() %>% fashion()
mtcars %>% correlate() %>% fashion(decimals = 1)
mtcars %>% correlate() %>% fashion(leading_zeros = TRUE)
mtcars %>% correlate() %>% fashion(na_print = "*")

# But doesn't have to include correlate()
mtcars %>% fashion(decimals = 3)
c(0.234, 134.23, -.23, NA) %>% fashion(na_print = "X")
```

---

first\_col

*Add a first column to a data.frame*

---

**Description**

Add a first column to a data.frame. This is most commonly used to append a rowname column to create a cor\_df.

**Usage**

```
first_col(df, ..., var = "rowname")
```

**Arguments**

df	Data frame
...	Values to go into the column
var	Label for the column. Default is "rowname"

**Examples**

```
first_col(mtcars, 1:nrow(mtcars))
```



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focus_if	<i>Conditionally focus correlation data frame</i>
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### Description

Apply a predicate function to each column of correlations. Columns that evaluate to TRUE will be included in a call to `focus`.

### Usage

```
focus_if(x, .predicate, ..., mirror = FALSE)
```

### Arguments

<code>x</code>	Correlation data frame or object to be coerced to one via <code>as_cordf</code> .
<code>.predicate</code>	A predicate function to be applied to the columns. The columns for which <code>.predicate</code> returns TRUE will be included as variables in <code>focus</code> .
<code>...</code>	Additional arguments to pass to the predicate function if not anonymous.
<code>mirror</code>	Boolean. Whether to mirror the selected columns in the rows or not.

### Value

A tibble or, if `mirror = TRUE`, a correlation data frame.

### Examples

```
library(dplyr)
any_greater_than <- function(x, val) {
  mean(abs(x), na.rm = TRUE) > val
}

x <- correlate(mtcars)

x %>% focus_if(any_greater_than, .6)
x %>% focus_if(any_greater_than, .6, mirror = TRUE) %>% network_plot()
```

---

network_plot	<i>Network plot of a correlation data frame</i>
--------------	---

---

### Description

Output a network plot of a correlation data frame in which variables that are more highly correlated appear closer together and are joined by stronger paths. Paths are also colored by their sign (blue for positive and red for negative). The proximity of the points are determined using multidimensional clustering.



**Usage**

```
network_plot(
  rdf,
  min_cor = 0.3,
  legend = TRUE,
  colours = c("indianred2", "white", "skyblue1"),
  repel = TRUE,
  curved = TRUE,
  colors
)
```

**Arguments**

rdf	Correlation data frame (see <a href="#">correlate</a> ) or object that can be coerced to one (see <a href="#">as_cordf</a> ).
min_cor	Number from 0 to 1 indicating the minimum value of correlations (in absolute terms) to plot.
legend	Boolean indicating whether a legend mapping the colors to the correlations should be displayed.
colours, colors	Vector of colors to use for n-color gradient.
repel	Should variable labels repel each other? If TRUE, text is added via <a href="#">geom_text_repel</a> instead of <a href="#">geom_text</a>
curved	Should the paths be curved? If TRUE, paths are added via <a href="#">geom_curve</a> ; if FALSE, via <a href="#">geom_segment</a>

**Examples**

```
x <- correlate(mtcars)
network_plot(x)
network_plot(x, min_cor = .1)
network_plot(x, min_cor = .6)
network_plot(x, min_cor = .7, colors = c("red", "green"), legend = TRUE)
```

---

pair_n	<i>Number of pairwise complete cases.</i>
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---

**Description**

Compute the number of complete cases in a pairwise fashion for x (and y).

**Usage**

```
pair_n(x, y = NULL)
```

**Arguments**

- `x` a numeric vector, matrix or data frame.
- `y` NULL (default) or a vector, matrix or data frame with compatible dimensions to `x`. The default is equivalent to `y = x` (but more efficient).

**Value**

Matrix of pairwise sample sizes (number of complete cases).

**Examples**

```
pair_n(mtcars)
```

---

<code>rearrange</code>	<i>Re-arrange a correlation data frame</i>
------------------------	--

---

**Description**

Re-arrange a correlation data frame to group highly correlated variables closer together.

**Usage**

```
rearrange(x, method = "PC", absolute = TRUE)
```

**Arguments**

- `x` `cor_df`. See [correlate](#).
- `method` String specifying the arrangement (clustering) method. Clustering is achieved via [seriate](#), which can be consulted for a complete list of clustering methods. Default = "PCA".
- `absolute` Boolean whether absolute values for the correlations should be used for clustering.

**Value**

`cor_df`. See [correlate](#).

**Examples**

```
x <- correlate(mtcars)

rearrange(x) # Default settings
rearrange(x, method = "HC") # Different seriation method
rearrange(x, absolute = FALSE) # Not using absolute values for arranging
```

---

retract	<i>Creates a data frame from a stretched correlation table</i>
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**Description**

retract does the opposite of what stretch does

**Usage**

```
retract(.data, x, y, val)
```

**Arguments**

.data	A data.frame or tibble containing at least three variables: x, y and the value
x	The name of the column to use from .data as x
y	The name of the column to use from .data as y
val	The name of the column to use from .data to use as the value

**Examples**

```
x <- correlate(mtcars)
xs <- stretch(x)
retract(xs)
```

---

rplot	<i>Plot a correlation data frame.</i>
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**Description**

Plot a correlation data frame using ggplot2.

**Usage**

```
rplot(
  rdf,
  legend = TRUE,
  shape = 16,
  colours = c("indianred2", "white", "skyblue1"),
  print_cor = FALSE,
  colors
)
```

**Arguments**

rdf	Correlation data frame (see <a href="#">correlate</a> ) or object that can be coerced to one (see <a href="#">as_cordf</a> ).
legend	Boolean indicating whether a legend mapping the colors to the correlations should be displayed.
shape	<a href="#">geom_point</a> aesthetic.
colours, colors	Vector of colors to use for n-color gradient.
print_cor	Boolean indicating whether the correlations should be printed over the shapes.

**Value**

Plots a correlation data frame

**Examples**

```
x <- correlate(mtcars)
rplot(x)

# Common use is following rearrange and shave
x <- rearrange(x, absolute = FALSE)
x <- shave(x)
rplot(x)
rplot(x, print_cor = TRUE)
rplot(x, shape = 20, colors = c("red", "green"), legend = TRUE)
```

---

shave	<i>Shave off upper/lower triangle.</i>
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---

**Description**

Convert the upper or lower triangle of a correlation data frame (`cor_df`) to missing values.

**Usage**

```
shave(x, upper = TRUE)
```

**Arguments**

x	cor_df. See <a href="#">correlate</a> .
upper	Boolean. If TRUE, set upper triangle to NA; lower triangle if FALSE.

**Value**

cor\_df. See [correlate](#).

## Examples

```
x <- correlate(mtcars)
shave(x) # Default; shave upper triangle
shave(x, upper = FALSE) # shave lower triangle
```

---

stretch	<i>Stretch correlation data frame into long format.</i>
---------	---

---

## Description

stretch is a specified implementation of `tidyr::gather()` to be applied to a correlation data frame. It will gather the columns into a long-format data frame. The `rowname` column is handled automatically.

## Usage

```
stretch(x, na.rm = FALSE, remove.dups = FALSE)
```

## Arguments

x	cor_df. See <a href="#">correlate</a> .
na.rm	Boolean. Whether rows with an NA correlation (originally the matrix diagonal) should be dropped? Will automatically be set to TRUE if mirror is FALSE.
remove.dups	Removes duplicate entries, without removing all NAs

## Value

tbl with three columns (x and y variables, and their correlation)

## Examples

```
x <- correlate(mtcars)
stretch(x) # Convert all to long format
stretch(x, na.rm = FALSE) # omit NAs (diagonal in this case)

x <- shave(x) # use shave to set upper triangle to NA and then...
stretch(x, na.rm = FALSE) # omit all NAs, therefore keeping each
# correlation only once.
```

# Index

as\_cordf, [2](#), [3](#), [8](#), [9](#), [12](#)

as\_matrix, [3](#)

cor, [2](#)

correlate, [3](#), [3](#), [7](#), [9](#), [10](#), [12](#), [13](#)

dice, [5](#)

fashion, [5](#)

first\_col, [6](#)

focus, [7](#), [8](#)

focus\_(focus), [7](#)

focus\_if, [8](#)

geom\_curve, [9](#)

geom\_point, [12](#)

geom\_segment, [9](#)

geom\_text, [9](#)

geom\_text\_repel, [9](#)

network\_plot, [8](#)

pair\_n, [9](#)

rearrange, [10](#)

retract, [11](#)

rplot, [11](#)

select, [7](#)

seriate, [10](#)

shave, [12](#)

stretch, [13](#)

tibble, [4](#)