NME

Network Modeling for Epidemics

1

Individual Based Models (IBMs)

aka “Agent based models”

Key features and differences from DCMs

- Represent each individual member of the population explicitly
  - The population is a data frame (in R speak)
    - Each row is an individual
    - Each column is an attribute (infection status, age, sex, etc.)

- Use discrete individual events instead of aggregate stock and flow rates to implement the epidemic processes
  - Events (contact, transmission, recovery, etc.) happen to individuals
  - Outcomes are governed by a draw from a probability distribution
    - Typically a discrete distribution when working in discrete time
    - Like a coin flip – the Bernoulli distribution
    - Binomial or Poisson distributions for positive values
    - Geometric distribution for waiting times, etc.

IBM pseudocode

```
# Initial conditions
     # create a data.frame (nrow = # of agents, ncols = # of attributes)
     # assign infection status (S, I, R) as one attribute
     # assign all other attributes
# Simulate epidemic
for (at = 1:num.timesteps) {
     # infection
          # draw the number of contacts for that step
          # draw 1 pair of agents for each contact
          # filter to just the discordant SI pairs
          # flip coin for each pair to determine if transmission
          # do bookkeeping for new infections
     # recovery
          # identify infected elements
          # flip coin for each case to determine recovery
          # do bookkeeping for recoveries
      # update other attributes
          # exact code depends on the nature of the attribute
}
# process output
```

Each process can be made to depend on the attributes of the agents

IBM strengths

- Shows the stochastic variability in these systems
  - Important to understand the typical stochastic variability (noise) and distinguish this from systematic effects (signal) when interpreting patterns in epidemic surveillance data
- Can handle multiple forms of heterogeneity with relative ease
  - With individuals identified, they just get labeled with their attribute, and all of the attribute-based heterogeneity in processes can then be implemented
- Very simple models have closed form solutions for the persistence threshold (related to the reproduction number R_0)
  - For examples, see this article
  - But in general, closed forms are not available, and you observe persistence or extinction probabilities via simulation.

IBM pseudocode and the contact network

```
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```

This is where a network model would be plugged in, with a more detailed specification of the process

IBM representations of the contact network

IBMs in the literature use a wide range of methods to represent heterogeneity in the contact process, e.g.:

- random mixing or something close to it
- "scale free" distributions for #s of partners
- simple spatial models (e.g. "lattice", "nearest neighbor" or "gravity" models)
- queuing processes and "stub matching"

Not realistic for many pathogen transmission systems

- General statistical model for networks

The topic of this course!