

Setting Physical Activity Goals with a Virtual Coach: Vicarious Experiences, Personalization and Acceptance

Bayesian Analyses

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This file is meant to guide you through the steps needed to reproduce our results for our four hypotheses from Table 3 as well as the Cronbach's alpha value reported for the acceptance index measure in the "Data Preparation and Analysis Strategies"-section.

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Examine Output of Code Run by Us

To see the output of the code as run by us, refer to the "analysis.pdf"-file.

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/goals_bayesian_firstaid`, or
 - Pull the Docker image from Dockerhub via `docker pull gbna4/goals_bayesian_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/goals_bayesian_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 run the analysis using the "analysis.Rmd"-workbook. To knit a pdf-file from the Rmd-file, you can use the "Knit"-button in R Studio.

Knitting R Markdown Only

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/goals_bayesian_firstaid .`
 - Pull the Docker image from Dockerhub via `docker pull gbna4/goals_bayesian_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/goals_bayesian_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

This directory contains the following files and folders:

- Data: Data needed for the analysis,
- Figures: Figure 3 from the paper as created by us,
- analysis.pdf: Output of the analysis as run by us,
- analysis.Rmd: Workbook so you can run the analysis yourself,
- Dockerfile: Dockerfile to build the Docker image yourself,
- 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.