Syphilis transmission model: How to run it

To run the “plain” (no screening interventions) model, run syph\_model\_main\_code.R – if you want to see a counterfactual for a case without contact tracing, set showCounterfactual to TRUE, otherwise set it to FALSE.

To run the model with screening interventions, run syph\_model\_interv\_code.R (the plotting code doesn’t all work yet). In this, the baseline is “2016 levels”, and the interventions are described in comments in model.pred.interv.fun.R as well as in Documents/syph\_MS\_draft.docx

Syphilis transmission model: current status

* Model is built
* Good calibration files exist for both Louisiana and Massachusetts
* Contact tracing has been implemented, but we still need to understand its behavior and make sure it is debugged (see below)
* Plan is to calibrate the model to the 5 years for which we have data and then evaluate screening interventions projecting 10 years into the future
* Methods, parameter tables, and technical appendix are written (except for contact tracing – will try to do this before I leave PPML)
* Draft of manuscript has been started.

Some outstanding issues/considerations

* Figure out why removing contact tracing makes incidence drop instead of increase.
* Since contact-tracing data only exists for Louisiana from 2011 on, and for Massachusetts from 2005 on, we will need some kind of smoothing in screening rates to be able to usefully test the effect of removing contact tracing.
* Get more plotting code for interventions working (several half-completed plot attempts exist right now, as well as one showing cumulative incidence across the calibration period that works). This may require the list outputted by model.out.interv.fun.R to include more pieces of information.
* Stratify Massachusetts contact tracing percentages by primary & secondary vs early latent (as is already done for Louisiana).
* Write data management code that can read in raw contact-tracing numerator and denominator data for an arbitrary number of years and levels of aggregation or disaggregation and calculate percent contact-traced within the code (this was a suggestion of Josh’s that was put on the back burner because other things were more pressing).
* Parameters for immunity after treatment (carried over from Ashleigh’s status report from last year, since this came up at a recent meeting and immunity may also be influencing contact tracing results)
  + No decision made with respect to how to model this
  + Currently have different durations for primary and secondary, early latent, and late latent (and allowing these to vary in calibration)
  + Sent a document to Tom, Harrell, and Andres (Documents/immunity\_params.docx) asking for guidance from their colleagues at DSTDP but have not heard back