

# rempsysc: Convenience functions for psychology

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## Summary

`{rempsysc}` is an R package of convenience functions that make the analysis-to-publication workflow faster, easier, and less error-prone. It enables the creation of publication-ready APA (American Psychological Association) tables exportable to Word (via `{flextable}`) and easily customizable APA-compliant plots (via `{ggplot2}`). It makes it easy to run statistical tests, check assumptions, and automate various tasks common in psychology research and social sciences more broadly.

## Statement of need

There are many reasons to use R ([R Core Team, 2022](#)) for analyzing and reporting data from research studies, such as being compatible with the ideals of open science ([Quintana, 2020](#)). However, R has a major downside for 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 does come together to produce packages that make using R increasingly easier and more user-friendly (e.g., the *easystats* ecosystem [Lüdtke et al., 2019/2023](#)). The `{rempsysc}` package (Really Easy Methods for Psychology) 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. `{rempsysc}` does not generate publication-ready text summarizing analyses; for this, see the `{report}` package ([Makowski et al., 2021/2023](#)). Instead, `{rempsysc}` focuses on the production of publication-ready tables and figures. Below, I go over a few quick examples of those.

## Examples Features

### Publication-Ready Tables

Many researchers using R still copy-paste the values from the R console to their manuscript, or retype them manually. Yet, this approach increases the risks of copy-paste and retyping errors so common in psychology. This problem is not trivial given that according to some estimates, up to 50% of articles in psychology have at least one statistical error ([Nuijten et al., 2016](#)). Ideally, one should be able to format the table directly in R, and to export it to Word directly.

Formatting a table properly in R is already a tedious and time-consuming task, but fortunately several packages take care of this step (e.g., the `{broom}` or `{report}` packages, [Makowski et al., 2021/2023](#); [Robinson et al., 2022](#), and there are several others), and there are several others). Exporting these formatted tables to Microsoft Word remains a challenge however. Some packages do export to Word (e.g., the `{apaTables}` package [Stanley & Spence, 2018](#)),

38 but their formatting is often rigid especially when using analyzes or table formats that are not  
39 supported by default.

40 {rempsysc} solves this problem by allowing maximum flexibility: you manually create the data  
41 frame exactly the way you want, and then only use the nice\_table() function on the resulting  
42 data frame. nice\_table() works on any data frame, even non-statistical ones like mtcars.

43 One of its main benefits however is the automatic formatting of statistical symbols and its  
44 integration with other packages. We can for example create a {broom} table and then apply  
45 nice\_table() on it. It suits particularly well the pipe workflow.

```
46 library(rempsysc)
47
48 lm(mpg ~ cyl + wt * hp, mtcars) |>
49   broom::tidy(conf.int = TRUE) |>
50   nice_table(broom = "lm")
```

Term	<i>b</i>	<i>SE</i>	<i>t</i>	<i>p</i>	95% CI
(Intercept)	49.49	3.66	13.51	< .001	[41.97, 57.01]
cyl	-0.37	0.51	-0.72	.479	[-1.41, 0.68]
wt	-7.63	1.52	-5.01	< .001	[-10.75, -4.51]
hp	-0.11	0.03	-3.64	.001	[-0.17, -0.05]
wt × hp	0.03	0.01	3.23	.003	[0.01, 0.04]

51  
52 We can do the same with a {report} table.

```
53 stats.table <- lm(mpg ~ cyl + wt * hp, mtcars) |>
54   report::report() |>
55   as.data.frame()
56
57 nice_table(stats.table)
```

Parameter	Fit	$b$	95% CI ( $b$ )	$t$	$df$	$p$	$\beta$	95% CI ( $\beta$ )
(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							

58

59 The {report} package provides quite comprehensive tables, so one may request an abbreviated  
60 table with the 'short' argument. For convenience, it is also possible to highlight significant  
61 results for better visual discrimination, using the 'highlight' argument.<sup>1</sup> Once satisfied with  
62 the table, we can add a title and note.

```
63 my_table <- nice_table(  
64   stats.table, short = TRUE, highlight = 0.001,  
65   title = c("Table 1", "A Pretty Regression Model"),  
66   note = c("The data was extracted from the 1974 Motor Trend US magazine.",  
67            "Greyed rows represent statistically significant differences, p < .001.")  
68 my_table
```

<sup>1</sup>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

**Table 1**

*A Pretty Regression Model*

Parameter	<i>b</i>	<i>t</i>	<i>df</i>	<i>p</i>	$\beta$	95% CI ( $\beta$ )
<b>(Intercept)</b>	<b>49.49</b>	<b>13.51</b>	<b>27</b>	<b>&lt; .001</b>	<b>-0.18</b>	<b>[-0.36, -0.01]</b>
cyl	-0.37	-0.72	27	.479	-0.11	[-0.42, 0.20]
<b>wt</b>	<b>-7.63</b>	<b>-5.01</b>	<b>27</b>	<b>&lt; .001</b>	<b>-0.62</b>	<b>[-0.85, -0.40]</b>
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.

Greyed rows represent statistically significant differences,  $p < .001$ .

69

70 One can then easily save the resulting table to Word with `flextable::save_as_docx()`,  
71 specifying the object name and desired path.

72 `flextable::save_as_docx(my_table, path = "my_table.docx")`

73 Additionally, tables created with `nice_table()` are {flextable} objects (Gohel & Skintzos,  
74 2022), and can be modified as such.<sup>2</sup>

## 75 **Formattting Results of Analyses**

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

### 78 **t tests**

```
79 nice_t_test(data = mtcars,  
80             response = c("mpg", "disp", "drat"),  
81             group = "am",  
82             warning = FALSE) |>  
83 nice_table()
```

Dependent Variable	<i>t</i>	<i>df</i>	<i>p</i>	<i>d</i>	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]

84

<sup>2</sup>A great resource for this is the {flextable} e-book: <https://ardata-fr.github.io/flextable-book/>

## 85 Contrasts

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

Dependent Variable	Comparison	df	t	p	d	95% CI
mpg	4 - 8	28	3.66	.001	3.59	[2.75, 4.46]
	6 - 8	28	1.29	.207	1.44	[0.78, 2.00]
	4 - 6	28	3.64	.001	2.15	[1.35, 3.06]
disp	4 - 8	28	-6.04	<.001	-4.80	[-5.75, -3.83]
	6 - 8	28	-4.86	<.001	-3.29	[-4.24, -2.25]
	4 - 6	28	-2.70	.012	-1.51	[-2.23, -0.88]

91

## 92 Regressions

```
93 data <- lapply(mtcars, scale)  
94 model1 <- lm(mpg ~ disp + wt * hp, data)  
95 model2 <- lm(qsec ~ drat + wt * hp, data)  
96 my.models <- list(model1, model2)  
97  
98 nice_lm(my.models) |>  
99   nice_table(highlight = TRUE)
```

Dependent Variable	Predictor	df	$\beta$	t	p	$sr^2$	95% CI
mpg	disp	27	-0.06	-0.35	.728	.00	[0.00, 0.01]
	wt	27	-0.63	-4.39	<.001	.08	[0.00, 0.16]
	hp	27	-0.32	-3.00	.006	.04	[0.00, 0.09]
	wt × hp	27	0.31	3.71	.001	.06	[0.00, 0.12]
qsec	drat	27	-0.03	-0.18	.862	.00	[0.00, 0.01]
	wt	27	0.49	2.37	.025	.07	[0.00, 0.19]
	hp	27	-1.05	-6.92	<.001	.62	[0.40, 0.83]
	wt × hp	27	0.02	0.10	.922	.00	[0.00, 0.00]

100

## 101 Simple Slopes

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

Dependent Variable	Predictor (+/-1 SD)	df	$\beta$	$t$	$p$	$sr^2$	95% CI
mpg	wt (LOW-hp)	27	-0.94	-5.60	< .001	.13	[0.02, 0.25]
	wt (MEAN-hp)	27	-0.63	-4.39	< .001	.08	[0.00, 0.16]
	wt (HIGH-hp)	27	-0.32	-1.94	.063	.02	[0.00, 0.05]
qsec	wt (LOW-hp)	27	0.47	1.56	.131	.03	[0.00, 0.10]
	wt (MEAN-hp)	27	0.49	2.37	.025	.07	[0.00, 0.19]
	wt (HIGH-hp)	27	0.51	2.41	.023	.07	[0.00, 0.19]

## 105 Correlation Matrices

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

111 The `{apaTables}` package (Stanley & Spence, 2018) allows exporting the correlation matrix  
 112 to Word in an APA format, and in many cases this already meets the formal requirements of  
 113 APA style. However, the Word format is not suitable for large matrices, as it will often spread  
 114 beyond the document's margin limits.

115 Another approach is to export the matrix to an image, like the `{correlation}` package does  
 116 (Makowski et al., 2020).<sup>3</sup> For very small matrices, this works extremely well, and the colour is  
 117 an immense help to quickly identify which correlations are strong or weak, positive or negative,  
 118 and significant or non-significant. Again, however, this does not work so well for large matrices  
 119 because labels might overlap or navigating the large figure becomes difficult.

120 When the goal is more exploratory in nature, and one has large matrices, it can be beneficial  
 121 to export them to Excel. `{rempsyc}` combines the idea of using a coloured correlation matrix  
 122 from the `{correlation}` package with the idea of exporting to Excel using `{openxlsx2}` (Barbone  
 123 & Garbuszus, 2023).

124 `{rempsyc}` also provides some usability improvements, like freezing the first row and column so  
 125 as to be able to easily see which variables correlate with which other variables, regardless of  
 126 how far or deep those variables are located within the matrix.

127 The colour represents the strength of the correlation, whereas the stars represent different  
 128 significance thresholds for the  $p$  value is.<sup>4</sup> The exact  $p$  values are provided in a second tab for  
 129 reference purposes, so all information is readily available in just one function call.

```
130 cormatrix_excel(data = infert,
131                 filename = "cormatrix1",
132                 select = c("age", "parity", "induced", "case", "spontaneous",
```

<sup>3</sup>Exporting the correlation matrix to an image through the `{correlation}` package also requires the `{see}` package (Lüdtke, Patil, et al., 2021)

<sup>4</sup>For convenience, colours are only used when the corresponding  $p$  value is at least smaller than .05

133 "stratum", "pooled.stratum"))

	A	B	C	D	E	F	G	H	I
1	Parameter	age	parity	induced	case	spontaneous	stratum	pooled.stratum	
2	age	1.0	.08	-.10	.0	-.08	-.21 ***	-.17 *	
3	parity	.08	1.0	.45 ***	.01	.31 ***	-.31 ***	.12	
4	induced	-.10	.45 ***	1.0	.02	-.27 ***	-.10	.16 *	
5	case	.0	.01	.02	1.0	.36 ***	.0	.0	
6	spontaneous	-.08	.31 ***	-.27 ***	.36 ***	1.0	.06	.21 ***	
7	stratum	-.21 ***	-.31 ***	-.10	.0	.06	1.0	.75 ***	
8	pooled.stratum	-.17 *	.12	.16 *	.0	.21 ***	.75 ***	1.0	
9									

	A	B	C	D	E	F	G	H	I
1	Parameter	age	parity	induced	case	spontaneous	stratum	pooled.stratum	
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	spontaneous	.186	.0	.0	.0	.0	.341	.001	
7	stratum	.001	.0	.113	.952	.341	.0	.0	
8	pooled.stratum	.006	.059	.010	.939	.001	.0	.0	
9									

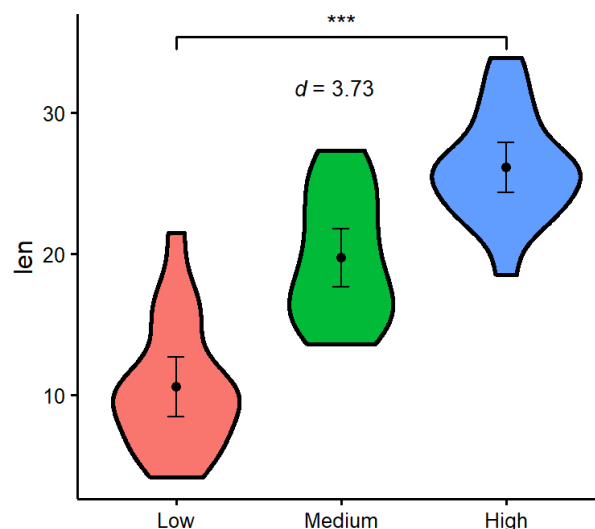
## 136 Publication-Ready Figures

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

141 This is why {rempsyc} setups a few default plot types, ready to be saved to your preferred  
 142 format (.pdf, .tiff, or .png).

## 143 Violin Plots

```
144 nice_violin(data = ToothGrowth,
145             group = "dose",
146             response = "len",
147             xlabels = c("Low", "Medium", "High"),
148             comp1 = 1,
149             comp2 = 3,
150             has.d = TRUE,
151             d.y = 30)
```



152

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

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

```
156 ggplot2::ggsave('nice_violinplotthere.pdf', width = 7, height = 7,  
157                  unit = 'in', dpi = 300)
```

158 Recommended dimensions for saving {rempsyc} figures is 7 inches wide and 7 inches high  
159 at 300 dpi, which makes sure that the resolution is high enough even if saving to non-vector  
160 graphics formats like .png. That said, scalable vector graphics formats like .pdf or .eps are  
161 still recommended for high-resolution submissions to scientific journals.

## 162 Scatter Plots

163 Figures are {ggplot2} objects (Wickham, 2016), and can be modified as such.

```
164 nice_scatter(data = mtcars,  
165              predictor = "wt",  
166              response = "mpg",  
167              group = "cyl",  
168              has.confband = TRUE)
```



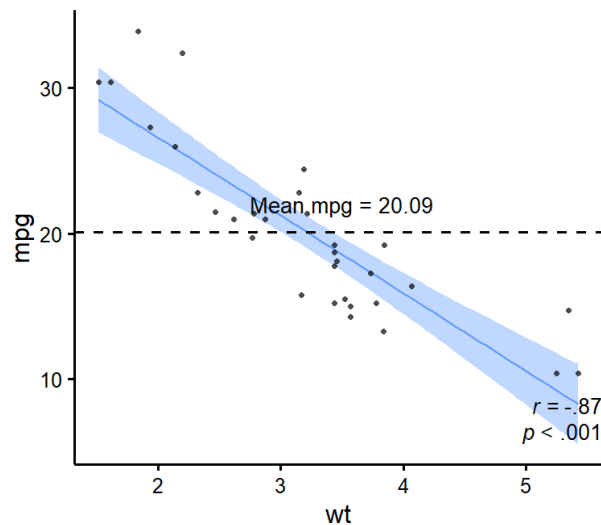
169



```

170 nice_scatter(data = mtcars,
171               predictor = "wt",
172               response = "mpg",
173               has.confband = TRUE,
174               has.r = TRUE,
175               has.p = TRUE) +
176   ggplot2::geom_hline(yintercept = mean(mtcars$mpg), colour = "black",
177                       linewidth = 1.4, linetype = "dashed") +
178   ggplot2::annotate("text", x = 3.5, y = 22, size = 7,
179                       label = paste("Mean mpg =", round(mean(mtcars$mpg), 2)))

```



```

180
181 For an example of such use in publication, see Krol et al. (2020).

```

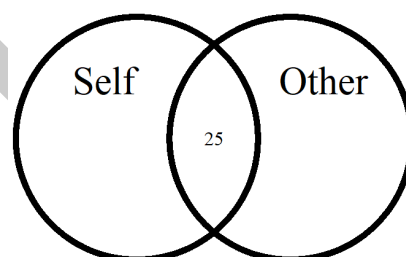
### 182 Overlapping Circles

183 For psychologists using the Inclusion of Other in the the Self Scale (Aron et al., 1992), it can  
 184 be useful to interpolate the original discrete scores (1 to 7) into a group average representation  
 185 of the conceptual self-other overlap. For example, assuming the group mean is 3.5 on the 1 to  
 186 7 scale, `overlap_circle()` will draw a 25% area overlap from interpolation:

```

187 overlap_circle(3.5)

```



```

188
189 For an example of such use in publication, see Thériault et al. (2021).

```

## 190 Testing assumptions

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

196 That said, if for whatever reason one wants to check objective assumption tests for a linear  
197 model, *rempsysc* makes this easy with the `nice_assumptions()` function, which provide *p*  
198 values for normality (Shapiro–Wilk), homoscedasticity (Breusch–Pagan) and autocorrelation of  
199 residuals (Durbin–Watson) in one call.

## 200 Categorical Predictors

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

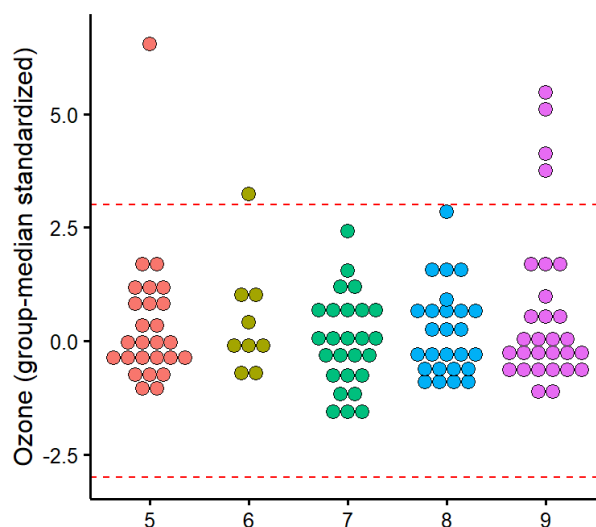
```
204 nice_normality(data = iris,  
205               variable = "Sepal.Length",  
206               group = "Species",  
207               shapiro = TRUE,  
208               histogram = TRUE,  
209               title = "Density (Sepal Length)")
```



210

211 Similarly for univariate outliers using median absolute deviations from the median (MAD, Leys  
212 et al., 2013).

```
213 plot_outliers(airquality,  
214              group = "Month",  
215              response = "Ozone")
```



216

217 Univariate outliers based on the median/MAD can also be simply requested with `find_mad()`.<sup>5</sup>

218 `find_mad(airquality, names(airquality), criteria = 3)`

219

220 `## 8 outlier(s) based on 3 median absolute deviations for variable(s):`

221 `## Ozone, Solar.R, Wind, Temp, Month, Day`

222 `##`

223 `## Outliers per variable:`

224 `##`

225 `## $Ozone`

226 `## Row Ozone_mad`

227 `## 1 30 3.218284`

228 `## 2 62 3.989131`

229 `## 3 99 3.488081`

230 `## 4 101 3.025573`

231 `## 5 117 5.261028`

232 `## 6 121 3.333911`

233 `##`

234 `## $Wind`

235 `## Row Wind_mad`

236 `## 1 9 3.049871`

237 `## 2 48 3.225825`

238 Homoscedasticity can also be checked numerically with `nice_var()` or visually with

239 `nice_varplot()`.

240 `nice_var(data = iris,`

241 `variable = names(iris[1:4]),`

242 `group = "Species") |>`

243 `nice_table()`

<sup>5</sup>Once one has identified outliers, it is also possible to winsorize them with the `winsorize_mad()` function.

Species	Setosa	Versicolor	Virginica	Variance.ratio	Criteria	Heteroscedastic
Sepal.Length	0.12	0.27	0.40	3.30	4.00	FALSE
Sepal.Width	0.14	0.10	0.10	1.50	4.00	FALSE
Petal.Length	0.03	0.22	0.30	10.20	4.00	TRUE
Petal.Width	0.01	0.04	0.07	6.80	4.00	TRUE

244

```
245 nice_varplot(data = iris,  
246               variable = "Sepal.Length",  
247               group = "Species")
```



248

## 249 Utility functions

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

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

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

260 There are other functions that the reader can explore at their leisure on the package [official](#)  
261 [website](#). However, hopefully, this overview has given the reader a gentle introduction to this  
262 package.

## Licensing and Availability

The `{rempsyc}` package is licensed under the GNU General Public License (GPL v3.0). It 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/>. All code is open-source and hosted on GitHub, and bugs can be reported at <https://github.com/rempsyc/rempsyc/issues/>.

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