All the work was done in R version 3.4.4

Before running the codes, set the fault directory to where the codes folder is located by using setwd("path").

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.