Epidemic Modeling Basics

Deterministic Compartmental Models

Models have three basic components

- **Elements** – "actors" in the model
- **States** – attributes of system elements
- **Transitions** – rates of movement between states

All models, simple and complex, have these same building blocks

Model component 1: Elements

Elements can be:

- Persons
- Animals
- Environmental reservoirs (water, soil)
- Vectors (e.g., mosquitoes)
- Pathogens

Example: Measles transmission requires people

Brief digression…

Hosts and pathogens: do we need to represent both as elements in the system?

- This week, we won't (*focus is on "between-host" dynamics*)
  - In a simple model we represent the pathogen via the effect on the host
    - Susceptible / Infected / Recovered with immunity
    - Duration of infection (influences recovery time)
    - Stage of infection (may influence infectivity or activity)

- But, we can (*by adding "within-host dynamics"*)
  - Explicitly govern pathogen reproduction and vital dynamics
  - Allow the pathogen to evolve

Model component 2: States

States – attributes of elements. For example:

- **Host states**
  - Infection status (Susceptible, Infected, Recovered…)
  - Demographic characteristics (male, female, …)
- **Pathogen states**
  - life cycle stage (e.g., larvae, reproductive adult, …)

Example: A simple measles model will have three host states:

susceptible (S)

infected (I)

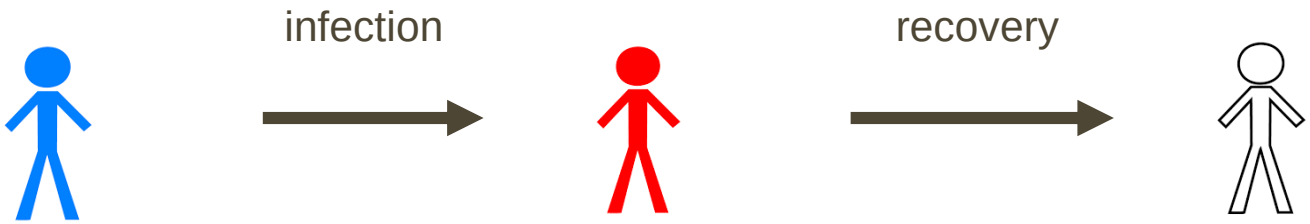
recovered w/ immunity (R)

Model component 3: Transitions

Transitions – movement between states

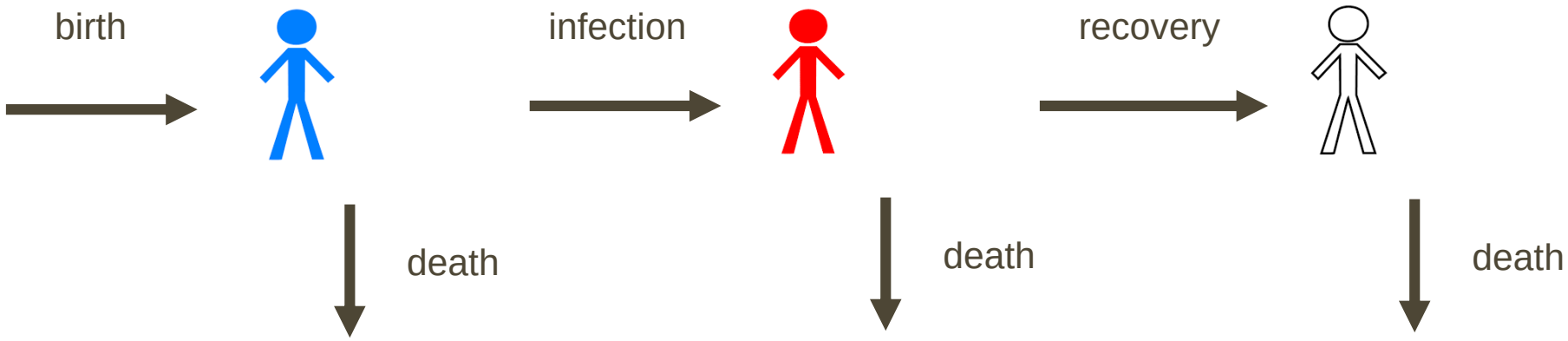
- **Deterministic**: fixed *rate* of transition between states.
  - Uses a population mean rate to govern process of movement
- **Stochastic**: *probability* that an element transitions between states.
  - Uses a full probability distribution of rates to govern the process of movement.

Example: The simple measles model has two transitions:



Model component 3: Transitions

- Transitions can also come in from outside the model, or move out of the model



Key transition: Infection

Many different modes of transmission:

STD/HIV:	direct body fluid contact (sex, needles, MTC)
Measles, Influenza:	respiratory, air-borne
Diarrheal diseases:	fecal-oral
Malaria:	vector-borne (mosquitoes)
Schistosomiasis:	water and vector-borne
Cholera:	water and food-borne

We're going to focus on direct, person-to-person transmission, because this is where contact networks matter most

Deterministic compartmental models

- A form of dynamic modeling in which people are represented only in terms of the aggregate count present in each state ("compartment")
- Within each compartment, people are homogeneous
- Transitions ("flows") are also represented in terms of number of people moving along them at any time point

Deterministic compartmental models

- May be discrete time or continuous time
  - We will focus on discrete time in the presentation
  - Most published models, and most packages (including EpiModel) solve in continuous time
- Compartmental models are usually deterministic – one will get the exact same results from a model each time one runs it
- Measures are of EXPECTED counts (across an infinite number of stochastic runs)
- This means compartments and transitions do not have to represent whole numbers of people

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
$s(t)$ = 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

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

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 $= s(t)$

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
α = act rate per unit time

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

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
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

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
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

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
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

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

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?

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

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

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

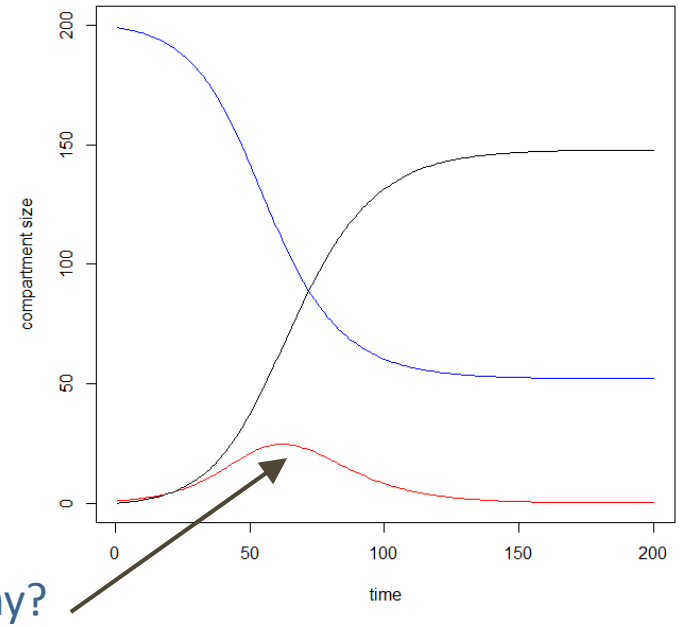
Difference equations

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:



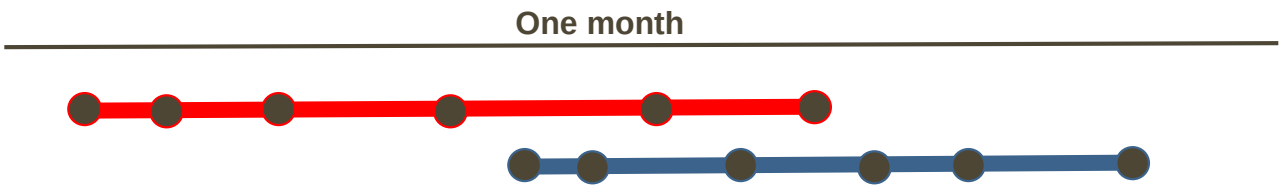
What happens on Day 62? Why?

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 today

DCMs: SIR model

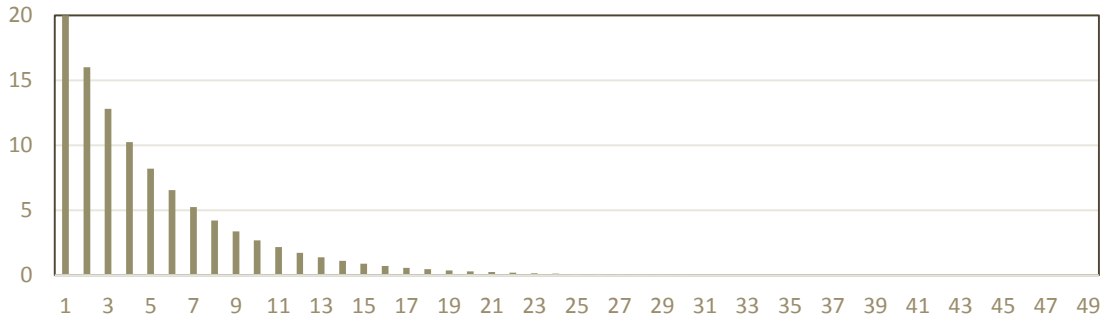
- Relationship between duration and recovery rate
  - Imagine a disease with a constant recovery rate of 0.2.
    - I.e., on Day 1 of infection, you have a 20% probability of recovering.
    - If you don't recover on Day 1, you have a 20% probability of recovering on Day 2. Etc.

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	$\frac{1}{p}$



DCMs: R_0

- $\boldsymbol{R_0}$ = the number of secondary infections stemming directly from the first infected case in a susceptible population – that is, one that has not experienced the disease before

  = duration infected x acts per time step x transmission per act $= \tau\alpha\mathrm{D}$

  = $\tau\alpha/\rho$ (for the basic SIR model)

- R_0 tells whether an epidemic is likely to occur or not:
  - $R_0 > 1$: one infected individual will on average infect >1 person total. In a deterministic model, the disease will grow
  - $R_0 < 1$: one infected individual will on average infect < 1 person total. In a deterministic model, the disease will fade away
  - $R_0 = 1$: we are right on the threshold between an epidemic and not. In a deterministic model, the disease will putter along