Simulation setup:

1. Generate (static) network with specified structure (degree dist and/or homophily)
2. Simulate epidemic spread over network – yields times of transitions and genetic distances
3. Sample egos from network to get “behavioral survey”
4. Define priors based on genetics and survey
5. Fit Bayesian model to epidemic data to get estimates of network properties (degree dist and/or homophily?)

Things that we could vary:

* Network size
* Degree distribution
* Distribution of attribute in population
* Strength of homophily
* Epidemic parameters – transmissibility, times in compartments
* Sampling coverage for behavioral survey
* Biased sampling for behavioral survey
* Strength of prior
* Add noise to dates to reduce accuracy of epidemic data
* Sampling of genetic data?

To make an interesting first paper, I think implementing some form of biased sampling for the behavioral survey will be important – we need to be doing something that couldn’t be achieved directly from the behavioral survey itself. Evaluating the contribution of the different data sources is another interesting question. I’m thinking we evaluate that by varying the survey coverage, adding noise to dates, and changing the variance of the prior induced by the genetics. I don’t really want to get into sampling the genetic network and inferring distances, etc.

Of the things listed above, network size, distribution of the attribute in the population, and epidemic parameters seem like low-priority items. They would contribute to a statement on generalizability of results, but wouldn’t be primary results themselves.

For unbiased sampling, vary num\_samples and set strong\_prior to FALSE.

For biased sampling, set num\_samples = N, strong\_prior to FALSE. Then replace the generated Prob\_Distr\_Params with an appropriate biased sample (avoids having to reprogram CCMnet).

Add output of degree distribution, or measure of distance of distribution from truth. Don’t save off all graphs.