NME

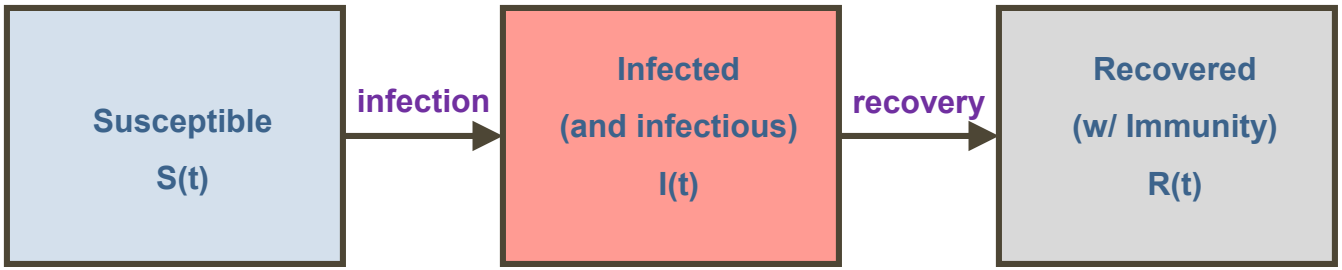
Network Modeling for Epidemics

1

Deterministic Compartmental Models (DCMs)

An overview of key principles

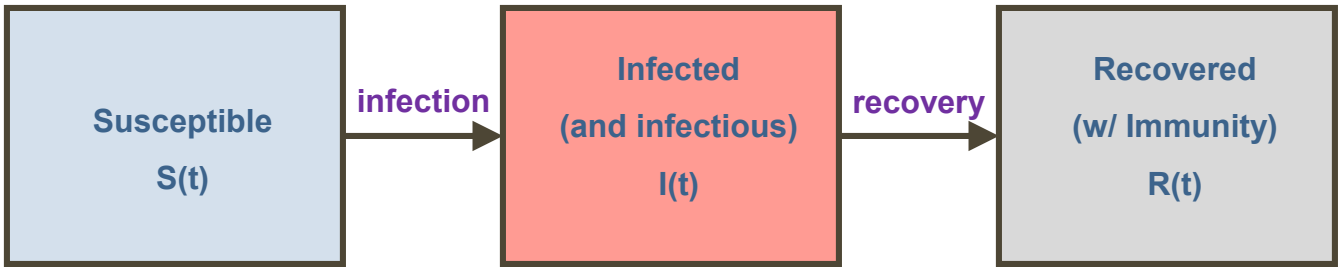
Stocks and flows



- Only the aggregate count in each state ("compartment") is represented, not individual persons
  - S(t) = # susceptibles at time t, etc.
  - Within each compartment, units are homogeneous and undifferentiated

- Transitions ("flows") represent the aggregate count that moves from one compartment to another at any time point
  - Flows are represented by differential equations (or difference equations if discrete time)
  - So you can get fractional values for the flows, not integral numbers of individuals

Flows represent changes in state



Change in # of susceptible persons per time unit

$$\frac{dS}{dt} = -\beta\, SI/N$$

Infection flow

Change in # of infected persons per time unit

$$\frac{dI}{dt} = \beta\, SI/N - \rho I$$

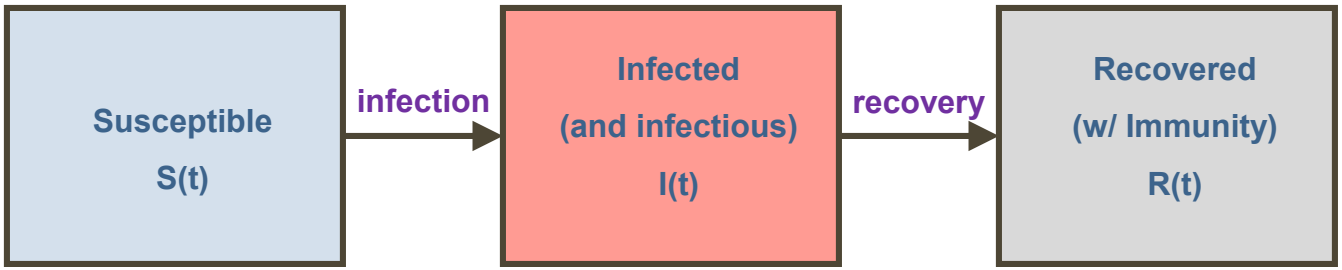
Recovery flow

Change in # of recovered persons per time unit

$$\frac{dR}{dt} = \rho I$$

- β and ρ are model parameters
- Q: Where are the contact events?
- A: embedded in the infection flow

The infection flow

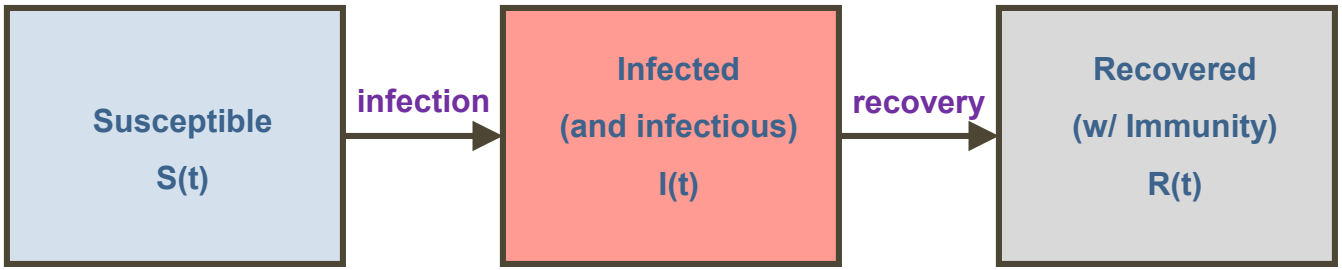


Common notation for infections $\beta SI/N$ where β is called the "force of infection"

Can be disaggregated as: $\tau c SI/N$ Where c = "contact rate"
τ = "transm. prob"

So: S susceptibles each have c contacts per unit time
I/N of the contacts are with infected elements in the population
each susceptible-infected contact has probability τ of transmitting

Assumptions in simple models



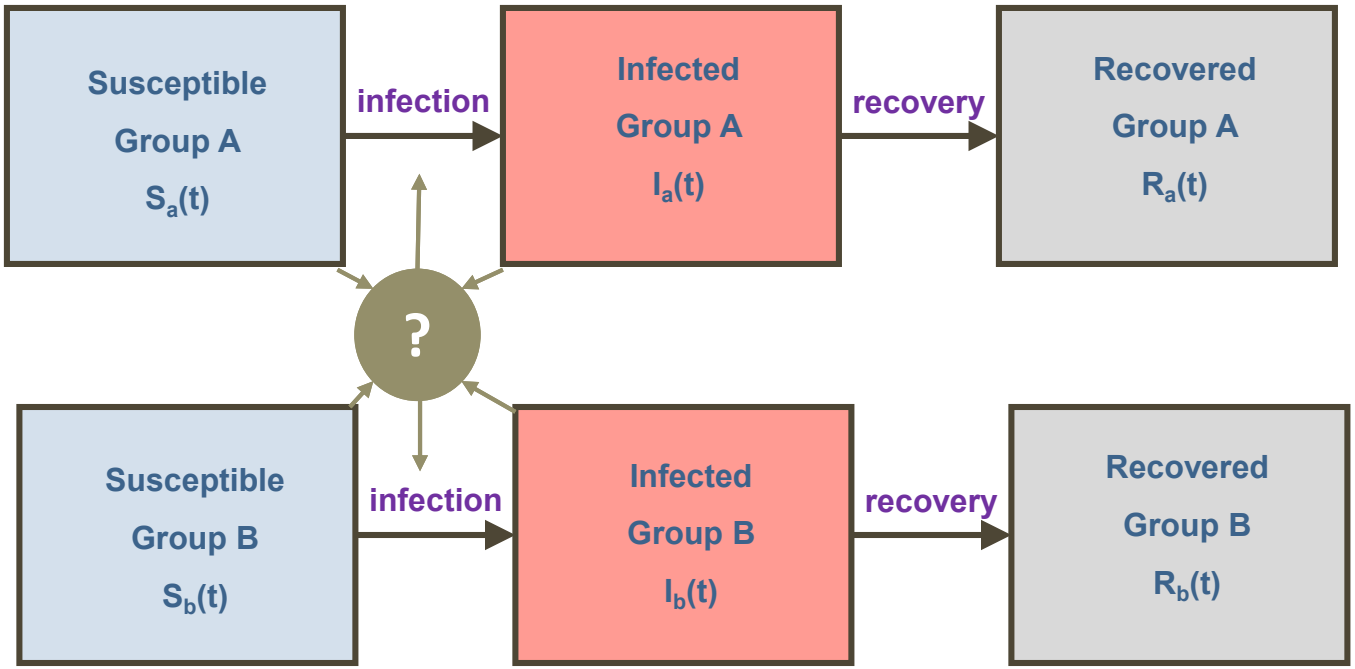
In this simple model: $\tau c\, SI/N$

where c = "contact rate"
τ = "transm. prob"

There are implicit assumptions:

- No attributes of the population elements or the pathogen influence the dynamics.
- Contacts are made at random, there are no patterns of preferential mixing
- Each contact is an independent event, there are no persistent partnerships, so each contact is with a new, randomly chosen member of the population

Attributes in DCMs: more stocks and flows



Example: A 2-group model, elements are A or B

- Doubles the number of infection compartments (a 3-group model would triple, etc.)
- Requires specifying the contact process within and between compartments

The number of states grows exponentially with additional heterogeneity

Features of DCMs

- Compartmental models are usually deterministic – each run gives the same result
- Outcomes = predicted values (and represent the means of an equivalent stochastic process over an infinite number of runs)
- Compartments and flows can represent fractional persons

DCM strengths

- Familiar to many (and familiarity breeds comfort)
- Have a long body of literature identifying properties of different classes of models
- Simple models have simple closed form expressions for R_0
  - Intuitively, the number of secondary infections for the first case is:

    Contact rate/timestep * duration infected * transmission prob/contact

    c D τ
  - So for a simple SIR DCM: $R_0 = cD\tau$

DCM limitations

- Do not show the stochastic variation in a system
  - Stochastic CMs do exist, but only address this one limitation
- Adding heterogeneity blows up quickly
  - Requires new compartments
    - adding a 2-group attribute means going from 3 compartments to 6
    - What if we want to also add another 5-group attribute, age and 4 categories of pathogen load? Testing and treatment status? Geographic location? Etc.
  - And if the heterogeneity isn't in discrete categories?

DCM limitations

Representing complex partnership network patterns is hard (or impossible, depending who you ask)

- Non-random mixing on a single attribute can be added into the incidence term easily enough
  - Classic example: age structured mixing
  - But additional questions arise in open populations where group sizes can change
- But adding multiple attributes is hard
- And detailed *partnership* patterns are harder
  - A tendency to only have one partner at a time? Differential by attribute?
  - For partnership duration to depend on attributes?
  - Remember that compartments only consider people in the aggregate; individuals are not uniquely identified
- If these things matter, then you're better off with an IBM.