1. Make sure packages *knitr* and *rmarkdown* are installed and that you load them before running *microbiomeExplorer*, as these packages are used to generate the reports.
2. Install *phantomjs* using the code below:

webshot::install\_phantomjs()

1. Install the package *installr* and then run the code below to install *pandoc*:

installr::install.pandoc()

The above steps work for Mac users only if the report cannot be directly generated. For Windows users, a solution to this issue had not been found at the time this document was written. But for a workaround, please see the next steps below:

1. Open me\_report.R within the tmp folder C:\Users\Owner\AppData\Local\Temp\RtmpsFfPir

Note that the last folder is sometimes a different name. Please sort your “Temp” folder by “Date Modified” and look for the most recent folder starting with the name “Rtmps”.

1. There will be a line that loads the data meData <- filterMEData(readData(...; below it should be a comment that says the name of your data file. You should replace the value within readData with a path pointing to your data file. (data within the temp folder is not available outside of the app)
2. Save the modified me\_report.R somewhere
3. Then you can set rscript to your version of me\_report.R rscript <- "me\_report.R" and then call knitr::spin(rscript, knit = FALSE)
4. If that goes through without issues, you could then try calling rmarkdown::render(rscript, output\_format = "all")

Please check the link below for more information about the issue or to see if the issue has been resolved on Windows without going through the workaround:

<https://github.com/zoecastillo/microbiomeExplorer/issues/9>