

Users' needs for a digital smoking cessation application and how to address them: A mixed-methods study

Bayesian Analysis of Correlations

Author: Nele Albers **Date:** June 2022

This file is meant to guide you through reproducing our Bayesian analysis of the correlations between user characteristics on the one hand and activity efforts and interaction scenario ratings on the other hand (Table 1).

We provide code for:

- the Bayesian analysis of the correlations between user characteristics on the one hand and activity efforts and interaction scenario ratings on the other hand (Table 1).

Examine Output of Code Run by Us

If you would like to examine the output of the code as run by us, have a look at:

- the file "Bayesian_analysis_correlations.pdf."

Run Code Yourself

This section is to explain how you can run the code yourself.

Requirements

You need to have Docker installed.

Steps to Reproduce Analyses

The reproduction of our code is based on Docker and R Studio. Take the following steps:

1. Make sure you have Docker installed. You can check if you do by running `docker -v`.
2. Navigate to the folder this README-file is in.
3. Now you have 2 options:
 - Build the Docker image via `docker build . -t gbna4/user_needs_paper_bayesian_correlations`, or
 - Pull the Docker image from Dockerhub via `docker pull gbna4/user_needs_paper_bayesian_correlations`.
4. Run the Docker container via `docker run -d -p 8787:8787 -v <path_to_this_directory>:/home/rstudio/analysis -e PASSWORD=<some_password> gbna4/user_needs_paper_bayesian_correlations`.
5. Go to localhost:8787.
6. Login with username 'rstudio' and the password chosen in step 4.
7. Navigate to the "analysis"-folder in R Studio.
8. Now you can reproduce the results via the .Rmd-file.

Knitting R Markdown

If you just want to knit an analysis file to a pdf-file, take the following steps:

1. Make sure you have Docker installed.
2. Navigate to the folder this README-file is in.
3. Now you have 2 options:
 - Build the Docker image via `docker build . -t gbna4/user_needs_paper_bayesian_correlations`, or
 - Pull the Docker image from Dockerhub via `docker pull gbna4/user_needs_paper_bayesian_correlations`.
4. Run an interactive session with the Docker container via `docker run -it -v <path_to_directory_of_this_README_file>:/home/rstudio/analysis gbna4/user_needs_paper_bayesian_correlations /bin/bash`.
5. In the interactive session, type `cd /home/rstudio/analysis` to navigate to the analysis-folder.
6. Start an R session via `R`.
7. Import rmarkdown via `library('rmarkdown')`.
8. Knit an R markdown file via `render("<analysis_file>.Rmd", output_file = "<desired_output_file_name>.pdf")`.

Explanation of Files in this Folder

This directory contains the following files and folders:

- Data: pre-processed data needed for the analysis,
- Bayesian_analysis_correlations.pdf: output of the analysis as run by us,
- Bayesian_analysis_correlations.Rmd: file for you to reproduce our analysis yourself,
- Dockerfile: the Dockerfile to build the Docker image yourself if you would like to,
- JAGS-4.3.0.tar.gz: we need jags for building the Docker image,
- README.md/README.pdf: this README-file, and
- references.bib: references used in the .Rmd-file.