

rempsyc: Convenience functions for psychology

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Software

- Review 🗗
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Summary

 $\{\text{rempsyc}\}\$ is an R package of convenience functions that make the analysis-to-publication workflow faster, easier, and less error-prone. It affords easily customizable APA plots (via $\{\text{ggplot2}\}\$) and nice APA tables exportable to Word (via $\{\text{flextable}\}\$). It makes it easy to run statistical tests, check assumptions, and automatize various tasks. It is a package mostly geared at researchers in the psychological sciences but people from all fields can benefit from it.

Statement of need

There are many reasons to use R (R Core Team 2022) for analyzing and reporting data from research studies. R is more compatible with the ideals of open science (Quintana 2020). In contrast to commercial software: (a) it is free to use; (b) it makes it easy to share a fully comprehensive analysis script; (c) it is transparent as anyone can look at the formulas or algorithms used in a given package; (d) the community can quickly contribute new packages based on current needs; (e) it generates better-looking figures; and (f) it helps reduce copypaste errors so common in psychology. The latter point is a substantial one because according to some estimates, up to 50% of articles in psychology have at least one statistical error (Nuijten et al. 2016).

However, R has a major downside for R novices: its steep learning curve due to its programmatic interface, in contrast to perhaps more user-friendly point-and-click software. Of course, this flexibility is also a strength, as the R community can, and increasingly does, mobilize to produce packages that make using R as easy as possible (e.g., the *easystats* ecosystem Lüdecke et al. [2019] 2023). The {rempsyc} package contributes to this momentum by providing convenience functions that remove as much friction as possible between your script and your manuscript (in particular, if you are using Microsoft Word).

There are mainly three things that go into a manuscript: text, tables, and figures. {rempsyc} does not generate publication-ready text summarizing analyses; for this, see the {report} package (Makowski et al. [2021] 2023). Instead, {rempsyc} focuses on the production of publication-ready tables and figures. Below, I go over a few quick examples of those.

Examples Features

33 Publication-Ready Tables

Formatting your table properly in R is already a time-consuming task, but fortunately several packages take care of the formatting within R [e.g., the {broom} or {report} packages, Robinson, Hayes, and Couch (2022); Makowski et al. ([2021] 2023); and there are several others]. Exporting these formatted tables to Microsoft Word remains a challenge however.



- Some packages do export to Word (e.g., Stanley and Spence 2018), but their formatting is often rigid especially when using analyzes that are not supported by default.
- 40 {rempsyc} solves this problem by allowing maximum flexibility: you manually create the data
- 41 frame exactly the way you want, and then only use the magical function, <code>nice_table()</code>, on
- the resulting data frame. nice_table() works on any data frame, even non-statistical ones
- 43 like mtcars.
- One of its main benefit however is the automatic formatting of statistical symbols and its
- integration with other packages. We can for example create a {broom} table and then apply
- nice_table() on it. It suits particularly well the pipe workflow.
- library(rempsyc)
 library(broom)
 model <- lm(mpg ~ cyl + wt * hp, mtcars)
 tidy(model, conf.int = TRUE) |>
 nice_table(broom = "lm")
- 52 Caption for example figure.
- We can do the same with a {report} table.
- 1 library(report)
 1 model <- lm(mpg ~ cyl + wt * hp, mtcars)
 1 stats.table <- as.data.frame(report(model))
 1 nice_table(stats.table)</pre>



Parameter	Fit	b	95% CI (b)	t	df	p	β	95% CI (β)
(Intercept)		49.49	[41.97, 57.01]	13.51	27	<.001	-0.18	[-0.36, -0.01]
cyl		-0.37	[-1.41, 0.68]	-0.72	27	.479	-0.11	[-0.42, 0.20]
wt		-7.63	[-10.75, -4.51]	-5.01	27	<.001	-0.62	[-0.85, -0.40]
hp		-0.11	[-0.17, -0.05]	-3.64	27	.001	-0.29	[-0.53, -0.04]
$wt \times hp$		0.03	[0.01, 0.04]	3.23	27	.003	0.29	[0.11, 0.47]
AIC	147.01							
AICc	150.37							
BIC	155.80							
R2	0.89							
R2 (adj.)	0.87							
Sigma	2.17							

The {report} package provides quite comprehensive tables, so one may request an abbreviated table with the short argument.

nice_table(stats.table, short = TRUE)



Parameter	b	t	df	p	β	95% CI (β)
(Intercept)	49.49	13.51	27	<.001	-0.18	[-0.36, -0.01]
cyl	-0.37	-0.72	27	.479	-0.11	[-0.42, 0.20]
wt	-7.63	-5.01	27	<.001	-0.62	[-0.85, -0.40]
hp	-0.11	-3.64	27	.001	-0.29	[-0.53, -0.04]
$wt \times hp$	0.03	3.23	27	.003	0.29	[0.11, 0.47]

For convenience, it is also possible to highlight significant results for better visual discrimination, using the highlight argument[1]. Once satisfied with the table, we can add a title and note.

my_table <- nice_table(
stats.table, short = TRUE, highlight = 0.001,
title = c("Table 1", "A Pretty Regression Model"),
note = c("The data was extracted from the 1974 Motor Trend US magazine.",

"* p < .05, ** p < .01, *** p < .001"))
my_table



Table 1A Pretty Regression Model

Parameter	b	t	df	p	β	95% CI (β)
(Intercept)	49.49	13.51	27	<.001	-0.18	[-0.36, -0.01]
cyl	-0.37	-0.72	27	.479	-0.11	[-0.42, 0.20]
wt	-7.63	-5.01	27	<.001	-0.62	[-0.85, -0.40]
hp	-0.11	-3.64	27	.001	-0.29	[-0.53, -0.04]
$wt \times hp$	0.03	3.23	27	.003	0.29	[0.11, 0.47]

Note. The data was extracted from the 1974 Motor Trend US magazine.

```
* p < .05, ** p < .01, *** p < .001
```

- One can then easily save the resulting table to Word with flextable::save_as_docx(), specifying the object name and desired path.
- 75 flextable::save_as_docx(my_table, path = "nice_tablehere.docx")
- Additionally, tables created with nice_table() are {flextable} objects (Gohel and Skintzos 2022), and can be modified as such[2].

78 Formattting Results of Analyses

⁷⁹ {rempsyc} also provides its own set of functions to prepare statistical tables before they can be fed to nice_table() and saved to Word.

t tests



Dependent Variable	t	df	p	d	95% CI
mpg	-3.77	18.33	.001	-1.48	[-2.27, -0.67]
disp	4.20	29.26	< .001	1.45	[0.64, 2.23]
drat	-5.65	27.20	< .001	-2.00	[-2.86, -1.12]

Contrasts

```
nice_contrasts(data = mtcars,
response = c("mpg", "disp"),
group = "cyl",
covariates = "hp") |>
nice_table(highlight = .001)
```

	Dependent Variable	Comparison	df	t	p	d	95% CI
-		4 - 8	28	3.66	.001	3.59	[2.72, 4.49]
	mpg	6 - 8	28	1.29	.207	1.44	[0.82, 2.00]
		4 - 6	28	3.64	.001	2.15	[1.35, 3.05]
		4 - 8	28	-6.04	<.001	-4.80	[-5.79, -3.85]
	disp	6 - 8	28	-4.86	<.001	-3.29	[-4.30, -2.17]
		4 - 6	28	-2.70	.012	-1.51	[-2.21, -0.90]

Regressions

```
model1 <- lm(mpg ~ cyl + wt * hp, mtcars)
model2 <- lm(qsec ~ disp + drat * carb, mtcars)

nice_lm(list(model1, model2)) |>
nice_table(highlight = TRUE)
```



Dependent Variable	Predictor	df	b	t	p	sr^2	95% CI
	cyl	27	-0.37	-0.72	.479	.00	[0.00, 0.01]
mno	wt	27	-7.63	-5.01	<.001	.11	[0.01, 0.20]
mpg	hp	27	-0.11	-3.64	.001	.06	[0.00, 0.12]
	wt × hp	27	0.03	3.23	.003	.04	[0.00, 0.10]
	disp	27	-0.01	-1.97	.059	.07	[0.00, 0.20]
~~~~	drat	27	0.23	0.20	.845	.00	[0.00, 0.01]
qsec	carb	27	1.15	0.72	.479	.01	[0.00, 0.06]
	$drat \times carb$	27	-0.48	-1.08	.289	.02	[0.00, 0.09]

Simple Slopes

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```
model1 <- lm(mpg ~ gear * wt, mtcars)
model2 <- lm(disp ~ gear * wt, mtcars)
my.models <- list(model1, model2)

nice_lm_slopes(my.models, predictor = "gear", moderator = "wt") |>
nice_table()
```

	Dependent Variable	Predictor (+/-1 SD)	df	b	t	p	sr ²	95% CI
_		gear (LOW-wt)	28	7.54	2.01	.054	.03	[0.00, 0.09]
	mpg	gear (MEAN-wt)	28	5.62	1.94	.062	.03	[0.00, 0.08]
		gear (HIGH-wt)	28	3.69	1.80	.083	.02	[0.00, 0.08]
		gear (LOW-wt)	28	50.51	0.67	.511	.00	[0.00, 0.02]
	disp	gear (MEAN-wt)	28	35.80	0.61	.545	.00	[0.00, 0.02]
		gear (HIGH-wt)	28	21.08	0.51	.616	.00	[0.00, 0.02]



#### Correlation Matrix

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111 It is also possible to export a colour-coded correlation matrix to Microsoft Excel. The
112 cormatrix_excel() function has several benefits over conventional approaches. The base R
113 cor() function for example does not use rounded values and the console is impractical for
114 large matrices. One may manually round values and export it to a .csv file, which is an
115 improvement but still unsatisfying.

The {apaTables} package (Stanley and Spence 2018) allows exporting the correlation matrix to Word in an APA format, and in many cases this is very satisfying for APA requirements.

Hovever, the Word format is not suitable for large matrices, as it will often spread beyond the document's margin limits.

Another approach is to export to an image, like {correlation} package does (Makowski et al. 2020). For very small matrices, this works extremely well, and the colour is an immense help to quickly identify which correlations are strong or weak, positive or negative. Again, however, this does not work so well for large matrices because labels might overlap or navigating the large figure becomes difficult.

When the goal is more exploratory, rather than reporting, and we have large matrices, it can be more useful to export it to Excel. In {rempsyc}, we combine the idea of using a coloured correlation matrix from the {correlation} package with the idea of exporting to Excel using {openxlsx2} (Barbone and Garbuszus 2023).

We also provide some quality of life-improvements, like freezing the first row and column so as to be able to easily see to which variables the correlations relate, regardless of how far or deep we are within the large correlation matrix.

The colour represents the strength of the correlation, whereas the stars represent how significant the p value is.[3] The exact p values are provided in a second tab for reference purposes, so all information is readily available in a convenient format.

	4	А	В	С	D	Е	F	G	н	1
ı	1	Paramete	age	parity	induced	case	spontaneo	stratum	pooled.str	atum
ı	2	age	1.0	.08	10	.0	08	21 ***	17 *	
ı	3	parity	.08	1.0	.45 ***	.01	.31 ***	31 ***	.12	
ı	4	induced	10	.45 ***	1.0	.02	27 ***	10	.16 *	
ı	5	case	.0	.01	.02	1.0	.36 ***	.0	.0	
ı	6	spontaneo	08	.31 ***	27 ***	.36 ***	1.0	.06	.21 ***	
Ы	7	stratum	21 ***	31 ***	10	.0	.06	1.0	.75 ***	
ı	8	pooled.str	17 *	.12	.16 *	.0	.21 ***	.75 ***	1.0	
	9									
		<b>← →</b>	r_value	p_val	ues	$\oplus$				



	А	В	С	D	E	F	G	н	1				
1	Paramete	age	parity	induced	case	spontaneo	stratum	pooled.str	ratum				
2	age	.0	.194	.113	.956	.186	.001	.006					
3	parity	.194	.0	.0	.889	.0	.0	.059					
4	induced	.113	.0	.0	.789	.0	.113	.010					
5	case	.956	.889	.789	.0	.0	.952	.939					
6	spontaneo	.186	.0	.0	.0	.0	.341	.001					
7	stratum	.001	.0	.113	.952	.341	.0	.0					
8	pooled.sti	.006	.059	.010	.939	.001	.0	.0					
9													
	√												

# **Publication-Ready Figures**

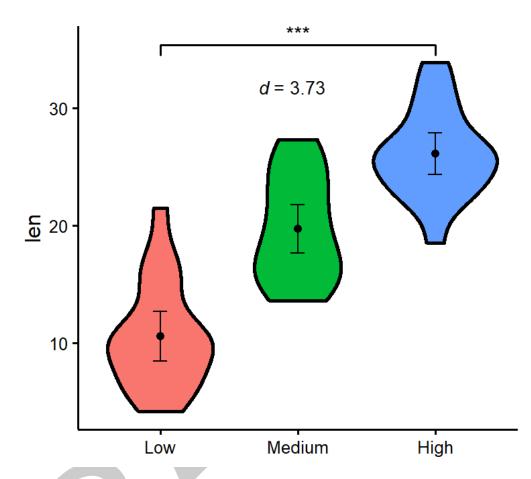
Preparing figures according to APA style, having them look good, and being able to save them in high-resolution with the proper ratios is often challenging. Working with {ggplot2} (Wickham 2016) provides tremendous flexibility, but an unintended consequence is that doing even trivial operations can at times be daunting.

This is why {rempsyc} prepares a few plot types for you, so they are ready to be saved to your preferred format (.pdf, .tiff, or .png).

#### Violin Plots

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For an example of such use in publication, see Thériault et al. (2021).

One can easily save the resulting figure with ggplot2::ggsave(), specifying the desired file name, extension, and resolution.

Recommended dimensions for saving {rempsyc} figures is 7 inches wide and 7 inches high at 300 dpi, which makes sure that the resolution is high enough even if saving to non-vector graphics formats like .png. That said, scalable vector graphics formats like .pdf or .eps are still recommended for high-resolution submissions to scientific journals. Additionally, figures are {ggplot2} objects (Wickham 2016), and can be modified as such.

#### 168 Scatter Plots

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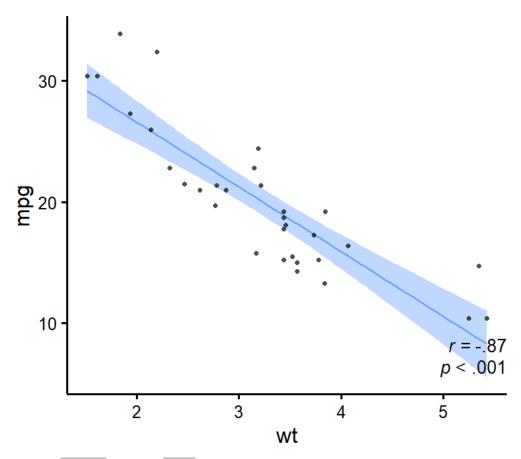
164

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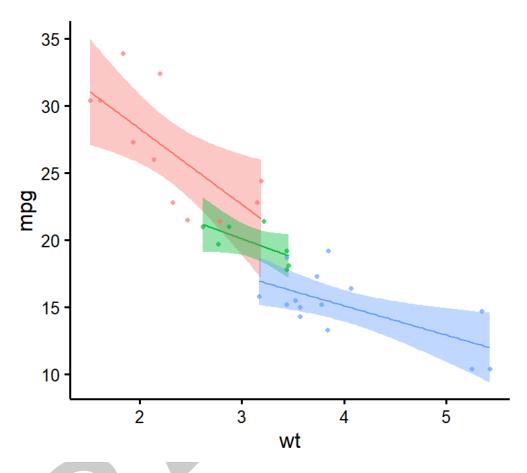
```
nice_scatter(data = mtcars,
predictor = "wt",
response = "mpg",
has.confband = TRUE,
has.r = TRUE,
has.p = TRUE)
```





```
nice_scatter(data = mtcars,
predictor = "wt",
response = "mpg",
group = "cyl",
has.confband = TRUE)
```





For an example of such use in publication, see Krol et al. (2020).

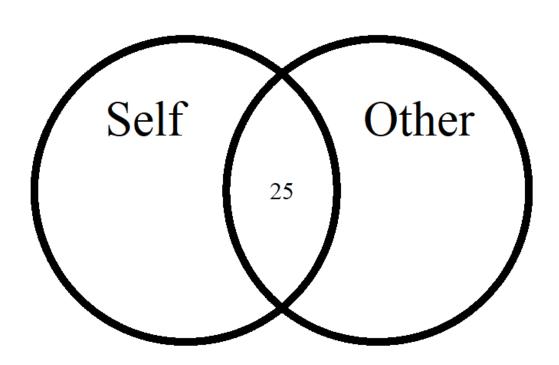
# 183 Overlapping Circles

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For psychologists using the Inclusion of Other in the the Self Scale (Aron, Aron, and Smollan 1992), it can be useful to interpolate the original discrete scores (1 to 7) into a group average representation of the conceptual self-other overlap.

overlap_circle(3.5)





For an example of such use in publication, see Thériault et al. (2021).

# 190 Testing assumptions

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When comes time to test assumptions of a linear model, the best option is the check_model()
function from *easystats*' {performance} package, which allows direct visual evaluation of assumptions (Lüdecke et al. 2021). Indeed, visual assessment of diagnostic plots is recommended over statistical tests since they are overpowered in large samples and underpowered in small samples (Kozak and Piepho 2018).

That said, if for whatever reason one wants to check objective asumption tests for a linear model, rempsyc makes this easy with the nice_assumptions() function, which provide p values for normality (Shapiro-Wilk), homoscedasticity (Breusch-Pagan) and autocorrelation of residuals (Durbin-Watson) in one call.

### Categorical Predictors

nice_normality() makes it easy to visually check normality in the case of categorical predictors (i.e., when using groups), through a combination of quantile-quantile plots, density plots, and histograms.

```
nice_normality(data = iris,
variable = "Sepal.Length",
```



```
group = "Species",
206
                             shapiro = TRUE,
207
                             histogram = TRUE,
208
                             title = "Density (Sepal Length)")
209
                       Density (Sepal Length)
                                           p = .460 (Shapiro-Wilk)
          1.0
          0.5
                                                                     Sample Quantiles
                                                                                                        p = .460 (Shapiro-Wilk)
          0.0
                                           p = .465 (Shapiro-Wilk)
       Density
0.5
                                                                                                                            versicolor
                                                                                                        p = .465 (Shapiro-Wilk)
          0.0
1.5
                                           p = .258 (Shapiro-Wilk)
          1.0
          0.5
          0.0
                                                                                                 6
                               Sepal.Length
                                                                                       Theoretical Quantiles
```

Similarly for univariate outliers using the median absolute deviation (MAD, Leys et al. 2013). plot_outliers(airquality,

group = "Month", response = "Ozone")

210

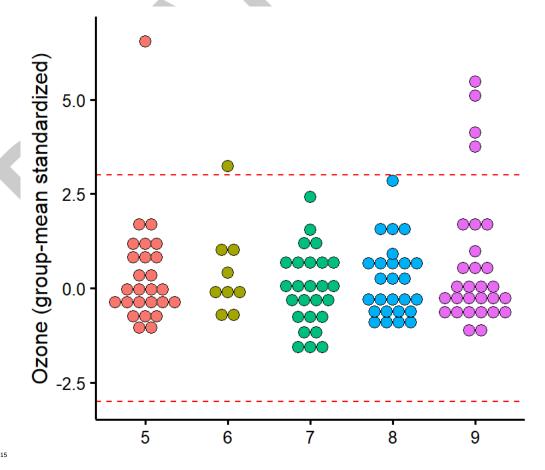
211

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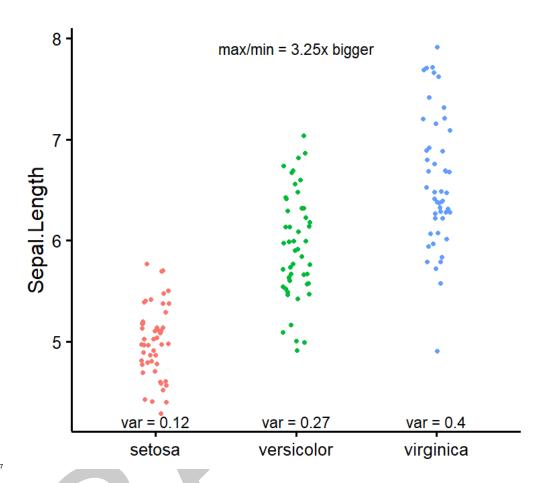
216



Univariate outliers based on the MAD can also be simply requested with find_mad().[4]



```
find_mad(airquality, names(airquality), criteria = 3)
217
218
    ## 8 outlier(s) based on 3 median absolute deviations for variable(s):
219
        Ozone, Solar.R, Wind, Temp, Month, Day
220
221
    ## Outliers per variable:
222
223
    ##
    ## $0zone
224
    ##
         Row Ozone_mad
225
    ## 1
         30
              3.218284
226
              3.989131
    ## 2
          62
227
              3.488081
    ## 3
         99
    ## 4 101 3.025573
229
    ## 5 117 5.261028
230
    ## 6 121 3.333911
231
    ##
232
    ## $Wind
233
         Row Wind_mad
234
    ##
          9 3.049871
235
    ## 1
    ## 2 48 3.225825
236
    Homoscedasticity can also be checked numerically with nice_var() or visually with
237
    nice_varplot().
238
    nice_var(data = iris,
239
              variable = names(iris[1:4]),
240
              group = "Species")
241
242
               Species Setosa Versicolor Virginica Variance.ratio Criteria
243
    ## 1 Sepal.Length 0.124
                                     0.266
                                               0.404
                                                                  3.3
244
    ## 2 Sepal.Width 0.144
                                                                              4
                                    0.098
                                               0.104
                                                                  1.5
245
    ## 3 Petal.Length 0.030
                                    0.221
                                                                 10.2
                                               0.305
                                                                              4
    ## 4 Petal.Width 0.011
                                    0.039
                                                0.075
                                                                  6.8
                                                                              4
247
         Heteroscedastic
    ##
248
    ## 1
                    FALSE
249
    ## 2
                    FALSE
250
    ## 3
                     TRUE
251
                     TRUE
    ## 4
252
253
    nice_varplot(data = iris,
                  variable = "Sepal.Length",
255
                  group = "Species")
256
```



# **Utility functions**

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Finally, with the idea of making the analysis workflow easier in mind, {rempsyc} also has a few other utility functions. nice_na() allows reporting item-level missing values per scale, as well as participant's maximum number of missing items by scale, as per recommendations (Parent 2013).

extract_duplicates() creates a data frame of only observations with a duplicated ID or participant number, so they can be investigated more thoroughly. best_duplicate() allows to follow-up on this investigation and only keep the "best" duplicate, meaning those with the fewer number of missing values, and in case of ties, the first one.

nice_reverse() permits the automatic reverse-coding of scores so common for psychology questionnaires, provided the minimum and maximum score values are known.

There are other functions that the reader can explore at their leisure on the package official website. However, hopefully, this overview has given the reader a gentle introduction to this package.

# **A**vailability

The {rempsyc} package is available on CRAN, and can be installed using install.packages("rempsyc").
The full tutorial website can be accessed at: https://rempsyc.remi-theriault.com/.



# Acknowledgements

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- [1] This argument can be used logically, as TRUE or FALSE, but can also be provided with a numeric value representing the cut-off threshold for the p value
- [2] A great resource for this is the {flextable} e-book: https://ardata-fr.github.io/flextable-book/
- [3] For convenience, colours are only used when the corresponding p value is at least smaller than .05
- Once one has identified outliers, it is also possible ot winsorize them with the winsorize_mad() function.