




rempsysc: Convenience functions for psychology

Rémi Thériault ¹

¹ Department of Psychology, Université du Québec à Montréal, Québec, Canada

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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.

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). 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](#)), but their formatting is often rigid especially when using analyzes or table formats that are not supported by default.

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

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

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

50
 51 We can do the same with a {report} table.

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

Parameter	Fit	<i>b</i>	95% CI (<i>b</i>)	<i>t</i>	<i>df</i>	<i>p</i>	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							

57

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

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

Table 1

A Pretty Regression Model

Parameter	<i>b</i>	<i>t</i>	<i>df</i>	<i>p</i>	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.

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

68

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

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

72 Additionally, tables created with `nice_table()` are `{flextable}` objects (Gohel & Skintzos,
73 2022), and can be modified as such.[2]

74 **Formattting Results of Analyses**

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

77 ***t* tests**

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

83

84 Contrasts

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

Dependent Variable	Comparison	<i>df</i>	<i>t</i>	<i>p</i>	<i>d</i>	95% CI
mpg	4 - 8	28	3.66	.001	3.59	[2.74, 4.39]
	6 - 8	28	1.29	.207	1.44	[0.80, 1.95]
	4 - 6	28	3.64	.001	2.15	[1.37, 3.10]
disp	4 - 8	28	-6.04	<.001	-4.80	[-5.72, -3.88]
	6 - 8	28	-4.86	<.001	-3.29	[-4.29, -2.28]
	4 - 6	28	-2.70	.012	-1.51	[-2.24, -0.89]

90

91 Regressions

```
92 model1 <- lm(mpg ~ cyl + wt * hp, mtcars)
93 model2 <- lm(qsec ~ disp + drat * carb, mtcars)
94
95 nice_lm(list(model1, model2)) |>
96   nice_table(highlight = TRUE)
```

Dependent Variable	Predictor	<i>df</i>	<i>b</i>	<i>t</i>	<i>p</i>	<i>sr</i> ²	95% CI
mpg	cyl	27	-0.37	-0.72	.479	.00	[0.00, 0.01]
	wt	27	-7.63	-5.01	<.001	.11	[0.01, 0.20]
	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]
qsec	disp	27	-0.01	-1.97	.059	.07	[0.00, 0.20]
	drat	27	0.23	0.20	.845	.00	[0.00, 0.01]
	carb	27	1.15	0.72	.479	.01	[0.00, 0.06]
	drat × carb	27	-0.48	-1.08	.289	.02	[0.00, 0.09]

97

98 Simple Slopes

```
99 model1 <- lm(mpg ~ gear * wt, mtcars)
100 model2 <- lm(displ ~ gear * wt, mtcars)
101 my.models <- list(model1, model2)
102
103 nice_lm_slopes(my.models, predictor = "gear", moderator = "wt") |>
104   nice_table()
```

Dependent Variable	Predictor (+/-1 SD)	df	b	t	p	sr ²	95% CI
mpg	gear (LOW-wt)	28	7.54	2.01	.054	.03	[0.00, 0.09]
	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]
displ	gear (LOW-wt)	28	50.51	0.67	.511	.00	[0.00, 0.02]
	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]

106 Correlation Matrices

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

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

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

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

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

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

```
131 cormatrix_excel(data = infert,
132                 filename = "cormatrix1",
```

```
133 select = c("age", "parity", "induced", "case", "spontaneous",
134           "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									

137 Publication-Ready Figures

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

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

144 Violin Plots

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



153

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

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

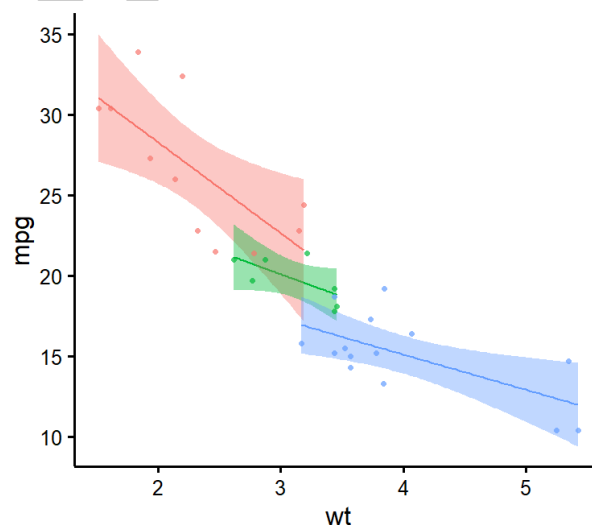
```
157 ggplot2::ggsave('nice_violinplotthere.pdf', width = 7, height = 7,  
158                  unit = 'in', dpi = 300)
```

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

163 Scatter Plots

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

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



170


```

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

```



```

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

```

183 Overlapping Circles

184 For psychologists using the Inclusion of Other in the the Self Scale (Aron et al., 1992), it can
 185 be useful to interpolate the original discrete scores (1 to 7) into a group average representation
 186 of the conceptual self-other overlap. For example, assuming the group mean is 3.5 on the 1 to
 187 7 scale, `overlap_circle()` will draw a 25% overlap from interpolation:

```

188 overlap_circle(3.5)

```



```

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

```

191 Testing assumptions

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

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

201 Categorical Predictors

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

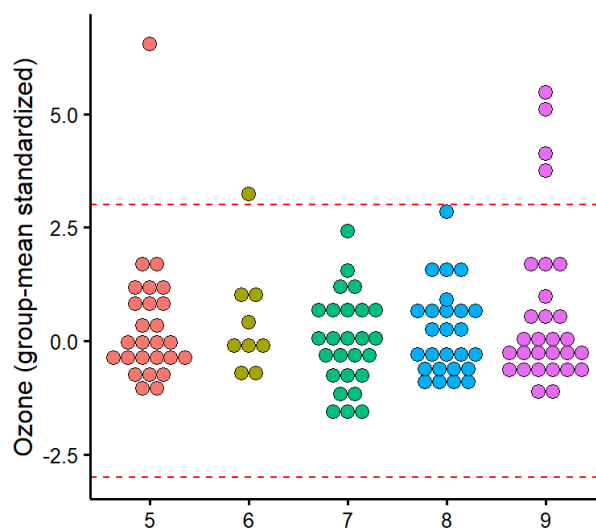
```
205 nice_normality(data = iris,  
206               variable = "Sepal.Length",  
207               group = "Species",  
208               shapiro = TRUE,  
209               histogram = TRUE,  
210               title = "Density (Sepal Length)")
```



211

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

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



217

218 Univariate outliers based on the median/MAD can also be simply requested with `find_mad()`.^[5]

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

220

221 `## 8 outlier(s) based on 3 median absolute deviations for variable(s):`

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

223 `##`

224 `## Outliers per variable:`

225 `##`

226 `## $Ozone`

227 `## Row Ozone_mad`

228 `## 1 30 3.218284`

229 `## 2 62 3.989131`

230 `## 3 99 3.488081`

231 `## 4 101 3.025573`

232 `## 5 117 5.261028`

233 `## 6 121 3.333911`

234 `##`

235 `## $Wind`

236 `## Row Wind_mad`

237 `## 1 9 3.049871`

238 `## 2 48 3.225825`

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

240 `nice_varplot()`.

241 `nice_var(data = iris,`

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

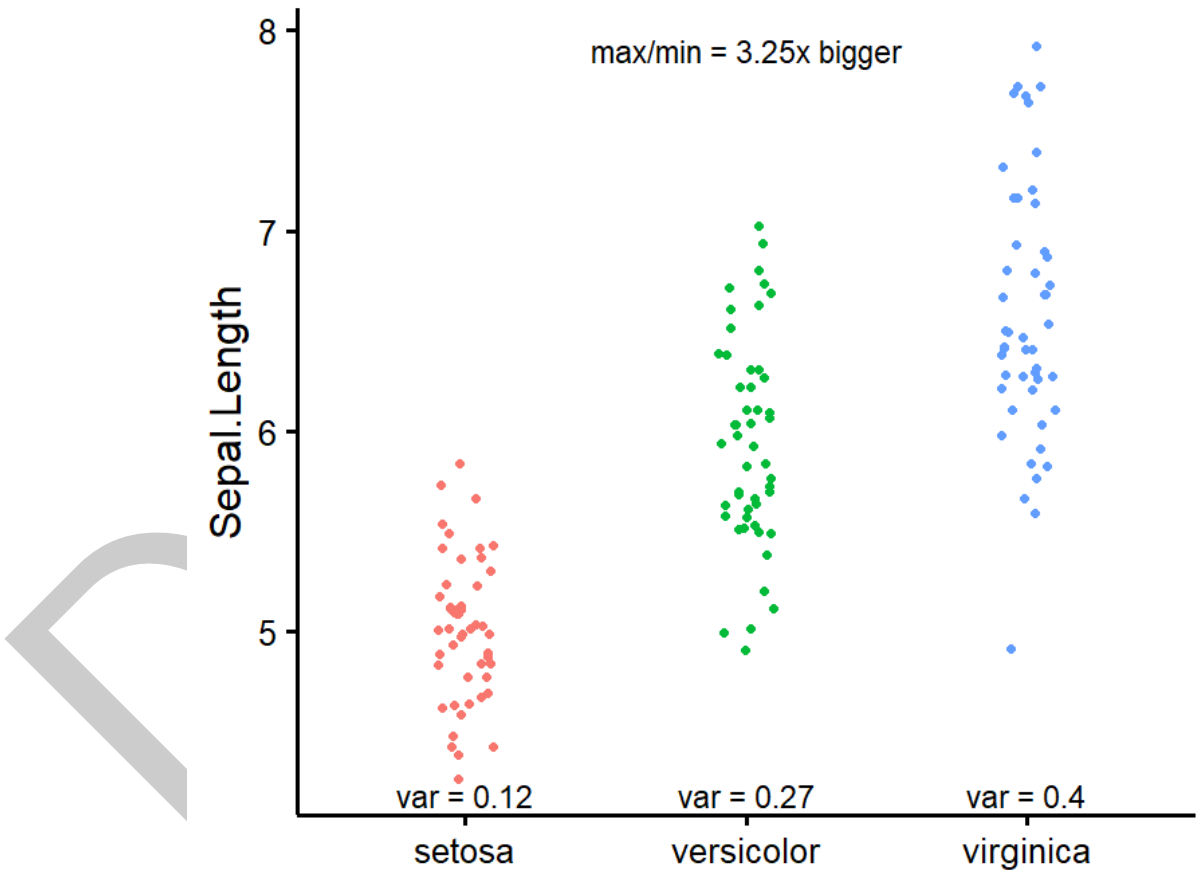
243 `group = "Species") |>`

244 `nice_table()`

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

245

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



249

250 Utility functions

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

255 extract_duplicates() creates a data frame of only observations with a duplicated ID or
256 participant number, so they can be investigated more thoroughly. best_duplicate() allows

257 to follow-up on this investigation and only keep the “best” duplicate, meaning those with the
258 fewer number of missing values, and in case of ties, the first one.

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

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

264 Licensing and Availability

265 The `{rempsys}` package is licensed under the GNU General Public License (GPL v3.0). It is
266 available on CRAN, and can be installed using `install.packages("rempsys")`. The full tutorial
267 website can be accessed at: <https://rempsys.remi-theriault.com/>. All code is open-source and
268 hosted on GitHub, and bugs can be reported at <https://github.com/rempsys/rempsys/issues/>.

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- 325 [1] This argument can be used logically, as 'TRUE' or 'FALSE', but can also be provided with
326 a numeric value representing the cut-off threshold for the p value
- 327 [2] A great resource for this is the {flextable} e-book: [https://ardata-fr.github.io/](https://ardata-fr.github.io/flextable-book/)
328 [flextable-book/](https://ardata-fr.github.io/flextable-book/)
- 329 [3] Exporting the correlation matrix to an image through the {correlation} package also requires
330 the {see} package (Lüdecke, Patil, et al., 2021)
- 331 [4] For convenience, colours are only used when the corresponding p value is at least smaller
332 than .05
- 333 [5] Once one has identified outliers, it is also possible to winsorize them with the
334 `winsorize_mad()` function.