

RRWM Assignment 2: Post-RRWM Report & Discussion

Poll: Were you able to reproduce the work based only on the program (not the code)?

Yes,

Here's the English translation in a clear academic style:

Based on the Word file of the analysis plan, the results can be reproduced without major difficulties.

```
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  2.049729   0.017799 115.161 < 2e-16 ***
sexFemale    0.087461   0.018454   4.739 2.16e-06 ***
age_group.L  0.023305   0.034020   0.685 0.49333
age_group.Q -0.034916   0.029499  -1.184 0.23658
age_group.C  0.064262   0.025620   2.508 0.01214 *
age_group^4  0.069552   0.023411   2.971 0.00297 **
age_group^5 -0.006681   0.021518  -0.310 0.75620
age_group^6 -0.027126   0.021071  -1.287 0.19798
marital_statusLiving common-law  0.025408   0.029233   0.869 0.38478
marital_statusWidowed  0.055981   0.042182   1.327 0.18448
marital_statusSeparated  0.255690   0.058494   4.371 1.24e-05 ***
marital_statusDivorced  0.103358   0.036744   2.813 0.00491 **
marital_statusSingle, never married  0.132770   0.029917   4.438 9.13e-06 ***
family_income.L -0.218268   0.027776  -7.858 4.09e-15 ***
family_income.Q  0.054217   0.024103   2.249 0.02450 *
family_income.C -0.025806   0.023513  -1.098 0.27243
family_income^4  0.048044   0.023234   2.068 0.03866 *
family_income^5 -0.001462   0.023002  -0.064 0.94931
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 0.9323529)

---
# Call:
# svyglm(formula = mental_health_num ~ sex + age_group + marital_status +
#   family_income, design = gss2017_svy)
# Survey design:
# called via srvyr
# Coefficients:
#              Estimate Std. Error t value Pr(>|t|)
# (Intercept)  2.049729   0.017799 115.161 < 2e-16 ***
# sexFemale    0.087461   0.018454   4.739 2.16e-06 ***
# age_group.L  0.023305   0.034020   0.685 0.49333
# age_group.Q -0.034916   0.029499  -1.184 0.23658
# age_group.C  0.064262   0.025620   2.508 0.01214 *
# age_group^4  0.069552   0.023411   2.971 0.00297 **
# age_group^5 -0.006681   0.021518  -0.310 0.75620
# age_group^6 -0.027126   0.021071  -1.287 0.19798
# marital_statusLiving common-law  0.025408   0.029233   0.869 0.38478
# marital_statusWidowed  0.055981   0.042182   1.327 0.18448
# marital_statusSeparated  0.255690   0.058494   4.371 1.24e-05 ***
# marital_statusDivorced  0.103358   0.036744   2.813 0.00491 **
# marital_statusSingle, never married  0.132770   0.029917   4.438 9.13e-06 ***
# family_income.L -0.218268   0.027776  -7.858 4.09e-15 ***
# family_income.Q  0.054217   0.024103   2.249 0.02450 *
# family_income.C -0.025806   0.023513  -1.098 0.27243
# family_income^4  0.048044   0.023234   2.068 0.03866 *
# family_income^5 -0.001462   0.023002  -0.064 0.94931
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Where did things go off track? Was there one error that caused everything to go wrong?

To assess what might have gone wrong, I carefully reviewed the script. Normally, running it should not cause any issues. However, although I used the `setwd()` function to set my working directory and access the database, executing the command to load the dataset kept returning an error, as shown above. It appears that the R Markdown file was forcing the use of a specific directory different from the one I had defined. To resolve this issue, I opened a new R script and manually copied each command from the R Markdown file to execute them separately.

```
> setwd("C:/Users/EG/Desktop/CanD 3/CAND3 Data")

Avis : The working directory was changed to C:/Users/EG/Desktop/CanD 3/CAND3 Data inside a notebook
chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir
option in the setup chunk to change the working directory for notebook chunks.

> library(readr)
> gss_12M0025_E_2017_c_31_F1 <- read_csv("gss-12M0025-E-2017-c-31_F1.csv")

Erreur : 'gss-12M0025-E-2017-c-31_F1.csv' does not exist in current working directory ('C:/Users/EG/
Desktop/CanD 3/CanD3 Formation/RVM/FABIO').

> getwd()
[1] "C:/Users/EG/Desktop/CanD 3/CanD3 Formation/RVM/FABIO"
> setwd("C:/Users/EG/Desktop/CanD 3/CAND3 Data")
```

What parts of the program left you uncertain about what to do?

In my case, the variable coding was clear.

Do you have any comments or reflections about the reproducibility exercise? For instance, has it changed your mind about the benefits (or costs) of open science?

This exercise is very useful. In fact, I recently submitted an article to a journal that required me to make my results reproducible by sharing the data I used via GitHub. However, I think reproducibility should be limited to sharing the **code files or scripts** developed by participants. Moreover, I believe that the words *program* and *reproducibility*, when used together, refer to writing lines of code using a software program and sharing them with the scientific community.

For those in fields where replication materials are not readily available, could an emphasis on reproducibility disadvantage researchers who use qualitative methods or restricted (e.g., administrative) data?

I don't think so. For researchers using qualitative methods, it is possible to share their "research protocol" with the scientific community, including the sampling procedure, the interview guides (individual and group), and the methods of analysis. As for restricted data, most scientific journals require authors to state that such data are only available upon request from the data-holding institution. Therefore, regardless of the field of research, there is always some framework that allows the reproducibility of results to be assessed — or at least approached.