

# Package ‘corrr’

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**Type** Package

**Title** Correlations in R

**Version** 0.4.5

**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.

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

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

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

---

### 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>
-----------	--

---

**Description**

Convert a correlation data frame to original matrix format.

**Usage**

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

**Arguments**

x	A correlation data frame. See <a href="#">correlate</a> or <a href="#">as_cordf</a> .
diagonal	Value (typically numeric or NA) to set the diagonal to

**Value**

Correlation matrix

**Examples**

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

---

autoplot.cor_df	<i>Create a correlation matrix from a cor_df object</i>
-----------------	---

---

**Description**

This method provides a good first visualization of the correlation matrix.

**Usage**

```
## S3 method for class 'cor_df'
autoplot(
  object,
  ...,
  method = "PCA",
  triangular = c("upper", "lower", "full"),
  barheight = 20,
  low = "#B2182B",
  mid = "#F1F1F1",
  high = "#2166AC"
)
```

**Arguments**

object	A cor_df object.
...	this argument is ignored.
method	String specifying the arrangement (clustering) method. Clustering is achieved via <a href="#">seriate</a> , which can be consulted for a complete list of clustering methods. Default = "PCA".
triangular	Which part of the correlation matrix should be shown? Must be one of "upper", "lower", or "full", and defaults to "upper".
barheight	A single, non-negative number. Is passed to <a href="#">ggplot2::guide_colourbar()</a> to determine the height of the guide colorbar. Defaults to 20, is likely to need manual adjustments.
low	A single color. Is passed to <a href="#">ggplot2::scale_fill_gradient2()</a> . The color of negative correlation. Defaults to "#B2182B".
mid	A single color. Is passed to <a href="#">ggplot2::scale_fill_gradient2()</a> . The color of no correlation. Defaults to "#F1F1F1".
high	A single color. Is passed to <a href="#">ggplot2::scale_fill_gradient2()</a> . The color of the positive correlation. Defaults to "#2166AC".

**Value**

A ggplot object

**Examples**

```
x <- correlate(mtcars)
autoplot(x)
autoplot(x, triangular = "lower")
autoplot(x, triangular = "full")
```

---

colpair\_map

*Apply a function to all pairs of columns in a data frame*


---

**Description**

colpair\_map() transforms a data frame by applying a function to each pair of its columns. The result is a correlation data frame (see [correlate](#) for details).

**Usage**

```
colpair_map(.data, .f, ..., .diagonal = NA)
```

**Arguments**

<code>.data</code>	A data frame or data frame extension (e.g. a tibble).
<code>.f</code>	A function.
<code>...</code>	Additional arguments passed on to the mapped function.
<code>.diagonal</code>	Value at which to set the diagonal (defaults to NA).

**Value**

A correlation data frame (`cor_df`).

**Examples**

```
## Using `stats::cov` produces a covariance data frame.
colpair_map(mtcars, cov)

## Function to get the p-value from a t-test:
calc_p_value <- function(vec_a, vec_b) {
  t.test(vec_a, vec_b)$p.value
}

colpair_map(mtcars, calc_p_value)
```

---

correlate

*Correlation Data Frame*


---

**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**

<code>x</code>	a numeric vector, matrix or data frame.
<code>y</code>	NULL (default) or a vector, matrix or data frame with compatible dimensions to <code>x</code> . The default is equivalent to <code>y = x</code> (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 "term" column
- Standardized variances (the matrix diagonal) set to missing values by default (NA) so they can be ignored in calculations.

The use argument and its possible values are inherited from `stats::cor()`:

- "everything": NAs will propagate conceptually, i.e. a resulting value will be NA whenever one of its contributing observations is NA
- "all.obs": the presence of missing observations will produce an error
- "complete.obs": correlations will be computed from complete observations, with an error being raised if there are no complete cases.
- "na.or.complete": correlations will be computed from complete observations, returning an NA if there are no complete cases.
- "pairwise.complete.obs": the correlation between each pair of variables is computed using all complete pairs of those particular variables.

As of version 0.4.3, the first column of a `cor_df` object is named "term". In previous versions this first column was named "rowname".

There is a `ggplot2::autoplot()` method for quickly visualizing the correlation matrix, for more information see `autoplot.cor_df()`.

### 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>
------	--

---

### 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 term column to create a `cor_df`.

**Usage**

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

**Arguments**

`df`                    Data frame  
`...`                 Values to go into the column  
`var`                 Label for the column, with the default "term"

**Examples**

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

---

focus

*Focus on section of a correlation data frame.*

---

## Description

Convenience function to select a set of variables from a correlation matrix to keep as the columns, and exclude these or all other variables from the rows. This function will take a [correlate](#) correlation matrix, and expression(s) suited for `dplyr::select()`. The selected variables will remain in the columns, and these, or all other variables, will be excluded from the rows based on 'same'. For a complete list of methods for using this function, see [select](#).

## Usage

```
focus(x, ..., mirror = FALSE)
```

```
focus_(x, ..., .dots, mirror)
```

## Arguments

<code>x</code>	<code>cor_df</code> . See <a href="#">correlate</a> .
<code>...</code>	One or more unquoted expressions separated by commas. Variable names can be used as if they were positions in the data frame, so expressions like 'x:y' can be used to select a range of variables.
<code>mirror</code>	Boolean. Whether to mirror the selected columns in the rows or not.
<code>.dots</code>	Use <code>focus_</code> to do standard evaluations. See <a href="#">select</a> .

## Value

A `tbl` or, if `mirror = TRUE`, a `cor_df` (see [correlate](#)).

## Examples

```
library(dplyr)
x <- correlate(mtcars)
focus(x, mpg, cyl) # Focus on correlations of mpg and cyl with all other variables
focus(x, -disp, -mpg, mirror = TRUE) # Remove disp and mpg from columns and rows

x <- correlate(iris[-5])
focus(x, -matches("Sepal")) # Focus on correlations of non-Sepal
# variables with Sepal variables.
```

---

focus_if	<i>Conditionally focus correlation data frame</i>
----------	---

---

### 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 = c("full", "range", "none"),
  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	How should the colors and legend for the correlation values be displayed? The options are "full" (the default) for -1 to 1 with a legend, "range" for the range of correlation values in rdf with a legend, or "none" for colors between -1 to 1 with no legend 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 = .2, colors = c("red", "green"), legend = "full")
network_plot(x, min_cor = .2, colors = c("red", "green"), legend = "range")
```

---

pair\_n

*Number of pairwise complete cases.*

---

**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>
---------	--

---

**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>
-------	---------------------------------------

---

**Description**

Plot a correlation data frame using ggplot2.

**Usage**

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

**Arguments**

<code>rdf</code>	Correlation data frame (see <a href="#">correlate</a> ) or object that can be coerced to one (see <a href="#">as_cordf</a> ).
<code>legend</code>	Boolean indicating whether a legend mapping the colors to the correlations should be displayed.
<code>shape</code>	<code>ggplot2::geom_point()</code> aesthetic.
<code>colours, colors</code>	Vector of colors to use for n-color gradient.
<code>print_cor</code>	Boolean indicating whether the correlations should be printed over the shapes.
<code>.order</code>	Either "default", meaning x and y variables keep the same order as the columns in x, or "alphabet", meaning the variables are alphabetized.

**Details**

Each value in the correlation data frame is represented by one point/circle in the output plot. The size of each point corresponds to the absolute value of the correlation (via the `size` aesthetic). The color of each point corresponds to the signed value of the correlation (via the `color` aesthetic).

**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)
```

---

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

---

**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 [correlate](#).  
`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 term column is handled automatically.

**Usage**

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

**Arguments**

`x` `cor_df`. See [correlate](#).  
`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 = TRUE) # omit NAs (diagonal in this case)

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

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