The current folder includes data and code for the HIV Testing Analysis in the article “Analysis of stepped-wedge cluster randomized trials: A tutorial using marginal models” by Turner et al.

For questions or comments about the code please contact John S. Preisser at [john\_preisser@unc.edu](mailto:john_preisser@unc.edu).

List of files:

1. hivtesting.sas7bdat = data set used for all of the following analyses
2. Cohort\_models\_BE\_Zmatrix\_twoalpha1\_strata.sas = SAS code to perform GEE/MAEE analyses under the constrained block exchangeable correlation
3. Cohort\_models\_BE\_Zmatrix\_twoalpha1\_strata.rtf = SAS output file from the above file
4. Cohort\_models\_BE\_Zmatrix\_fouralpha1\_strata.sas = SAS code to perform GEE/MAEE analyses under the extended 3-dependence correlation
5. Cohort\_models\_BE\_Zmatrix\_fouralpha1\_strata.rtf = SAS output file from the above file
6. binomial\_maee.R = R function to perform GEE/MAEE analyses for binary outcome data, revised from the binomial\_maee function in the geeCRT package, using a different inverse function – Eigen\_pinverse rather than ginv to aviod the warning from SVD function in the ginv function
7. HIV analysis.R = R code to perform all GEE/MAEE analyses, which sources the above file

NOTE: Make sure the current working directory is the current folder before running each program.