

Group assignment part II for EP16: Missing Values in Clinical Research

Multiple Imputation

13 – 17 May, 2019

Deadline & submission:

Assignments need to be submitted via Canvas no later than 14 June 2019.

Task:

Impute and analyze the dataset you have been assigned and provide documentation that explains all steps performed and allows to reproduce them.

You may either provide

- R syntax, output and textual explanations **combined in one document**, for example using rmarkdown or knitr (submit the `.Rnw` or `.Rmd` syntax file and the resulting `.pdf` or `.html` file), or
- **two separate documents**, where
 1. one document is a report explaining all steps you have performed, supported by relevant plots and output (which could be a standard Microsoft Word document or a PDF), and
 2. one R syntax file (with ending `.R`; do NOT copy R syntax into a word document!)

Write the names of all group members on ALL files that you submit.

Report:

The report needs to demonstrate

- that you are aware of all the characteristics of your data
- that you know what those characteristics imply for the imputation
- that you chose an appropriate imputation approach: you may use the packages we have used for imputation in complex settings (**mice** and **JointAI**, but also **smcfcs** or **jomo**), but using **mice** for imputation is sufficient for this assignment
- that you are aware of pro's and con's of the imputation approach you chose (mention limitations and, where possible, name approaches that could overcome these limitations)
- that you did not just automatically/blindly accept the default settings
- that you properly checked that the imputation was successful
- which adjustments you made to the imputation procedure to correct problems that have occurred, and that these adjustments fixed the problem

Moreover

- Use plots and other R output (this you may also copy into the microsoft word document, if necessary) to support your decisions.
- If you run into issues that you cannot fix, document that as well. (e.g., if R throws any warning messages include them in the report and, if possible, explain why they can be ignored or that you could not find a way to prevent them)
- Textual explanations can be brief, but should be written in complete sentences to be readable.

For example:

“Histograms of the continuous variables (see figure below) show that all continuous covariates, except for `xxx`, are approximately normally distributed, hence, we chose `method1` to impute `xxx` and `method2` to impute the other continuous variables.”

- The analysis model of interest is given for each dataset, but you need to decide yourself
 - if additional variables should be used as auxiliary variables
 - if variables need to be re-coded or re-scaled
- You do not need to check standard model assumptions in the final analysis model.
- Focus on the methodological part, an interpretation of the clinical finding is not needed.
- If you encounter any problems, email me.

Syntax file

The syntax file needs to follow the same structure as the report, so that the steps explained in the report can be followed in the R syntax in the same order.

Use sections in the report and provide the same sections in comments in the R syntax file (if you use a separate `.R` syntax file).

For example, if you have a structure

1. first section
2. second section
 - 2.1. first subsection
 - 2.2. second subsection

your syntax file you could look like this:

```
#####  
# 1. first section #####  
#####  
...  
  
#####  
# 2. second section #####  
#####  
  
# 2.1 first subsection -----  
3 + 3  
  
# transform with log  
log(3) + log(3)  
  
# 2.2 second subsection -----  
...
```