All the work was done in R version 3.4.4

This folder contains the codes and datasets for the application.

The dataset folder contains the raw datasets-rawDatasets.zip, and the final dataset we used-data.csv. The dataProcessing.R script is used to produce the final dataset.

1) In the analysis, we compare five methods-AIPTW, g computation, IPTW, PENCOMP, and naïve methods are used. To obtain the estimates, just run pencompRun.R, gcomputeRun.R, IPTWRun.R, naiveRun.R, and AIPTWRun.R, respectively. The following functions are needed.

   source("addFun.R") ###additional function for processing

   source("AIPTW.R") ###function for obtaining AIPTW estimate

   source("gcompute.R") ##function for obtaining g computation estimate

   source("gcomputeFunc.R") ###additional function for g computation

   source("IPTW.R") ###function for obtaining IPTW estimate

   source("naive.R") ###function for obtaining naive estimate

2) After obtaining the estimates, run the following R scripts in the FiguresandTables folder to reproduce the figures and tables regarding the application.

   a. balance.R is the R script to reproduce Table 3, which shows the balance results for the 8th window
   b. overlaps_Figure9_Table30-31.R is the R script to produce overlap distributions (Figure 9), summary of weights (Table 30), and overlap proportions (Table 31 in Appendix)
   c. Figure10.R—to produce Figure 10 in the main paper
   d. Figure11_Appendix.R—to produce Figure 11 in the Appendix
   e. overlaps_Figure9_Table30-31.R—produce Figure 9 (overlap distributions between treatment groups); Table 30 in the Appendix on summary of weights; and Table 31 in the Appendix on overlap proportions between treatment groups.
   f. sampleSizeTable29Appendix.R—to produce Table 29 in the Appendix, detailing the sample size of each treatment sequence within each 3-visit window.