# Foundations of dynamic modeling:
## The SIR Model Family
DAIDD 2020

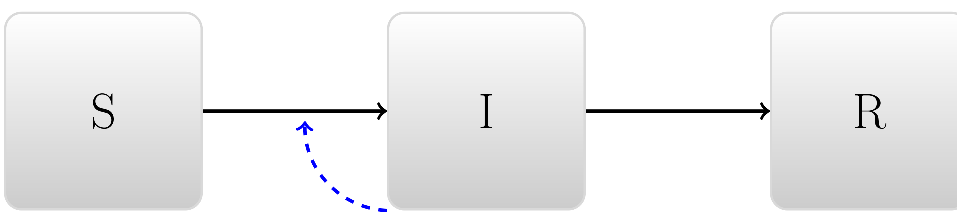
## Goals

- 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:**

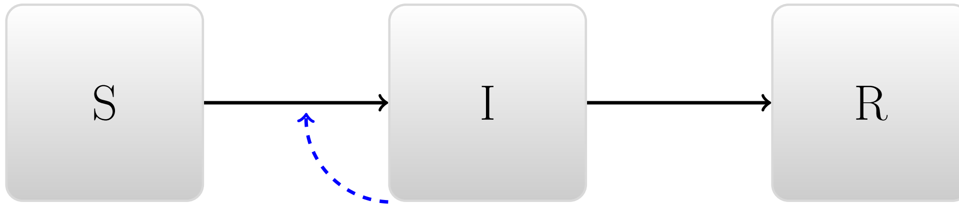



- Susceptible $\to$ Infectious $\to$ Recovered

## What determines transition rates?

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

## Conceptual modeling




## 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 $\gamma$
  - Total recovery rate is $\gamma I$
  - Mean time infectious is $D = 1/\gamma$

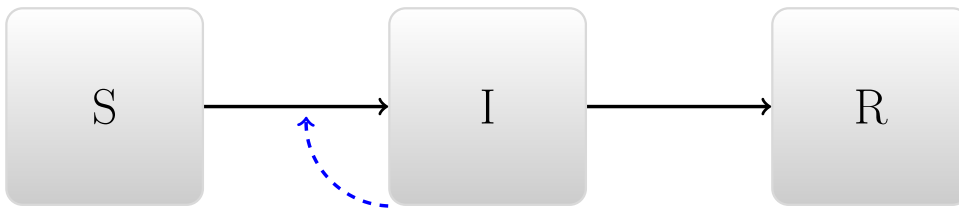
## Transmission

- 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 $\mathcal{T} = \beta SI/N$

## Conceptual modeling



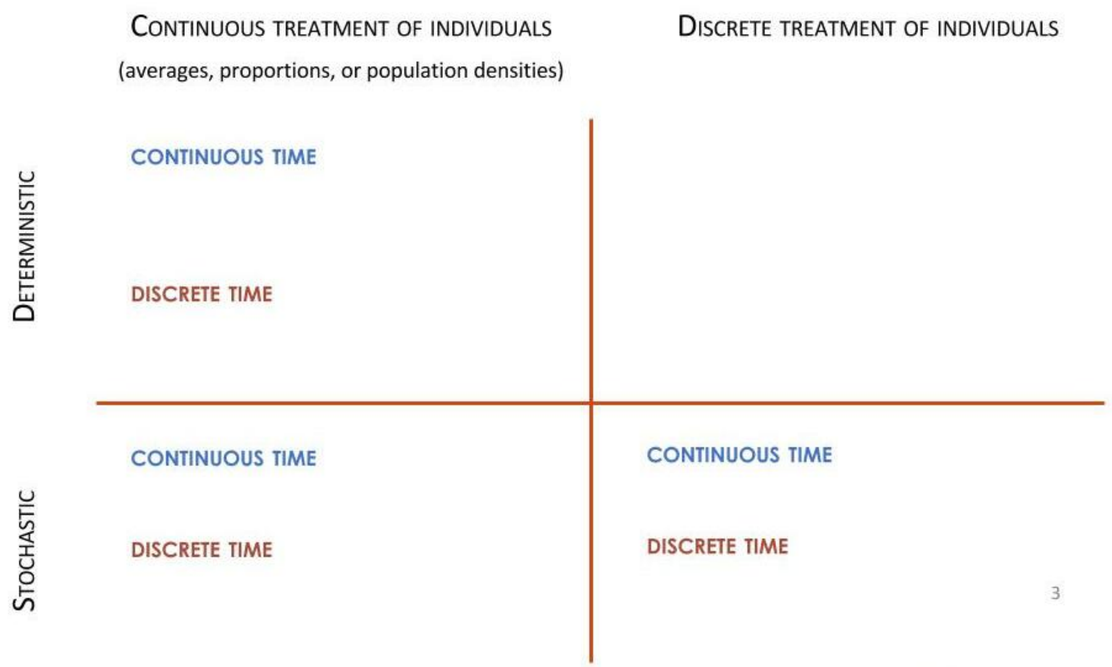

## The basic reproductive number

- $\mathcal{R}_0$ is the number of people who would be infected by an infectious individual *in a fully susceptible population.*
- $\mathcal{R}_0 = \beta/\gamma = \beta D = (cp)D$
  - $c$: Contact Rate
  - $p$: Probability of transmission (infectivity)
  - $D$: Average duration of infection
- A disease can invade a population if and only if $\mathcal{R}_0 > 1$.

## ODE implementation

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

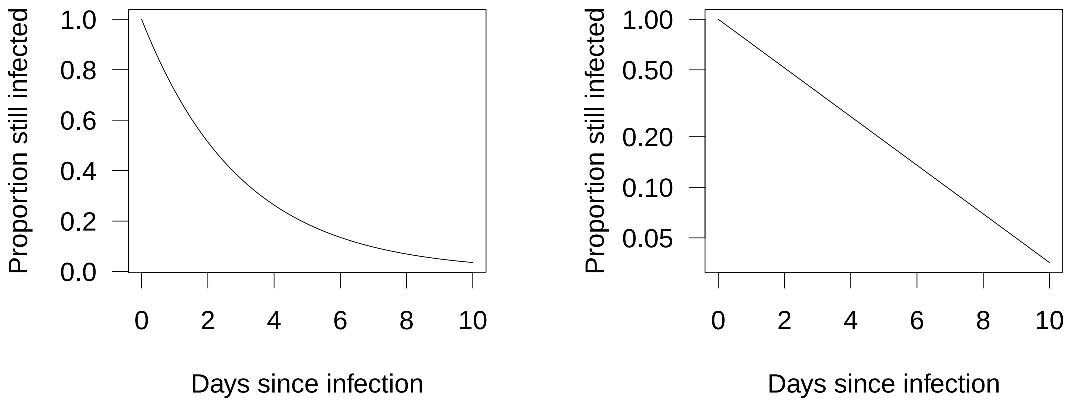
## Model taxonomy




## ODE assumptions

- Lots and lots of people
- Perfectly mixed

## ODE assumptions




- Waiting times are exponentially distributed
- Rarely realistic

## Scripts vs. spreadsheets

- Scripts are more transparent, less redundant
- Spreadsheets are more intuitive for simple problems

## More about transmission

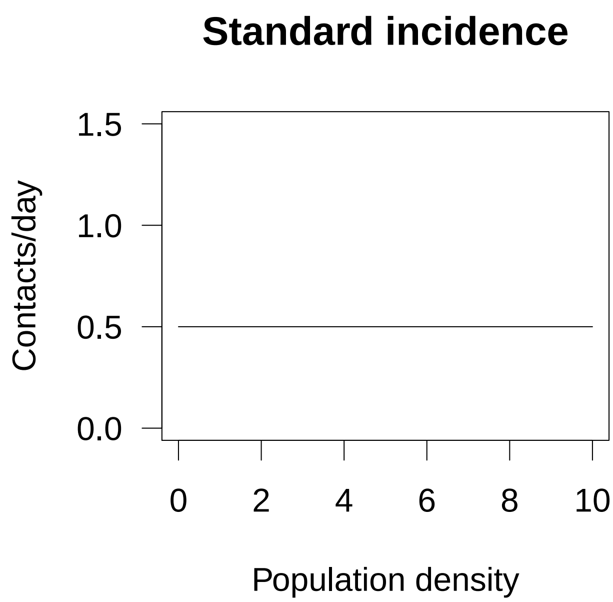
- $\beta = pc$
  - What is a contact?
  - What is the probability of transmission?
- Sometimes this decomposition is clear
- But usually it's not

## Population sizes

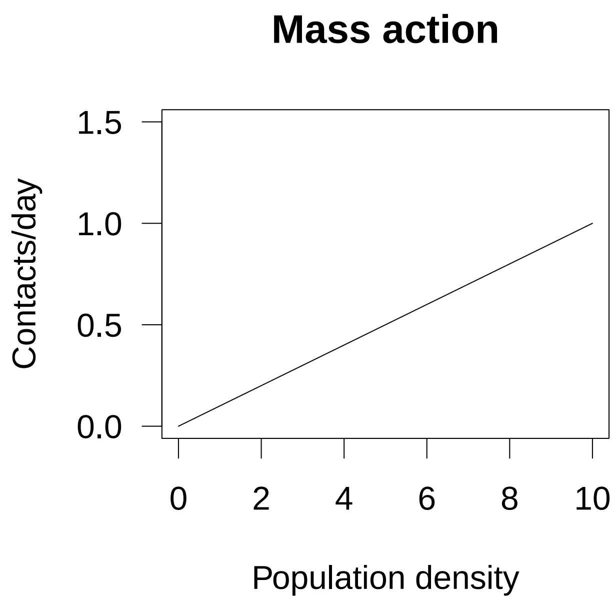
- How does $\beta$ change with population size?
- We can make different assumptions about this
  - It may increase with population size, or not
- If population size changes we have to *consider* the question

## Population sizes

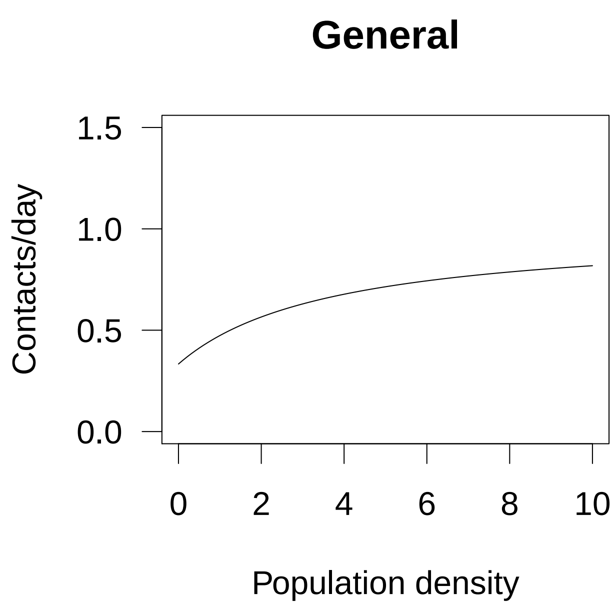
$$
\begin{aligned}
\frac{dS}{dt} &= -\beta(N)\frac{SI}{N} \\
\frac{dI}{dt} &= \beta(N)\frac{SI}{N} - \gamma I \\
\frac{dR}{dt} &= \gamma I
\end{aligned}
$$




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




- $\beta(N) = \alpha_0 N$
- $\mathcal{T} = \alpha_0 SI$
- Also known as *density-dependent* transmission



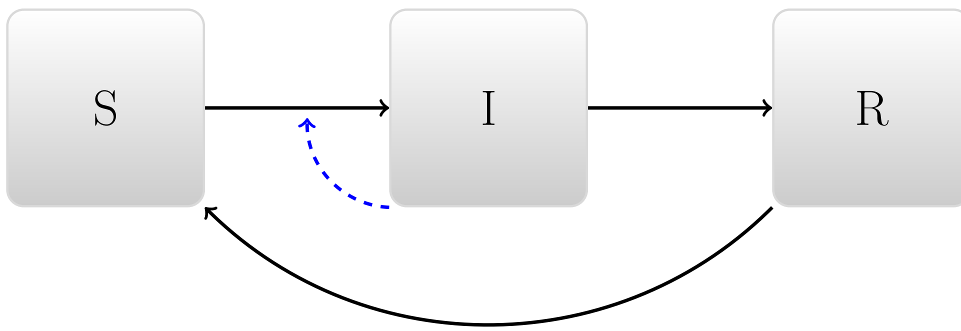

- Per-capita rate:
  - May not go to zero when $N$ does

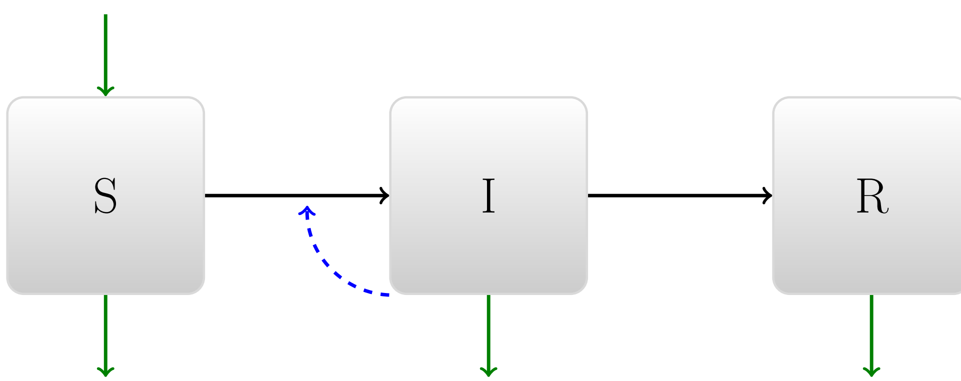
– May not go to $\infty$ when $N$ does

## Digression – units

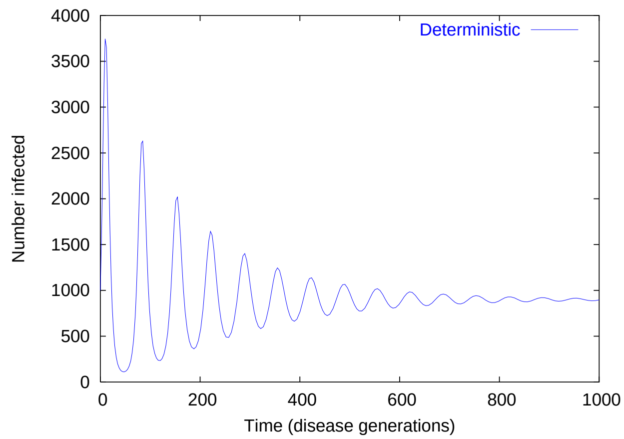
- $\mathcal{T} = \beta SI/N$ : [ppl/time]
- $\beta$ : [1/time]
  - The true $\beta$ always has people in the numerator and the denominator
  - $\beta/\gamma = \beta D$ : [1]
- $\mathcal{T} = \alpha SI$ : [ppl/time]
  - Mass-action incidence, $\alpha$ : [1/(people $\cdot$ time)]

## Closing the circle



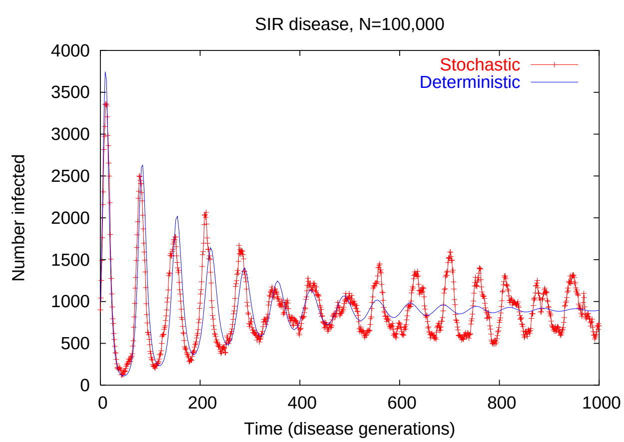



## Tendency to oscillate




- Many susceptibles → many infections → few susceptibles → few infections → ...
- 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)

## 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