

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

Acceptance of the Virtual Coach

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This file is meant to guide you through reproducing our reported acceptance of the virtual coach Sam from the "Materials"-section of our paper.

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 "acceptance.pdf."

Run Code Yourself

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

Requirements

You need to have Docker installed.

In addition, you need to download the public dataset on the acceptance of the virtual coach (<https://doi.org/10.4121/19934783.v1>). Save the file "Post_Questionnaire_Acceptance_Anonym_Preprocessed.xlsx" to the "Data"-folder in the folder that this README-file is in.

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_acceptance`, or
 - Pull the Docker image from Dockerhub via `docker pull gbna4/user_needs_paper_bayesian_acceptance`.
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_acceptance`.
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 acceptance results by means of the file "acceptance.Rmd."

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_acceptance .`
 - Pull the Docker image from Dockerhub via `docker pull gbna4/user_needs_paper_bayesian_acceptance .`
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_acceptance /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

This directory contains the following files and folders:

- Data: to save the data required for the analysis,
- Dockerfile: the Dockerfile to build the Docker image yourself if you would like to,
- acceptance.pdf: output of code for the acceptance of the virtual coach as run by us,
- acceptance.Rmd: file to run the code for the acceptance of the virtual coach 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.