

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). 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.

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

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 = "my_table.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 | 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] |

90

91 Regressions

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

| Dependent Variable | Predictor | df | β | 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] |

99

100 Simple Slopes

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

| Dependent Variable | Predictor (+/-1 SD) | df | β | 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] |

104 Correlation Matrices

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

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

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

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

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

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

```
129 cormatrix_excel(data = infert,
130                 filename = "cormatrix1",
131                 select = c("age", "parity", "induced", "case", "spontaneous",
132                           "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 | | | | | | | | | |
| | | r_values | p_values | | | | | | |
| 133 | | | | | | | | | |
| | 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 | | | | | | | | | |
| | | r_values | p_values | | | | | | |
| 134 | | | | | | | | | |

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} setups a few default plot types, ready to be saved to your preferred format (.pdf, .tiff, or .png).

Violin Plots

```
nice_violin(data = ToothGrowth,
            group = "dose",
            response = "len",
            xlabels = c("Low", "Medium", "High"),
            comp1 = 1,
            comp2 = 3,
            has.d = TRUE,
            d.y = 30)
```



151

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

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

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

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

161 Scatter Plots

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

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



168


```

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

```



```

179
180 For an example of such use in publication, see Krol et al. (2020).

```

181 Overlapping Circles

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

```

186 overlap_circle(3.5)

```



```

187
188 For an example of such use in publication, see Thériault et al. (2021).

```

189 Testing assumptions

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

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

199 Categorical Predictors

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

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



209

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

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



215

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

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

218

219 `## 8 outlier(s) based on 3 median absolute deviations for variable(s):`

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

221 `##`

222 `## Outliers per variable:`

223 `##`

224 `## $Ozone`

225 `## Row Ozone_mad`

226 `## 1 30 3.218284`

227 `## 2 62 3.989131`

228 `## 3 99 3.488081`

229 `## 4 101 3.025573`

230 `## 5 117 5.261028`

231 `## 6 121 3.333911`

232 `##`

233 `## $Wind`

234 `## Row Wind_mad`

235 `## 1 9 3.049871`

236 `## 2 48 3.225825`

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

238 `nice_varplot()`.

239 `nice_var(data = iris,`

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

241 `group = "Species") |>`

242 `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 |

243

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



247

248 Utility functions

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

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

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

259 There are other functions that the reader can explore at their leisure on the package [official](#)
260 [website](#). However, hopefully, this overview has given the reader a gentle introduction to this
261 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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- 323 [1] This argument can be used logically, as 'TRUE' or 'FALSE', but can also be provided with
324 a numeric value representing the cut-off threshold for the p value
- 325 [2] A great resource for this is the {flextable} e-book: <https://ardata-fr.github.io/flextable-book/>
326
- 327 [3] Exporting the correlation matrix to an image through the {correlation} package also requires
328 the {see} package (Lüdtke, Patil, et al., 2021)
- 329 [4] For convenience, colours are only used when the corresponding p value is at least smaller
330 than .05
- 331 [5] Once one has identified outliers, it is also possible to winsorize them with the
332 `winsorize_mad()` function.