

RMarkdown based APA Manuscript with ‘papaja’

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Author Note

We can include author notes for, e.g., attribution of data or expanding on roles/locations.

Abstract

This is a short example of a completely reproducible manuscript made entirely in RStudio with RMarkdown and various R scripts, functions, and packages.

Keywords: reproducible, manuscript, multivariate

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Introduction

The aim of this RMarkdown example is to show how to write a reproducible manuscript, which includes numerous bells-and-whistles—with contributions from R, Python, RMarkdown, and LaTeX. This “manuscript” will include only the best (nicest looking) parts from `1_a_Simple_RMarkdown_PDF.Rmd`

In order to help make this manuscript look nicer, we are changing some of the YAML (“yet another markup language”) header options, so that we remove line numbers, and allow for tables & figures to appear in text, as opposed to the end.

Methods

We first make our data with R

Then call off to python for the `.describe()` method

And then pass the `desc` object back to R and use the `kable()` and `kableExtra` packages to make a nice table of summary statistics for the measures of interest. In this particular part, we also show the code chunk. Furthermore, some particular packages—such as `papaja`—and certain advanced features from LaTeX require the use of `results='asis'` in chunk header.

```
apa_table(py$desc, caption = "A descriptive statistics table.",
  note = "This formatted through LaTeX via papaja::apa_table() from a python object fr
```

Procedure

Next we are going to use more features from LaTeX, including various additional LaTeX packages that we define in the YAML header. We can use a number of LaTeX features like inline calls, numbered equations, and, for example, algorithms. We will use each of those

Table 1

A descriptive statistics table.

	AGE	MOCA	CDRSB	WholeBrain	Hippocampus	MidTemp
count	665.00	665.00	665.00	665.00	665.00	665.00
mean	71.92	23.89	1.20	1,057,025.55	7,149.61	20,301.93
std	6.87	3.28	1.34	103,672.74	1,086.04	2,675.57
min	55.00	16.00	0.00	817,421.23	3,731.00	12,213.00
25%	67.20	22.00	0.00	984,409.91	6,510.00	18,535.00
50%	71.90	24.00	1.00	1,051,621.33	7,223.00	20,186.00
75%	76.60	26.00	2.00	1,120,569.50	7,834.00	22,088.00
max	89.60	30.00	5.50	1,486,035.64	10,602.00	32,189.00

Note. This formatted through LaTeX via `papaja::apa_table()` from a python object from the `.describe()` method, loaded from data in R and written through RMarkdown.

features to describe the covSTATIS method (see also our covSTATIS project repository). Our description of covSTATIS is extremely truncated here and is only meant to illustrate features of writing a manuscript in RMarkdown.

CovSTATIS is a multi-table principal components analysis, specifically designed to integrate and analyze multiple correlation or covariance matrices. Each correlation matrix— $\mathbf{R}_{[k]}$ —is double-centered by way of a centering matrix as $\mathbf{\Xi} = \mathbf{I} - \mathbf{1}(I^{-1})\mathbf{1}^T$ as

$$\mathbf{S}_{[k]} = \frac{1}{2}\mathbf{\Xi}\mathbf{R}_{[k]}\mathbf{\Xi}. \quad (1)$$

After we perform the double-centering in Eq. @ref(eq:double_center), we then compute α weights of each matrix where first we vectorize each $\mathbf{S}_{[k]}$ and storing those each

column vector in a new matrix as $\mathbf{Z} = [\text{vec}\{\mathbf{S}_{[1]}, \dots, \mathbf{S}_{[k]}, \dots, \mathbf{S}_{[K]}\}]$ and then decompose \mathbf{Z} with the singular value decomposition (SVD):

$$\mathbf{Z} = \mathbf{U}\mathbf{\Delta}\mathbf{V}^T. \quad (2)$$

The *alpha* weights are $\boldsymbol{\alpha} = \mathbf{v}_1 \times (\mathbf{v}_1^T \mathbf{1})^{-1}$. We then compute the compromise cross-product matrix as $\mathbf{S}_{[+]} = \sum_{i=1}^K \alpha_k \mathbf{S}_{[k]}$, and finally decompose $\mathbf{S}_{[+]}$ with the eigenvalue decomposition (EVD) as

$$\mathbf{S}_{[+]} = \mathbf{Q}\mathbf{\Lambda}\mathbf{Q}^T. \quad (3)$$

We can also outline these steps algorithmically as

Result: Decomposition of the compromise matrix— $\mathbf{S}_{[+]}$ —in covSTATIS

Input : $[\mathbf{R}_{[1]} \dots \mathbf{R}_{[k]} \dots \mathbf{R}_{[K]}]$

Output: $\mathbf{Q}, \mathbf{\Lambda}$

Define $\mathbf{S}_{[+]} = \mathbf{0}$

for $k = 1, \dots, K$ **do**

 | $\mathbf{S}_{[k]} \leftarrow \frac{1}{2} \mathbf{\Xi} \mathbf{R}_{[k]} \mathbf{\Xi}$

end

$\mathbf{Z} \leftarrow [\text{vec}\{\mathbf{S}_{[1]}, \dots, \mathbf{S}_{[k]}, \dots, \mathbf{S}_{[K]}\}]$

$\mathbf{U}\mathbf{\Delta}\mathbf{V}^T \leftarrow \text{SVD}(\mathbf{Z})$

$\boldsymbol{\alpha} \leftarrow \mathbf{v}_1 \times (\mathbf{v}_1^T \mathbf{1})^{-1}$

for $k = 1, \dots, K$ **do**

 | $\mathbf{S}_{[+]} \leftarrow \mathbf{S}_{[+]} + (\mathbf{S}_{[k]} \times \alpha_{[k]})$

end

$\mathbf{Q}\mathbf{\Lambda}\mathbf{Q}^T \leftarrow \text{EVD}(\mathbf{S}_{[+]})$

Algorithm 1: CovSTATIS algorithm

Data analysis

The `papaja` package includes the ability to generate a bibliography directly from all the loaded packages (via `cite_r()`). We used R (Version 3.5.1; R Core Team, 2018) and the R-packages *covstatis* (Version 0.1.0; it, n.d.), *dplyr* (Version 0.7.6; Wickham et al., 2018), *ExPosition* (Version 2.8.23; Beaton et al., 2014a), *factoextra* (Version 1.0.5; Kassambara & Mundt, 2017), *forcats* (Version 0.3.0; Wickham, 2018a), *ggplot2* (Version 3.0.0; Wickham, 2016), *gridExtra* (Version 2.3; Auguie, 2017), *GSVD* (Version 0.2.0; Beaton, n.d.), *here* (Version 0.1; Müller, 2017), *kableExtra* (Version 0.9.0; Zhu, 2018), *knitr* (Version 1.22.8; Xie, 2015), *ours* (Version 0.0.0.9000; Sunderland & Beaton, n.d.), *papaja* (Version 0.1.0.9842; Aust & Barth, 2018), *prettyGraphs* (Version 2.1.6; Beaton et al., 2014b), *purrr* (Version 0.2.5; Henry & Wickham, 2018), *readr* (Version 1.1.1; Wickham et al., 2017), *reticulate* (Version 1.9; Allaire, Ushey, & Tang, 2018), *RevoUtils* (Version 11.0.1; Corporation, 2018b, 2018a), *RevoUtilsMath* (Version 11.0.0; Corporation, 2018a), *stringr* (Version 1.3.1; Wickham, 2018b), *tibble* (Version 1.4.2; Müller & Wickham, 2018), *tidyr* (Version 0.8.1; Wickham & Henry, 2018), and *tidyverse* (Version 1.2.1; Wickham, 2017) for all our analyses.

Results

Need a scree plot here for covstatis...

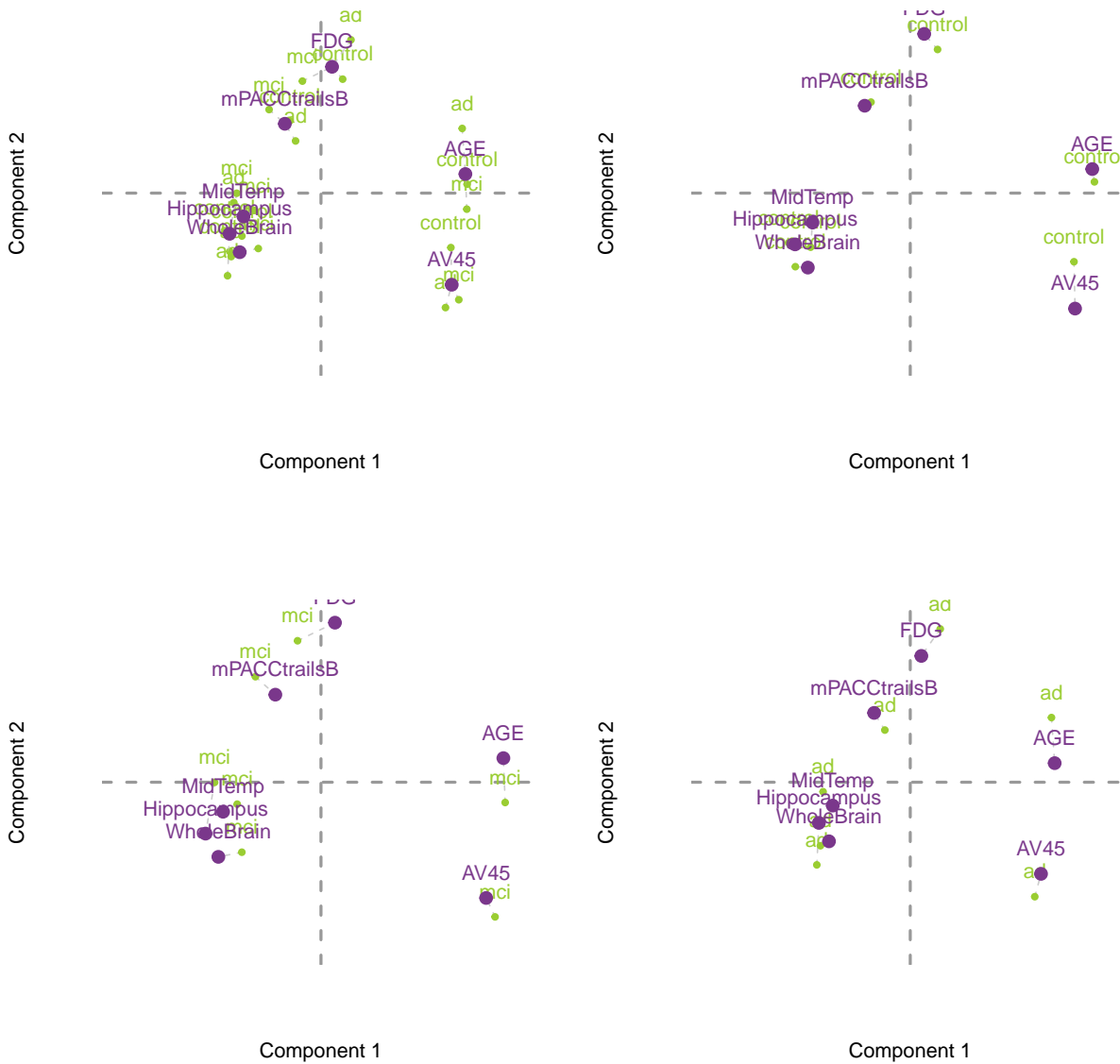


Figure 1. Using par() to make a layout of multiple base plots

Discussion

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