…Performing Correlation Analysis: Basic Tools

Comparing stats::cor.test, rstatix::cor_test, and correlation::cor_test

There are multiple packages that allow to perform basic correlation analysis and provide a sufficiently detailed output. By sufficiently detailed I mean more detailed than that of `stats::cor()`. Of those, I prefer `rstatix` and `correlation` (the latter is part of the `easystats` ecosystem). Both have the function `cor_test()`, and both are better than `stats::cor_test()` because they work in a pipe and return output as a dataframe.

Let's illustrate the use of `cor_test()` from both packages with the data collected by Gorman, Williams, and Fraser (2014), which is available as the `palmerpenguins` package. First, let's install and load the packages, then get data for one penguin species:

```
# install packages
install.packages("rstatix")
install.packages("correlation")
install.packages("palmerpenguins")

# load packages
library(dplyr)
library(rstatix)
library(correlation)
library(palmerpenguins)

# select Adelie penguins
adelie <- penguins %>%
  filter(species == "Adelie") %>%
  select(c(2, 3, 6)) %>% # keep only relevant data
  drop_na()
```

Advantages of `rstatix::cor_test()`:

- works in a pipe, unlike `stats::cor.test()`,
- output is a tibble dataframe, unlike `stats::cor.test()`, which returns a list, and unlike `correlation::cor_test()`, which returns a dataframe but not a tibble,
- supports quaziquotation, unlike `correlation::cor_test()` – you don't have to remember to put variable names in quotes.

Disadvantages of `rstatix::cor_test()`:

- only allows to calculate confidence intervals (CIs) for Pearson's \(r\), unlike `correlation::cor_test()`, which can calculate CIs for Spearman's rho \(\rho\) and Kendall's tau \(\tau\),
- knows only three methods for correlation analysis – Pearson's, Spearman's, and Kendall's – vs. 15 (!) methods available in `correlation::cor_test()` including the `"auto"` method, where R tries to guess the best method for you, and
- doesn't report sample size and/or degrees of freedom, unlike `correlation::cor_test()`.

Let's illustrate:

```
# rstatix::cor_test()
rstatix::cor_test(adelie, bill_length_mm, body_mass_g, method =
"spearman")

#> # A tibble: 1 x 6
#>   var1           var2          cor statistic        p method
#>
#> 1 bill_length_mm body_mass_g  0.55   258553. 2.77e-13 Spearman

# correlation::cor_test()
correlation::cor_test(adelie, x = "bill_length_mm", y = "body_mass_g",
method = "spearman")

#> Parameter1      |  Parameter2 |  rho |       95% CI |         S |
p |   Method | n_Obs
#> ------------------------------------------------------------
-----------------------------
#> bill_length_mm | body_mass_g | 0.55 | [0.42, 0.65] | 2.59e+05 | <
.001 | Spearman |   151
```

Most R packages, including `stats`, `rstatix`, and `correlation`, use Pearson's correlation coefficient \(r\) as the default method for correlation analysis, so you'll need to expressly assign a `method` argument if you need to compute a different coefficient.

Both `rstatix::cor_test()` and `correlation::cor_test()` support directional hypothesis testing, even though in the latter case the directional option is not documented in the help returned by `?correlation::cor_test`:

```
rstatix::cor_test(adelie, bill_length_mm, body_mass_g,
                  alternative = "greater")

#> # A tibble: 1 x 8
#>   var1           var2          cor statistic        p conf.low
conf.high method
#>
#> 1 bill_length_mm body_mass_g  0.55      8.01 1.48e-13    0.447
1 Pearson


correlation::cor_test(adelie, x = "bill_length_mm", y = "body_mass_g",
                      alternative = "greater")

#> Parameter1      |  Parameter2 |    r |       95% CI | t(149) |      p
|  Method | n_Obs
#> ------------------------------------------------------------
--------------------------
#> bill_length_mm | body_mass_g | 0.55 | [0.45, 1.00] |   8.01 | < .001
| Pearson |   151
```

Retrieving p-values and Confidence Intervals

Even if your analysis does not immediately return a p-value or a CI for your chosen method, `correlation` package provides two functions that can calculate them for nearly any method in existence: `cor_to_p()` and `cor_to_ci()`. These functions take:

- your correlation coefficient (or a correlation matrix),
- sample size,
- confidence level (95% set as default), and
- method (see `?correlation::cor_to_ci` for a full list).

Let's illustrate using the values returned by our analysis of correlation between bill length and body mass in Adelie penguins, for Spearman's \(\rho\) coefficient:

```
# p-value
correlation::cor_to_p(.55, n = 151, method = "spearman")

#> $p
#> [1] 2.581667e-13
#>
#> $statistic
#> [1] 8.038661

# CI with default confidence level
correlation::cor_to_ci(.55, n = 151, method = "spearman")

#> $CI_low
#> [1] 0.4239604
#>
#> $CI_high
#> [1] 0.6551406

# CI with 99% confidence level
correlation::cor_to_ci(.55, n = 151, ci = 0.99, method = "spearman")

#> $CI_low
#> [1] 0.3802826
#>
#> $CI_high
#> [1] 0.683883
```

As of the time of writing this, `cor_to_p()` and `cor_to_ci()` do not support directional hypothesis testing.

Correlation Matrix

A correlation matrix is simply a table containing correlation coefficients for pairs of variables. It is useful when you need to report coefficients (and sometimes their p-values too) for more than two variables. Here is what it looks like:

```
# clean up missing data
penguins <- drop_na(penguins)

# make correlation matrix
cmat <- rstatix::cor_mat(penguins, names(select_if(penguins,
is.numeric)))
cmat
```

```
#> # A tibble: 5 x 6
#>   rowname           bill_length_mm bill_depth_mm flipper_length_mm
body_mass_g   year
#> *
#> 1 bill_length_mm             1           -0.23              0.65
0.59   0.033
#> 2 bill_depth_mm            -0.23          1                -0.580
-0.47  -0.048
#> 3 flipper_length_mm         0.65        -0.580              1
0.87   0.15
#> 4 body_mass_g               0.59        -0.47               0.87
1      0.022
#> 5 year                      0.033       -0.048              0.15
0.022  1
```

You can reorder a correlation matrix by coefficient:

```
# correlation matrix, ordered by coefficient
rstatix::cor_reorder(cmat)
```

```
#> # A tibble: 5 x 6
#>   rowname           bill_depth_mm   year bill_length_mm
flipper_length_mm body_mass_g
#> *
#> 1 bill_depth_mm             1     -0.048         -0.23
-0.580      -0.47
#> 2 year                    -0.048  1               0.033
0.15        0.022
#> 3 bill_length_mm          -0.23   0.033           1
0.65        0.59
#> 4 flipper_length_mm       -0.580  0.15            0.65
1           0.87
#> 5 body_mass_g             -0.47   0.022           0.59
0.87        1
```

It is also possible to extract significance levels from the correlation matrix with `rstatix::cor_get_pval()`, which returns a table of numeric p-values:

```
# matrix of p-values
rstatix::cor_get_pval(cmat)
```

```
#> # A tibble: 5 x 6
#>   rowname           bill_length_mm bill_depth_mm flipper_length_mm
body_mass_g    year
#>
#> 1 bill_length_mm          0.             2.53e- 5          7.21e- 42
1.54e- 32 0.553
#> 2 bill_depth_mm           2.53e- 5       0.                4.78e- 31
7.02e- 20 0.381
#> 3 flipper_length_mm       7.21e-42       4.78e-31          0.
3.13e-105 0.00574
#> 4 body_mass_g             1.54e-32       7.02e-20          3.13e-105
```

```
0.        0.691
#> 5 year                   5.53e- 1      3.81e- 1         5.74e-  3
6.91e-  1 0
```

You can also get a correlation matrix with both coefficients (as numbers) *and* p-values (as symbols). By default, the symbols and their meanings are: **** \(\leq\) .0001, *** \(\leq\) .001, ** \(\leq\) .01, * \(\leq\) .05, no symbol \(=\) not significant. You can assign your own symbols and significance cut-off points with the `symbols` and `cutpoints` arguments, respectively.

```
rstatix::cor_mark_significant(cmat)
```

```
#>             rowname bill_length_mm bill_depth_mm flipper_length_mm
body_mass_g year
#> 1    bill_length_mm
#> 2     bill_depth_mm       -0.23****
#> 3 flipper_length_mm        0.65****      -0.58****
#> 4       body_mass_g        0.59****      -0.47****           0.87****
#> 5              year           0.033         -0.048             0.15**
0.022
```

If you don't like the matrix format, you can pivot the matrix to a long format with `rstatix::cor_gather()` as a dataframe of paired variables. The returned table will show both the coefficients and the p-values as numbers. Note that the table might get quite long depending on the number of correlated variables:

```
rstatix::cor_gather(cmat)
```

```
#> # A tibble: 25 x 4
#>    var1              var2              cor       p
#>
#>  1 bill_length_mm    bill_length_mm  1      0.
#>  2 bill_depth_mm     bill_length_mm -0.23   2.53e- 5
#>  3 flipper_length_mm bill_length_mm  0.65   7.21e-42
#>  4 body_mass_g       bill_length_mm  0.59   1.54e-32
#>  5 year              bill_length_mm  0.033  5.53e- 1
#>  6 bill_length_mm    bill_depth_mm  -0.23   2.53e- 5
#>  7 bill_depth_mm     bill_depth_mm   1      0.
#>  8 flipper_length_mm bill_depth_mm  -0.580  4.78e-31
#>  9 body_mass_g       bill_depth_mm  -0.47   7.02e-20
#> 10 year              bill_depth_mm  -0.048  3.81e- 1
#> # … with 15 more rows
```

An opposite function `rstatix::cor_spread()` spreads a long correlation dataframe into a correlation matrix:

```
cmat_long <- cor_gather(cmat)
rstatix::cor_spread(cmat_long)
```

```
#> # A tibble: 5 x 6
#>   rowname           bill_length_mm bill_depth_mm flipper_length_mm
body_mass_g   year
#>
#> 1 bill_length_mm             1           -0.23              0.65
```

```
0.59   0.033
#> 2 bill_depth_mm           -0.23        1              -0.580
-0.47  -0.048
#> 3 flipper_length_mm        0.65       -0.580           1
0.87   0.15
#> 4 body_mass_g              0.59       -0.47            0.87
1      0.022
#> 5 year                     0.033      -0.048           0.15
0.022  1
```

Reporting Correlation Analysis

Reporting as Text

Reporting correlation coefficients is pretty easy: you just have to say how big they are and what their significance value is. When reporting, keep the following things in mind (Field, Miles, and Field 2012, 241):

1. Coefficients are usually (for example, in APA style) reported to two decimal places. There should be no zero before the decimal point for the correlation coefficient or the probability value (because neither can exceed 1).
2. There are standard probabilities you can use when reporting \(p\) (.05, .01, .001, and .0001). If \(p \geq .001\), report the exact p-value, otherwise you can simply report \(p < .001\).
3. If you are reporting a one-tailed probability, you should expressly state so, as by default probabilities are assumed to be two-tailed.
4. Use a correct letter to represent your correlation coefficient, such as Pearson's \(r\), Kendall's \(\tau\), or Spearman's \(\rho\).
5. Remember to report your sample size (as \(n = sample\:size\)) or degrees of freedom (APA requires degrees of freedom in parentheses next to \(r\)). Just remember that for Pearson's \(r\), \(df = n\:–\:2\). For non-parametric tests, report only sample size.
6. It is also recommended to report the test statistic (for Pearson's \(r\), it would be \(t\)-statistic).
7. Confidence intervals should be provided whenever possible in addition to the results of the hypothesis test, with confidence level matched to the significance level chosen for the test (e.g. 95% CI for \(p \leq .05\), 99% CI for \(p \leq .01\)); if no inference to the population is intended, report standard deviation of the mean instead of CI (Sim and Reid 1999).

For example, the results of this test:

```
correlation::cor_test(adelie, x = "bill_length_mm", y = "body_mass_g")
```

```
#> Parameter1     |  Parameter2 |    r |       95% CI | t(149) |      p
|  Method | n_Obs
#> --------------------------------------------------------------
--------------------------
#> bill_length_mm | body_mass_g | 0.55 | [0.43, 0.65] |   8.01 | < .001
| Pearson |   151
```

Can be reported as follows:

> Our research shows a highly significant positive correlation between bill length and

> body mass among Adelie penguins: \(t\) = 8.01, \(p\) < .001, Pearson's \(r\)(149) = .55, \(n\) = 151, 95% CI [0.43, 0.65].

Reporting Spearman's or Kendall's correlation coefficients would be similar, but without degrees of freedom.[1]

Reporting as Table

You have no doubt noticed that the results of statistical models are often reported as nicely formatted tables in peer-reviewed journals. So far, our correlations have been reported as plain text tables with a monospaced font. Which means they look a bit ugly. Fortunately, R has a multitude of packages designed to format tables. You can find a brief overview of most (although certainly not all) of them here.

My criteria for choosing the best packages to format tables are simple. First and foremost, the package should be fully compatible with R Markdown, which I use for nearly all my writing (and you should too, because of how much better it is than ~~MS Word~~ legacy software with horrible UI).[2] This means that when you knit your Rmd, the table should render correctly in at least the following formats: HTML, PDF, Word, PowerPoint, and ideally, also OpenDocument and LaTeX. The package should also be easy to use and well-documented.

Upon some research, I think that the best options are:

- `huxtable` – supports most formats and is well-documented,
- `flextable` – the best documented, and
- `gtsummary` – the simplest. Although `gtsummary` renders natively as HTML only, its output can be converted to huxtable or flextable objects, which in turn can be rendered as pretty much anything. Also, `huxtable` and `flextable` are highly versatile and can be used to format any tables, regardless of their contents. `gtsummary` is primarily intended to format the output of commonly used statistical models.

I personally prefer `huxtable` because it supports the largest number of formats (for some to work, you may still need `flextable` to be installed) and has a simple, straightforward syntax.

```
# install packages for table formatting
install.packages("huxtable")
install.packages("flextable")
```

Avoid loading `huxtable` and `flextable` at the same time, as there will be conflicts between some of their functions. Or if you have to, call functions using the `packagename::` syntax.

Let's now demonstrate `huxtable` in action by formatting the results of our correlation analysis:

```
# load huxtable
library(huxtable)

# make huxtable
adelie_ht <- rstatix::cor_test(adelie,
                               bill_length_mm, body_mass_g,
                               method = "spearman") %>%
  as_huxtable() %>%
  set_all_padding(row = everywhere, col = everywhere, value = 6) %>%
  set_bold(1, everywhere) %>%
  set_top_border(1, everywhere, value = 0.8) %>%
  set_bottom_border(1, everywhere, value = 0.4) %>%
  set_caption("Correlation between Body Mass and Bill Length in Adelie
Penguins")

# render huxtable
adelie_ht
```

In some situations, you might need to render a huxtable object as an image, e.g. to combine it with a ggplot object or for other purposes. For example, I had to do this for compatibility with the `goodpress` package, which for some reason can't process `huxtable` HTML output. To render your huxtable as an image, you'll first need to convert it to a flextable object with `huxtable::as_flextable()`, and then render with `flextable::as_raster()`.[3]

```
# render huxtable as an image
adelie_ht %>%
  as_flextable() %>%
  flextable::as_raster(.)
```

Refer to the `huxtable` documentation for the details about what these functions do. Note that some table formatting options work only for the specific output types. For example, higher visual weight of the top border (`value = 0.8`) renders correctly in PDF, but in HTML both borders render as having equal weight. Not sure if this is a bug or a feature.

As a more advanced example, let's format our correlation matrix `cmat`. First, let's reorder it by correlation coefficient, and then let's render coefficients in different color fonts depending on the coefficient's sign and magnitude:

```
cmat_ht <- rstatix::cor_reorder(cmat) %>%
  as_huxtable() %>%
  set_all_padding(row = everywhere, col = everywhere, value = 6) %>%
  set_bold(1, everywhere) %>%
  set_background_color(evens, everywhere, "grey92") %>%
  map_text_color(-1, -1, by_colorspace("red4", "darkgreen")) %>%
  set_caption("Correlation Matrix for Pygoscelis Penguins") %>%
  set_col_width(everywhere, value = c(.16, .15, .11, .2, .2, .2)) %>%
  set_width(1.02) %>% # note how sum of col widths == total table width
  theme_article() # yes, there are themes!

cmat_ht %>%
  as_flextable() %>%
  flextable::as_raster(.)
```

In case you are using R Markdown for your reporting and are rendering to PDF, keep in mind that you won't be able to format table captions with HTML tags like here: `set_caption("`**`Correlation Matrix for Pygoscelis Penguins`**`")`, because they will be rendered literally (as "" **and** ""). However, this works for HTML.

Also keep in mind that the best YAML settings for PDF output would be:

```
output:
  pdf_document:
    latex_engine: xelatex
```

This will work well for complex or unusual LaTeX syntax, which may otherwise cause “Unicode character … not set up for use with LaTeX when knitting to pdf” error.

Just to illustrate how PDF output would look, here is this post rendered to PDF from R Markdown. Looks nice, doesn’t it?

Visualizing Correlation Matrix

`rstatix` has a function to visualize correlation matrices: `cor_plot()`. However, `rstatix::cor_plot()` does not return a ggplot object, and thus:

- can’t take `ggplot2` themes or custom theme objects,
- makes it harder to define a custom color palette, and
- most importantly, `rstatix::cor_plot()` output can’t be further customized or annotated using `ggplot2` themes or packages such as `ggpubr`.[4]

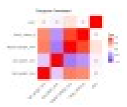
Therefore, I would instead recommend using `ggcorrplot::ggcorrplot()` which returns a ggplot object that can be altered, customized, or annotated using a broad ecosystem of `ggplot2`-based packages. Another great package is `latex2exp`. It allows you to render LaTeX expressions inside plot objects, which is very handy if you’d like to use special symbols or Greek letters in your plot’s text elements.

```
# install ggcorrplot and ggpubr
install.packages("ggcorrplot")
install.packages("ggpubr")
install.packages("latex2exp")

# load ggcorrplot and ggpubr
library(ggcorrplot)
library(ggpubr)
```

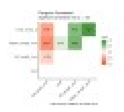
There are two main ways to visualize a correlation matrix: as a square plot where correlations are duplicated (remember that \(CORxy = CORyx\)) and self-correlations (\(r = 1\)) are included, and as a half-square plot where correlation coefficients are not duplicated and self-correlations are excluded. Optionally, you can also add correlation coefficients to the plot, mark statistically non-significant correlations or completely exclude them, change the plot’s color scheme, etc. Since `ggcorrplot()` returns a `ggplot2` object, it can be further altered (e.g. by adding subtitle, annotations, captions, etc.) using `ggpubr::ggpar()`, `ggpubr::annotate_figure()`, and similar functions.

```
# ggcorrplot - basic
ggcorrplot(cmat, title = "Penguins Correlated")
```



Let’s now customize the plot by removing self-correlations, leaving non-significant coefficients blank, assigning a different color palette, reordering the plot by correlation coefficient, choosing plot theme, and adding subtitle and caption. Pay attention to comments in the code:

```
# ggcorrplot - customized
ggcorrplot(cmat, # takes correlation matrix
           title = "Penguins Correlated",
           ggtheme = theme_classic, # takes ggplot2 and custom themes
           colors = c("red", "white", "forestgreen"), # custom color
palette
           hc.order = TRUE, # reorders matrix by corr. coeff.
           type = "upper", # prevents duplication; also try "lower"
           lab = TRUE, # adds corr. coeffs. to the plot
           insig = "blank", # wipes non-significant coeffs.
           lab_size = 3.5) %>%
  # add subtitle and caption; note rendering LaTeX symbols in ggplot
objects
  ggpubr::ggpar(subtitle = latex2exp::TeX("Significant correlations
only (p$\\leq$.05)",
                                          output = "text"),
                caption = "Data: Gorman, Williams, and Fraser 2014")
```



Note how you can render LaTeX symbols inside ggplot objects with `latex2exp::TeX()` function.

Hopefully, I've managed to provide some useful tips on performing and reporting correlation analysis. The next post in this series will be dedicated to robust methods for correlation analysis.

This post is also available as a PDF.

Bibliography

Field, Andy, Jeremy Miles, and Zoë Field. 2012. *Discovering Statistics Using R*. First edit. London, Thousand Oaks, New Delhi, Singapore: SAGE Publications.