### Chris Lab Notebook

# Chris Hoover 5/11/2020

### **TODOs**

5/11/20 Clarify source of iterations/updating with Josh 5/11/20 Get  $R_0$  equation as function of model parameters from NextGen matrix \* Completed 5/11/20; see LEMMA\_model

### 5/11/2020

#### Goals:

- \* Familiarize with model
- \* Code model in STAN and try some initial fits to get idea of runtimes, outputs
- \* Start brainstorming potential improvements to model

### Package/Model functionality

### R/InputsFromSpreadsheets.R

Contains functions to read user inputs and translate them into model inputs, generate parameter sets to sample from. Also main wrapper function that users run to generate report: CredibilityIntervalFromExcel

#### R/CredibilityInterval.R

contains functions to run model, check which model runs "fit" input data (e.g. which parameter sets generate predictions that agree with input data)

#### R/CombinedModels.R

contains functions to run seir model

### R/CreateOutputs.R

Takes model posteriors and generate plots of projections, posterior distributions and comparison to prior distributions

#### Overall process

- $1. \ User \ calls \ Credibility Interval From Excel \ which \ processes \ data \ in \ excel \ spreadsheet \ and \ then \ calls \ Credibility Interval$
- 2. CredibilityInterval does some more preprocessing of model inputs and then calls RunSim1

- 3. RunSim1 calls RunSim which uses FitSEIR to generate reasonable estimates of when the outbreak started based on comparison of model generated outputs to observed data done with CalcError function. Once FitSEIR has found a best start data for each parameter set, Seir is run.
- 4. The output of RunSim1 comes from running Seir which produces model estiamtes from the input parameter estimate and best guess start date. InBounds is then called to determine if the output of Seir is within the user provided uncertainty bounds of the observed data.
  - \*\* There seems to be some sort of iteration updating going on that I can't quite figure out

### Test Run

```
file.copy(system.file("extdata", "SF-April13.xlsx", package = "LEMMA", mustWork = TRUE), "example.xlsx"
LEMMA::CredibilityIntervalFromExcel("example.xlsx")
```

Works for the most part except for a fairly obscure ggplot error

### 5/15/2020

Didn't make it to STAN on the 11th, so want to try and get an idea of some of the advantages and disadvantages STAN has compared to other approaches and maybe get around to coding up a version of the model in STAN

### **STAN Pros**:

- Hamiltonian MCMC in STAN is quite fast and would generate more posterior samples
- Could incorporate priors to constrain some of the parameters like hospitalization rate
- Could place a prior on  $t_0$  and fit epidemic start time more explicitly

### **STAN Cons:**

• Not sure how to implement the same type of model fit in STAN that incorporates the min and max guess (i.e. confirmed hospitalizations and hospitalizations + 30% suspected cases). Could put a distribution on it, but could end up being a bit wonky

### 5/18/2020

Fixed some algebra slip-ups in the  $\mathcal{R}_0$  calculation for the model in the LEMMA\_model document

### Potential improvements/ideas (running list)

Network models to examine sub-epidemics (like Mission study), implications for effectiveness of SiP, opening back up

Intro paper on network models here with corresponding R package and website with tutorials

#### Questions

- What are the characteristics of a network that gives rise to the findings of the Mission study?
- What are the implications of such a network for efficacy/limitations of SiP intervention? What are the implications for lifting SiP? i.e. how does the network change once SiP is lifted and how does transmission then propagate through this post-SiP network?
- How can test-trace-isolate be used to limit transmission through such a network?

### Concepts

- Degree or connectivity (k) number of neighbors an individual has; degree distribution  $(p_k)$  population level characteristic of connectivity
- **Size** of the network described by **distance** between two nodes the length of the shortest path between them in the network; **diameter** of the network is the largest **distance** in the network
- Mixing matrix describes how individuals of type *i* within the network are connected to individuals of type *j* where "type" can refer to any characteristic that differs between individuals. **Assortative** mixing describes a network pattern in which individuals are more likely to interact with like individuals
- local clustering (φ) how many pairs are shared between pairs of individuals in the network,
   e.g. given two pairs, how many of the networks between the two pairs will look like triangles in which
   A relates to B, B relates to C, AND A also relates to C.
- Betweenness/Centrality Importance of particular individuals within the network; number of paths between i and j that pass through a particular node

### Continuous time, stochastic model versions

I've got a continuous time stochastic model built with the adaptivetau package that's got a slightly different structure that I could work on building out a bit more/make more user friendly with similar input/output functionality. Would having three models all running projections help or make things more confusing? Maybe have this going on behind the scenes and convey where there's more or less agreement between the models to DPHs?

## Quantifying impact: how many cases/hospitalizations/deaths avoided due to SiP?

### Erlang distributed latent period, hospitalization length

Maybe a bit more of an academic exercise, but compartmental models make an implicit assumption that wait times between model states are exponentially distributed, which is rarely the case. Implementing "box cars", we can relax this assumption to make wait times Erlang (special case of a gamma distribution in which the shape parameter is a positive integer) distributed. Would be good for both E and H states given we have data on the distributions of latent period and hospitalization times we could fit to

Make some priors endogenous (e.g. non-adjustable), focus users on things most likely to vary by region/area/population:

- Population Size
- Start date of projection
- End date of projection
- Percent infected who are hospitalized
- Average hospital length of stay
- Timing and effectiveness  $(\mathcal{R}_e)$  of interventions