TITLE: "Sharing information across patient subgroups to draw conclusions from sparse treatment networks"

AUTHORS: Theodoros Evrenoglou, Silvia Metelli, Johannes-Schneider Thomas, Spyridon Siafis, Rebecca Turner, Stefan Leucht, Anna Chaimani

MAIN AUTHOR OF THE CODE: Theodoros Evrenoglou, tevrenoglou@gmail.com

R version 4.0.3 (2020-10-10)

Platform: x86_64-w64-mingw32/x64 (64-bit)

Running under: Windows 10 x64 (build 19045)

Matrix products: default

locale:

[1]   LC_COLLATE=English_United   States.1252   LC_CTYPE=English_United   States.1252 LC_MONETARY=English_United States.1252

[4] LC_NUMERIC=C   LC_TIME=English_United States.1252

attached base packages:

[1] stats   graphics grDevices utils   datasets methods   base

other attached packages:

[1] gplots_3.1.3   igraph_1.2.6   mvtnorm_1.1-1   ggsci_2.9   remotes_2.2.0   nmajags_0.1-0

[7] devtools_2.3.2 usethis_1.6.3 curl_5.0.0   R2jags_0.6-1   rjags_4-10   coda_0.19-4

[13] netmeta_2.1-0   meta_6.2-1   forcats_0.5.0 stringr_1.4.0 dplyr_1.0.10   purrr_0.3.4

[19] readr_1.4.0 tidyr_1.1.2   tibble_3.1.8   ggplot2_3.3.5 tidyverse_1.3.0 readxl_1.3.1

loaded via a namespace (and not attached):

[1] nlme_3.1-149   bitops_1.0-7   fs_1.5.2   lubridate_1.7.9.2 httr_1.4.2   rprojroot_2.0.2

[7] tools_4.0.3   backports_1.2.0 utf8_1.1.4   R6_2.5.0   R2WinBUGS_2.1-21 metafor_3.0-2

[13] KernSmooth_2.23-17 DBI_1.1.0   colorspace_2.0-0 withr_2.5.0   tidyselect_1.2.0

[18] prettyunits_1.1.1 processx_3.4.4   compiler_4.0.3   cli_3.6.0   rvest_0.3.6   xml2_1.3.2

[24] desc_1.2.0   caTools_1.18.0   scales_1.2.1   callr_3.5.1   digest_0.6.27

[29] minqa_1.2.4   pkgconfig_2.0.3   lme4_1.1-27.1   sessioninfo_1.1.1 dbplyr_2.0.0

[34] rlang_1.0.6   rstudioapi_0.13   generics_0.1.0   jsonlite_1.7.1   gtools_3.8.2   magrittr_2.0.3

[40] Matrix_1.2-18   Rcpp_1.0.10   munsell_0.5.0   fansi_0.4.1   abind_1.4-5   lifecycle_1.0.3

[46] stringi_1.5.3   CompQuadForm_1.4.3 mathjaxr_1.0-1   MASS_7.3-53   pkgbuild_1.1.0

[51] grid_4.0.3   parallel_4.0.3   crayon_1.3.4   lattice_0.20-41   haven_2.3.1   splines_4.0.3

[57] hms_0.5.3   ps_1.4.0   pillar_1.8.1   boot_1.3-25   pkgload_1.1.0   magic_1.5-9

[63] reprex_0.3.0   glue_1.6.2   modelr_0.1.8   vctrs_0.5.1   nloptr_1.2.2.2 testthat_3.0.4

[69] cellranger_1.1.0 gtable_0.3.0   assertthat_0.2.1 broom_0.7.9   memoise_1.1.0

[74] ellipsis_0.3.2

INSTRUCTIONS:

Access: All the files described in this document can also be accessed through the public GitHub repository at: https://github.com/TEvrenoglou/codes_sharing_information. Through this link you can download the *Data_and_Codes* folder in your personal device.

Code execution process:

1. Set the folder *Data_and_Codes* as the current working directory
2. Run the scripts **1-11** as these are listed below in the Codes folder description. This will reproduce all the figures and tables given in the **main manuscript** and the **Appendix 1**. The rest of the files in the **Codes** folder involve parts of the code which are sourced within the master files to facilitate the analysis and the reproduction of the results. Finally, the `nmajags` library used in our code, is currently available only through GitHub. Please make sure to install it using the code:

```
library(remotes)
remotes::install_github("guido-s/nmajags")
```

Note that **Figure 1** of the main manuscript was created using the online tool: https://www.nmastudioapp.com/ and thus there is no code to reproduce this figure. **Figure 1** though does not involve any numerical results but only a graphical representation of the data.

Folder **Codes**: It contains both **R** and **JAGS** code. There is no specific order to run the analyses and reproduce the results. However, we suggest the one given below.

1. **master_naive_synthesis.R**, contains the code to run the naive synthesis NMA model and to gather and save the results. The code ends by saving the results in the *"Results"* folder. These results are also readily available as part of the *"basic_comparisons_all.xlsx"* and *"SUCRAS.xlsx"* files in the "Intermediate results" folder. Finally, the **Table 10** of the **Appendix 1** can also be reproduced using this code.
2. **master_data_based_beta_no_downweight.R**, contains the code to run the two-stage NMA model with data based beta priors and no downweight. Through the code you can also gather and save the

results. The code ends by saving the results in the *"Results"* folder. These results are also readily available as part of the *"basic_comparisons_all.xlsx"* and *"SUCRAS.xlsx"* files in the "Intermediate results" folder. Finally, the **Table 11** and the **Figure 8** of the **Appendix 1** can also be reproduced using this code.

3. **master_data_based_beta_RoB_downweight.R**, contains the code to run the two-stage NMA model with data based beta priors and downweight according to the risk of bias criterion. Through the code you can also gather and save the results. The code ends by saving the results in the *"Results"* folder. These results are also readily available as part of the *"basic_comparisons_all.xlsx"* and *"SUCRAS.xlsx"* files in the "Intermediate results" folder. Finally, the **Table 12** and the **Figure 9** of the **Appendix 1** can also be reproduced using this code.

4. **master_data_based_beta_NCT_downweight.R**, contains the code to run the two-stage NMA model with data based beta priors and downweight according to the non common treatment criterion. Through the code you can also gather and save the results. The code ends by saving the results in the *"Results"* folder. These results are also readily available as part of the *"basic_comparisons_all.xlsx"* and *"SUCRAS.xlsx"* files in the "Intermediate results" folder. Finally, the **Table 13** and the **Figure 10** of the **Appendix 1** can also be reproduced using this code.

5. **master_expert_opinion_beta_no_downweight.R**, contains the code to run the two-stage NMA model with expert opinion based beta priors and no downweight. Through the code you can also gather and save the results. The code ends by saving the results in the *"Results"* folder. These results are also readily available as part of the *"basic_comparisons_all.xlsx"* and *"SUCRAS.xlsx"* files in the "Intermediate results" folder. Finally, the **Table 14** and the **Figure 11** of the **Appendix 1** can also be reproduced using this code.

6. **master_expert_opinion_beta_RoB_downweight.R**, contains the code to run the two-stage NMA model with expert opinion based beta priors and downweight according to the risk of bias criterion. Through the code you can also gather and save the results. The code ends by saving the results in the *"Results"* folder. These results are also readily available as part of the *"basic_comparisons_all.xlsx"* and *"SUCRAS.xlsx"* files in the "Intermediate results" folder. Finally, the **Table 15** and the **Figure 12** of the **Appendix 1** can also be reproduced using this code.

7. **master_expert_opinion_beta_NCT_downweight.R**, contains the code to run the two-stage NMA model with expert opinion based beta priors and downweight according to the non common treatment criterion. Through the code you can also gather and save the results. The code ends by saving the results in the *"Results"* folder. These results are also readily available as part of the *"basic_comparisons_all.xlsx"* and *"SUCRAS.xlsx"* files in the "Intermediate results" folder. Finally, the **Table 16** and the **Figure 13** of the **Appendix 1** can also be reproduced using this code.

8. **master_NMA_with_non_informative_priors.R**, contains the code to run the NMA model that assigns non-informative priors to the treatment effect parameters. Through the code you can also gather and save the results. The code ends by saving the results in the *"Results"* folder. These results are also readily available as part of the *"basic_comparisons_all.xlsx"* and *"SUCRAS.xlsx"* files in the "Intermediate results" folder. Finally, the **Table 17** of the **Appendix 1** can also be reproduced using this code.

9. **master_figure_2_and_appendix_figures_2-7.R**, contains the code to reproduce the **Figure 2 of the main manuscript** and the **Figures 2-7** of the **Appendix 1**. Please, make sure that you have installed the ggplot2 version 3.3.5.

10. **master_community_detection_appendix_figure_1_table_1.R**, contains the code to reproduce the **Figure 1** and the **Table 1** of the **Appendix 1**.

11. **master_consistency_checks.R**, contains the code to reproduce the **Tables 2-9** of the **Appendix 1**.

12. **helpers.R**, contains R functions to facilitate the analysis across the different master files. The *cd()* function in this file was obtained from the online supplementary material of the manuscript by Law et al. (https://bmcmedresmethodol.biomedcentral.com/articles/10.1186/s12874-019-0689-9).

The following files are included in the **Code** folder and contain **JAGS codes** which are sourced across the "master" files.

- **NMA_model_data_based_beta.R**, contains the JAGS code used for the first stage of the proposed approach. It performs network meta-analysis with data based priors for beta.

- **NMA_model_expert_based_beta.R**, contains the JAGS code used for the first stage of the proposed approach. It performs network meta-analysis with expert opinion based priors for beta.

- **NMA_model_with_informative_priors.R**, contains the JAGS code used for the second stage of the proposed approach. It performs network meta-analysis with the informative priors constructed at the first stage.

- **standard_NMA_model.R**, contains the JAGS code to perform network meta-analysis using non-informative priors.

- **NMA_model_node_splitting.R**, contains the JAGS code to fit the NMA node-splitting model. The code was obtained from the online supplementary material of the manuscript by Dias et al. (https://onlinelibrary.wiley.com/doi/10.1002/sim.3767).

- **pairwiseMA_data_expert_based_priors.R**, contains the JAGS code to fit the pairwise meta-analysis model and construct priors for the beta parameter according to the (i) data based and (ii) expert opinion based approach.

Folder **Data** contains:

- file **data.xlsx**, contains the main dataset of the analysis.
- file **expert_opinion.xlsx**, contains the expert opinions used in master files **5-7**.
- file **GP_pooled_data.xlsx**, contains the pooled General patient results that are used in the master files **5-7**.

Folder **Results**: It contains all the tables and figures presented in the **main manuscript** and in the **Appendix 1**. These results are given either in "xlsx" or "tiff" format for tables and figures respectively. All the tables and figures included in that file can be reproduced from the master files **1-11** in the **Code** folder.

Folder **Intermediate results**: It contains all the results of the analysis that can be used to reproduce the **Figure 2** of the main manuscript and **Tables 2-9** and **Figures 2-7** of the **Appendix 1**. These files are sourced within the respective master files.

DATA AVAILABILITY: Data for the application are available through the **Data** folder.

All the paths in the files are relative, based on the assumption that the working directory is set properly as stated in the "Code execution" section.