Foundations of dynamic modeling:

The SIR Model Family

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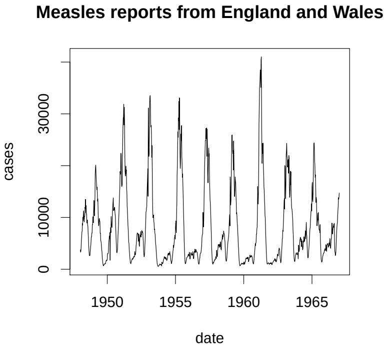
DAIDD 2019

Goals

- This lecture will:
  - introduce the idea of dynamical modeling
  - explain why dynamical modeling is a key tool for understanding infectious disease
  - discuss and demonstrate simple dynamical models from the SIR model family
  - investigate some insights that can be gained from these models

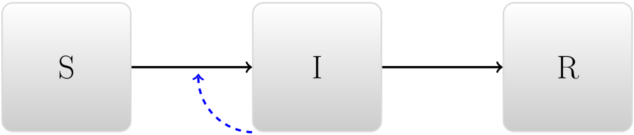
Dynamical modeling connects scales



- Start with rules about how things change in short time steps
  - Usually based on *individuals*
- Calculate results over longer time periods
  - Usually about *populations*

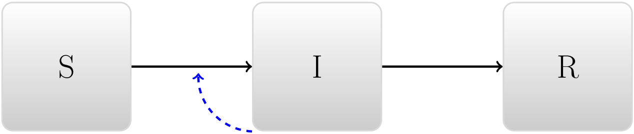
Compartmental models

Divide people into categories:



- Susceptible → Infectious → Recovered

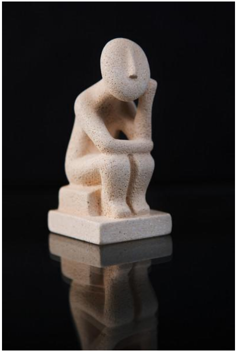
What determines transition rates?



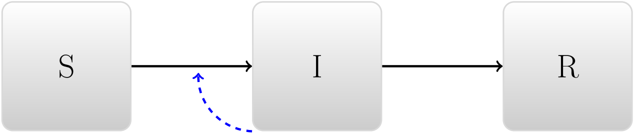
- People get better independently
- People get infected by infectious people

Conceptual modeling (present)

$$S \longrightarrow I \longrightarrow R$$

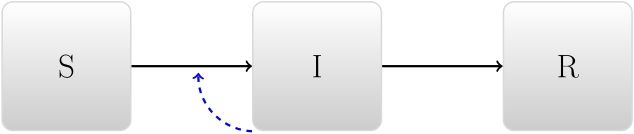


Conceptual modeling



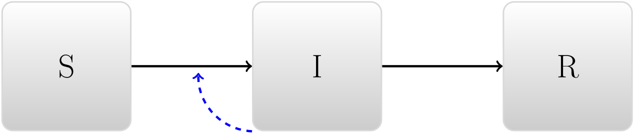
- What is the final result?
- When does disease increase, decrease?

Dynamic implementation



- Requires assumptions about recovery and transmission
- The *conceptually simplest* implementation uses Ordinary Differential Equations (ODEs)
  - Other options may be more realistic
  - Or simpler in practice

Recovery



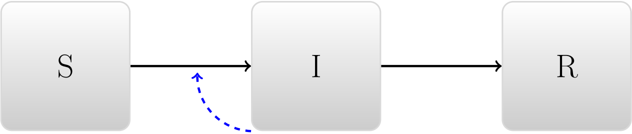
- Infectious people recover at *per capita* rate γ
  - Total recovery rate is γI
  - Mean time infectious is $D = 1/\gamma$

Transmission

$$\begin{tikzcd} S \arrow[r] & I \arrow[r] & R \end{tikzcd}$$

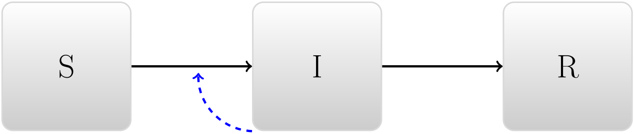
- Susceptible people get infected by:
  - Going around and contacting people (rate c)
  - Some of these people are infectious (proportion I/N)
  - Some of these contacts are effective (proportion p)
- Per capita rate of becoming infected is $cpI/N \equiv \beta I/N$
- Population-level transmission rate is $\mathcal{T} = \beta SI/N$

Another perspective on transmission



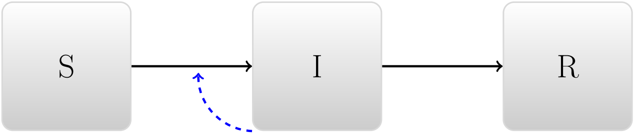
- Infectious people infect others by:
  - Going around and contacting people (rate c)
  - Some of these people are susceptible (proportion S/N)
  - Some of these contacts are effective (proportion p)
- Per capita rate of infecting others is $cpS/N \equiv \beta S/N$
- Population-level transmission rate is $\mathcal{T} = \beta SI/N$

ODE implementation



$$
\begin{aligned}
\frac{dS}{dt} &= -\beta\frac{SI}{N} \\
\frac{dI}{dt} &= \beta\frac{SI}{N} - \gamma I \\
\frac{dR}{dt} &= \gamma I
\end{aligned}
$$

Spreadsheet implementation



Model taxonomy (present)

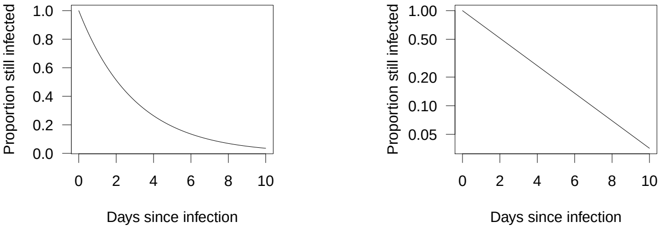
	CONTINUOUS TREATMENT OF INDIVIDUALS (averages, proportions, or population densities)	DISCRETE TREATMENT OF INDIVIDUALS
DETERMINISTIC	CONTINUOUS TIME DISCRETE TIME	
STOCHASTIC	CONTINUOUS TIME DISCRETE TIME	CONTINUOUS TIME DISCRETE TIME

3

ODE assumptions

- Lots and lots of people
- Perfectly mixed

ODE assumptions



- Waiting times are exponentially distributed
- Rarely realistic

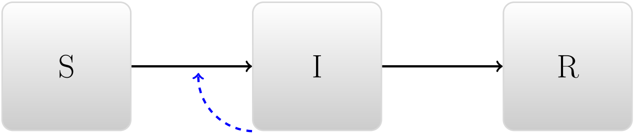
More about transmission

- $\beta = pc$
  - What is a contact?
  - What is the probability of transmission?
- Sometimes this decomposition is clear
- But usually it's not

Population sizes

- How does β change with population size?
- Recall that β is the *per capita* rate of contacts

Population sizes (present)



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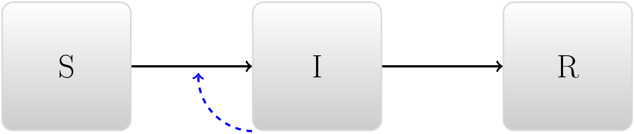
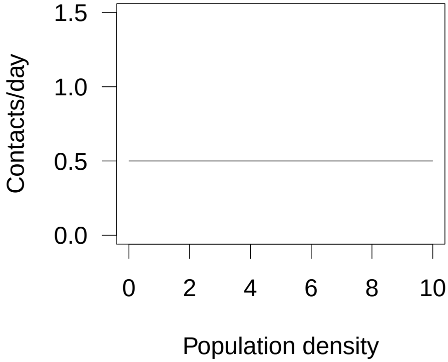
Population sizes



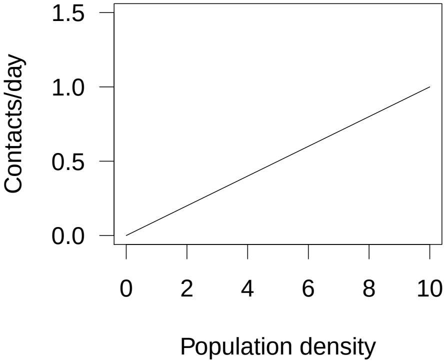
$$\begin{aligned}
\frac{dS}{dt} &= -\beta(N)\frac{SI}{N} \\
\frac{dI}{dt} &= \beta(N)\frac{SI}{N} - \gamma I \\
\frac{dR}{dt} &= \gamma I
\end{aligned}$$

Standard incidence



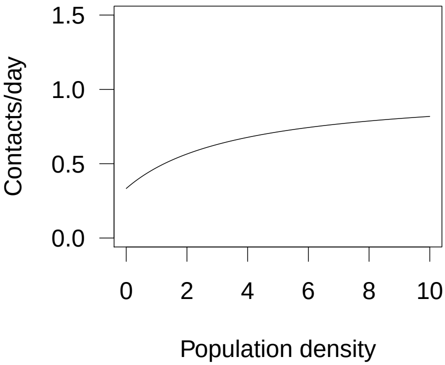
- $\beta(N) = \beta_0$
- $\mathcal{T} = \frac{\beta_0 SI}{N}$
- Also known as *frequency-dependent* transmission

Mass action



- $\beta(N) = \beta_1 N$
- $\mathcal{T} = \beta_1 SI$
- Also known as *density-dependent* transmission

General



- Per-capita rate:
  - May not go to zero when N does
  - May not go to ∞ when N does

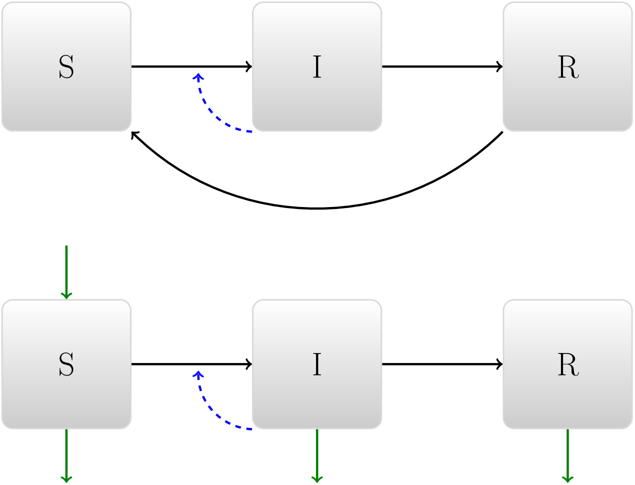
Digression – units

- $\mathcal{T} = \beta SI/N$: $[\mathrm{ppl}/\mathrm{time}]$

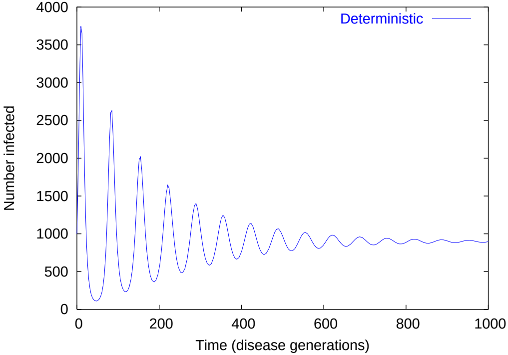
- β : $[1/\mathrm{time}]$
  - The true β always has people in the numerator and the denominator
  - $\beta/\gamma = \beta D$: $[1]$

- Components of β may have different units
  - Standard incidence, β_0 : $[1/\mathrm{time}]$
  - Mass-action incidence, β_1 : $[1/(\mathrm{people} \cdot \mathrm{time})]$

Closing the circle

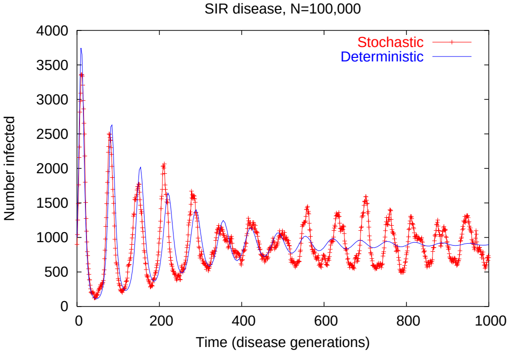


Tendency to oscillate



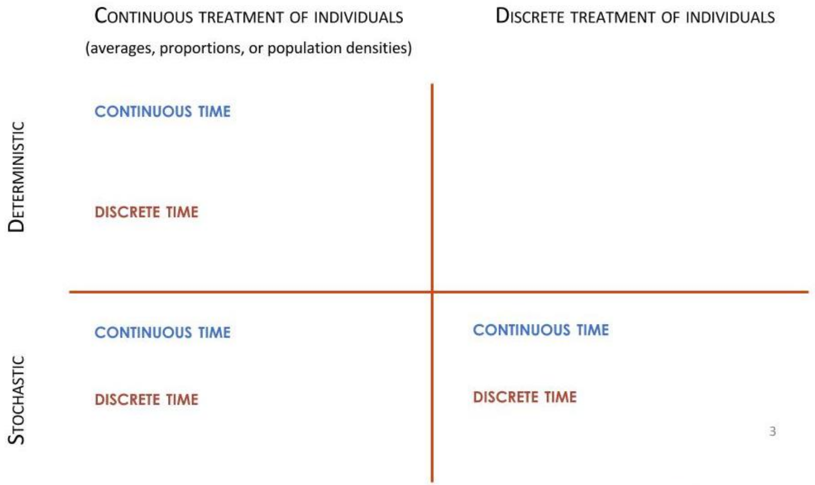
- Many susceptibles $\rightarrow$ many infections $\rightarrow$ few susceptibles $\rightarrow$ few infections $\rightarrow$ ...
- Oscillations in simple models tend to be "damped"

With individuality



- Treating individuals as individuals can produce substantial oscillations even in large populations
- Interaction between random effects and the different time scales (of infection and recovery)

Model taxonomy (present)



Summary

- Dynamic models are an essential tool because they allow us to link between scales
- There are many ways to construct and implement dynamic models
- Very simple models can provide useful insights
  - Reproductive numbers and thresholds
  - Tendency for oscillation (and tendency for damping)
- More complex models can provide more detail, but also require more assumptions, and more choices
- Understanding simple models can help guide our understanding of more complicated models

Title: Foundations of dynamic modeling:
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