

Attitudes Toward a Virtual Smoking Cessation Coach: Relationship and Willingness to Continue

Bayesian Analysis of Correlations

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This file is meant to guide you through reproducing our Bayesian analysis of the correlations between user variables and attitude ratings reported in the "Results"-section of the paper.

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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 results 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/attitudes_perstech_firstaid`, or
 - Pull the Docker image from Dockerhub via `docker pull gbna4/attitudes_perstech_firstaid`.
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/attitudes_perstech_firstaid`.
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. If the "analysis"-folder is empty, check that you have used the correct path in the command for running the Docker container. Also, sharing the folder content may not work if you use a drive other than the C drive.
8. Now you can reproduce the results via the .Rmd-file in the "analysis"-folder. You can also knit a pdf-file from the Rmd-file via the "Knit"-button in R

Studio.

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/attitudes_perstech_firstaid`, or
 - Pull the Docker image from Dockerhub via `docker pull gbna4/attitudes_perstech_firstaid`.
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/attitudes_perstech_firstaid /bin/bash`.
5. In the interactive session, type `cd /home/rstudio/analysis` to navigate to the "analysis"-folder. See the previous section in case your "analysis"-folder is empty.
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:

- Bayesian_analysis_correlations.pdf: Output of Bayesian analysis when run by us,
- Bayesian_analysis_correlations.Rmd: File for you to reproduce our analysis results,
- Dockerfile: To build the Docker image yourself,
- JAGS-4.3.0.tar.gz: Needed for building the Docker image,
- preprocessed_data.csv: Required data,
- README.md/README.pdf: This README-file, and
- references.bib: References used in the .Rmd-file.