NME 2021

Network Modeling for Epidemics

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Deterministic Compartmental Models

The workhorse of epidemic modelers

And a good place to build intuition

Deterministic compartmental models

- Only the aggregate count in each state ("compartment") is represented, not the individual persons
- Within each compartment, people are homogeneous
- Transitions ("flows") are represented in terms of rates
  - The fraction of the aggregate count that moves from one compartment to another at any time point

Deterministic compartmental models

- May be discrete time or continuous time
  - We will focus on discrete time in what follows because it's easier to understand
  - Most published models, and most packages (including EpiModel) solve in continuous time
- Compartmental models are usually deterministic – each run gives exactly the same result
- Measures = EXPECTED counts (across an infinite number of stochastic runs)
- Compartments and flows can represent fractional persons

DCMs: SIR model

Here R stands for:

- **Recovered** with immunity
- Also sometimes called "**removed**" in the literature – but be careful
  - *Removed* from the infection process
  - *Not removed* from the contact process

DCMs: SIR model

New infections per unit time (incidence)
What is a reasonable expression for this quantity?

t = time

State variables

$s(t)$ = expected number of susceptible people at time t
$i(t)$ = expected number of infected people at time t
$r(t)$ = expected number of recovered people at time t

Parameters

α = act rate per unit time
τ = prob. of transmission given S-I act
ρ = recovery rate

DCMs: SIR model

A new infection requires: a susceptible person to have an act with an infected person and for infection to transmit because of that act

t = time
$s(t)$ = expected number of susceptible people at time t
$i(t)$ = expected number of infected people at time t

Expected incidence at time t =

DCMs: SIR model

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Expected incidence at time t $= s(t)$

DCMs: SIR model

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$s(t)$ = expected number of susceptible people at time t
$i(t)$ = expected number of infected people at time t
α = act rate per unit time

Expected incidence at time t $= s(t)\alpha$

DCMs: SIR model

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t = time
$s(t)$ = expected number of susceptible people at time t
$i(t)$ = expected number of infected people at time t
α = act rate per unit time

Expected incidence at time t $= s(t)\alpha \frac{i(t)}{s(t)+i(t)+r(t)}$

DCMs: SIR model

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t = time
$s(t)$ = expected number of susceptible people at time t
$i(t)$ = expected number of infected people at time t
α = act rate per unit time
τ = "transmissibility" = prob. of transmission given S-I act

Expected incidence at time t $= s(t)\alpha \frac{i(t)}{s(t)+i(t)+r(t)}\tau$

DCMs: SIR model

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$s(t)$ = expected number of susceptible people at time t
$i(t)$ = expected number of infected people at time t
α = act rate per unit time
τ = "transmissibility" = prob. of transmission given S-I act
$n(t)$ = total population = $s(t) + i(t) + r(t)$

Expected incidence at time t $= s(t)\alpha \frac{i(t)}{s(t)+i(t)+r(t)}\tau$

$= s(t)\alpha \frac{i(t)}{n(t)}\tau$

DCMs: SIR model

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Expected incidence at time t

$$= s(t)\alpha \frac{i(t)}{s(t)+i(t)+r(t)}\tau$$

$$= s(t)\alpha \frac{i(t)}{n(t)}\tau$$

$$= s(t)\alpha \frac{i(t)}{n}\tau$$

Careful: only for a "closed" population can the time subscript be dropped for n

DCMs: SIR model

New recoveries per unit time
What is a reasonable expression for this quantity?

t = time
$s(t)$ = expected number of susceptible people at time t
$i(t)$ = expected number of infected people at time t
$r(t)$ = expected number of recovered people at time t
α = act rate per unit time
τ = prob. of transmission given S-I act
ρ = recovery rate

DCMs: SIR model

- Much simpler process: expected number of recoveries at time t equals $\rho\, i(t)$
- Reminder: Expected incidence at time $t \quad = s(t)\alpha\frac{i(t)}{n}\tau$
- How do we turn this into a system of equations?

$$s(t+1) = s(t) - s(t)\alpha\frac{i(t)}{n}\tau$$

$$i(t+1) = i(t) + s(t)\alpha\frac{i(t)}{n}\tau - \rho i(t)$$

$$r(t+1) = r(t) + \rho i(t)$$

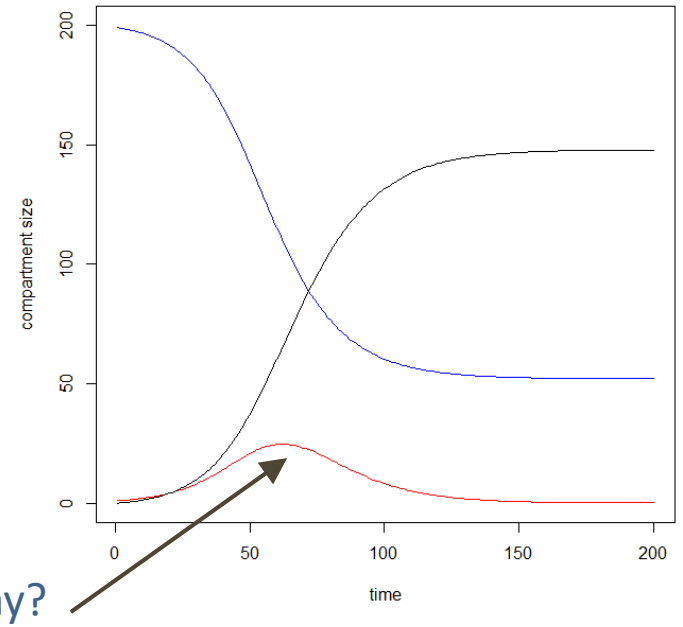
Difference equations

DCMs: SIR model

Add in a set of initial conditions: $s(0) = 999, i(0) = 1, r(0) = 0$

and a set of parameter values $\alpha = 0.6, \tau = 0.3, \rho = 0.1$

And one has the full trajectory of each state over time:



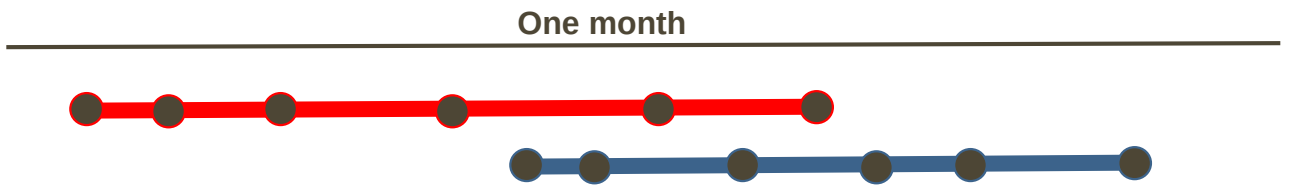
What happens on Day 62? Why?

Brief digression: contacts and acts

- The epi modeling literature typically uses the term “contact” – so why do we use “act”?
- Because “contact” is an ambiguous word in this context
  - E.g. think of sexual activity - when we say “# of contacts per year”
    - Does it mean number of sex acts?
    - Or numbers of different partners?
- To be explicit, we will make the distinction between “acts” and “partners” throughout this workshop
- This distinction matters for disease dynamics *when there are repeated acts with the same person*

Brief digression: contacts and acts

- If multiple acts occur within partnerships, DCMs take one of two forms.



1. Define a contact as an act. Model each act as a separate independent event, ignoring the persistent nature of the partnerships
2. Define a contact as a partnership. Compress all of the acts over the partnership into a single instance in time

- We'll return to this later

DCMs: SIR model

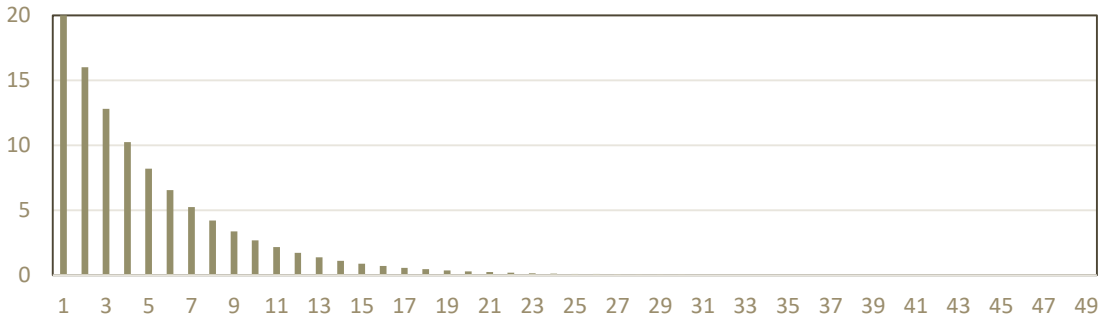
- Relationship between duration of infection and recovery rate
  - Imagine a disease with a constant recovery rate of 0.2.
    - I.e., on Day 1 of infection, you have a 20% probability of recovering.
    - If you don't recover on Day 1, you have a 20% probability of recovering on Day 2. Etc.

DCMs: SIR model

- Now, imagine 100 people who start out infected on the same day.
  - How many recover after being infected 1 day? 100*0.2 = 20
  - How many recover after being infected 2 days? 80*0.2 = 16
  - How many recover after being infected 3 days? 64*0.2 = 12.8
  - What is this distribution called? Geometric
  - What is the mean (expected) duration spent infected? 1/0.2 = 5 days

1/ρ = *D*

Geometric	
Parameters	$0 < p \leq 1$ success probability (real)
Support	$k \in \{1, 2, 3, \ldots\}$
Probability mass function (pmf)	$(1-p)^{k-1} p$
Cumulative distribution function (CDF)	$1 - (1-p)^k$
Mean	$\frac{1}{p}$



R_0 : A key summary metric

Definition: The expected number of secondary infections generated by the first infected case in a population that has never seen this infection before

A single number that summarizes the epidemic potential in a population

- What happens if the first infected case recovers before transmitting to someone else?
- … nothing.

R_0 and the "persistence threshold"

There is an epidemic persistence threshold at $R_0 = 1$

Value of R_0	Implication
< 1	The first infected individual will on average infect < 1 person total. In a deterministic model, the epidemic will always go extinct
> 1	The first infected individual will on average infect >1 person total. In a deterministic model, the epidemic will always grow
= 1	We are right on the threshold between an epidemic and extinction. In a deterministic model, the epidemic will just putter along

DCMs: R_0

- So, how do we calculate R_0 for a DCM?
  - Intuitively, for that first case, the expected number of secondary infections generated is:

duration infected x act rate per timestep x transmission rate per act

D α τ

- For a simple SIR DCM: $R_0 = \frac{\alpha\tau}{\rho}$ Because $\mathrm{D} = \frac{1}{\rho}$