

Foundations of dynamic modeling: The SIR Model Family

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MMED2018

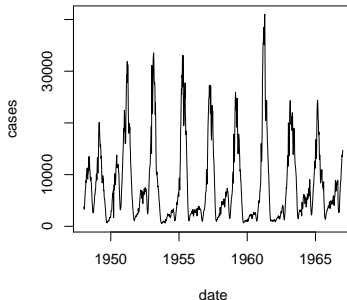
Goals

- ▶ 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

Dynamic modeling connects scales



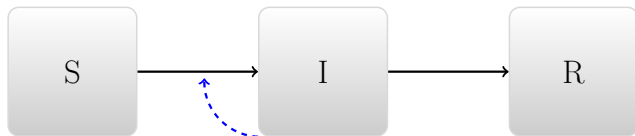
Measles reports from England and Wales



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

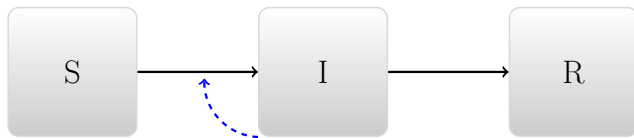
Compartmental models

Divide people into categories:



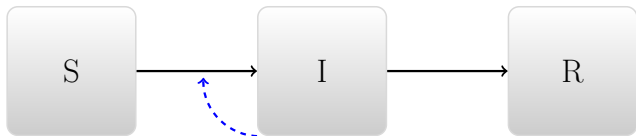
- Susceptible \rightarrow Infectious \rightarrow Recovered

What determines transition rates?

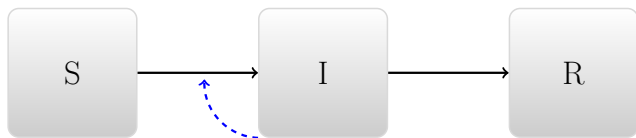


- ▶ People get better independently
- ▶ People get infected by infectious people

Conceptual modeling

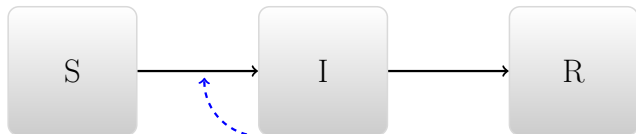


Conceptual modeling



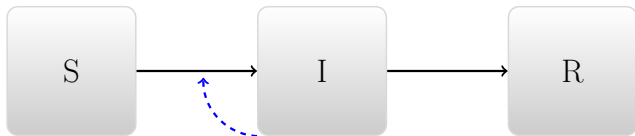
- ▶ What is the final result?
- ▶ When does disease increase, decrease?

Dynamic implementation



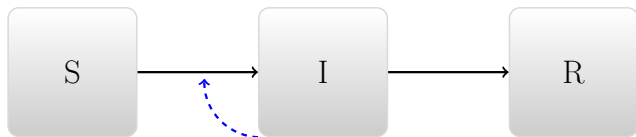
- ▶ Requires assumptions about recovery and transmission
- ▶ The *conceptually simplest* implementation uses Ordinary Differential Equations (ODEs)
 - ▶ Other options may be more realistic
 - ▶ Or simpler in practice

Recovery



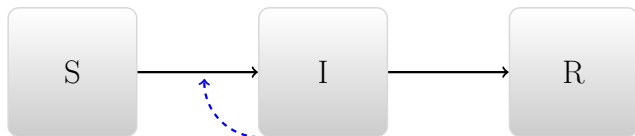
- ▶ Infectious people recover at *per capita* rate γ
 - ▶ Total recovery rate is γI
 - ▶ Mean time infectious is $D = 1/\gamma$

Transmission



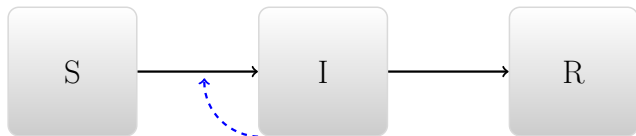
- ▶ Susceptible people get infected by:
 - ▶ Going around and contacting people (rate c)
 - ▶ Some of these people are infectious (proportion I/N)
 - ▶ Some of these contacts are effective (proportion p)
- ▶ Per capita rate of becoming infected is $cpl/N \equiv \beta I/N$
- ▶ Population-level transmission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

Another perspective on transmission



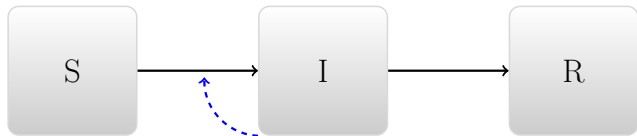
- ▶ Infectious people infect others by:
 - ▶ Going around and contacting people (rate c)
 - ▶ Some of these people are susceptible (proportion S/N)
 - ▶ Some of these contacts are effective (proportion p)
- ▶ Per capita rate of infecting others is $cpS/N \equiv \beta S/N$
- ▶ Population-level transmission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

ODE implementation



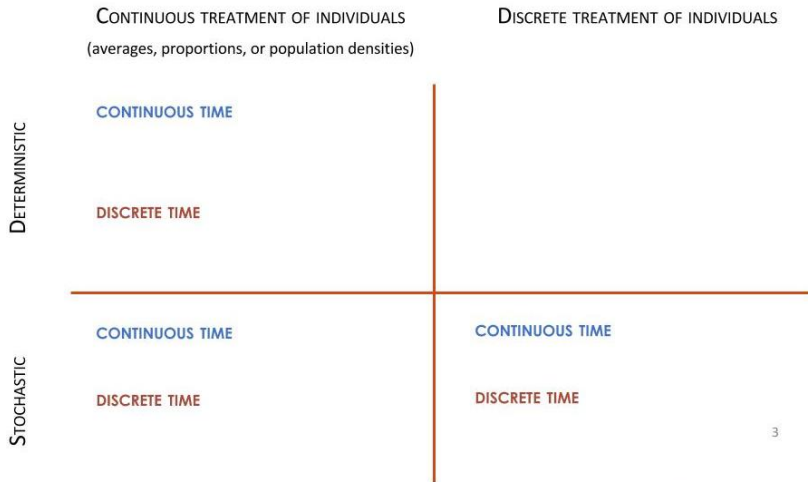
$$\begin{aligned}\frac{dS}{dt} &= -\beta \frac{SI}{N} \\ \frac{dI}{dt} &= \beta \frac{SI}{N} - \gamma I \\ \frac{dR}{dt} &= \gamma I\end{aligned}$$

Spreadsheet implementation

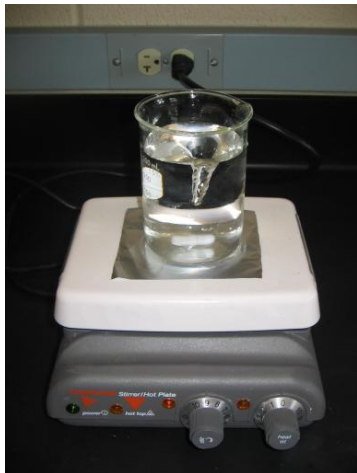


<http://tinyurl.com/SIR-MMED-2018>

Model taxonomy

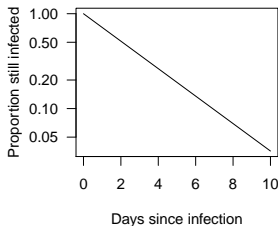
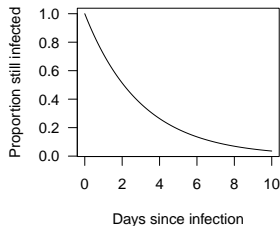


ODE assumptions



- ▶ Lots and lots of people
- ▶ Perfectly mixed

ODE assumptions



- ▶ Waiting times are exponentially distributed
- ▶ Rarely realistic

Scripts vs. spreadsheets

	Susceptibles people	Infectious people	Removed people	Total people
0	999	1	0	1000
1	998.6004	1.1996	0.2	1000
2	998.121231584064	1.438848415936	0.43992	1000
3	997.546773522873	1.72553679393953	0.7276896831872	1000
4	996.858252058318	2.06895089970737	1.07279704197511	1000
5	996.033271747327	2.48014103075661	1.48658722191658	1000
6	995.045150553223	2.97223401870901	1.9826154280679	1000
7	993.862147734573	3.56079003361749	2.5770622318097	1000
8	992.446573962396	4.26420579907117	3.2892202385332	1000
9	990.753775388012	5.10416321364044	4.14206139834744	1000
10	988.730987798368	6.1061181605567	5.16289404107552	1000
11	986.316064502168	7.29981782464567	6.38411767318688	1000
12	983.430093466813	8.71982529507146	7.844081238116	1000
13	980.005937097253	10.4060166056164	9.58804629713029	1000

```
return(as.list(  
  Sdot = - beta*S*I/N,  
  Idot = S*I/N - I/D,  
  Rdot = I/D  
))
```

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

More about transmission

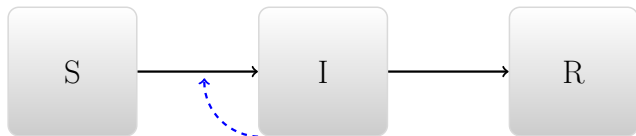


- ▶ $\beta = pc$
 - ▶ What is a contact?
 - ▶ What is the probability of transmission?
- ▶ Sometimes this decomposition is clear
- ▶ But usually it's not

Population sizes

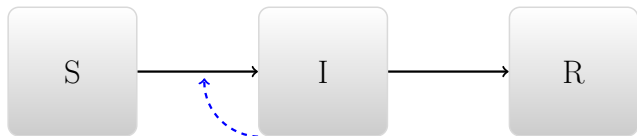
- ▶ How does β change with population size?
- ▶ Recall that β is the *per capita* rate of contacts

Population sizes



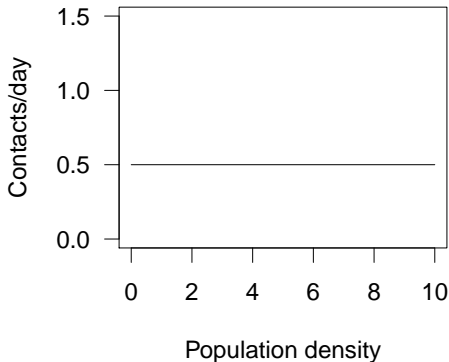
$$\begin{aligned}\frac{dS}{dt} &= -\beta \frac{SI}{N} \\ \frac{dI}{dt} &= \beta \frac{SI}{N} - \gamma I \\ \frac{dR}{dt} &= \gamma I\end{aligned}$$

Population sizes



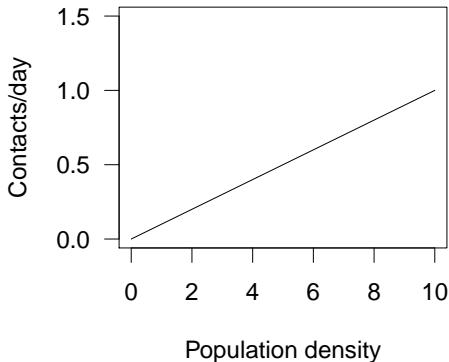
$$\begin{aligned}\frac{dS}{dt} &= -\beta(N)\frac{SI}{N} \\ \frac{dI}{dt} &= \beta(N)\frac{SI}{N} - \gamma I \\ \frac{dR}{dt} &= \gamma I\end{aligned}$$

Standard incidence



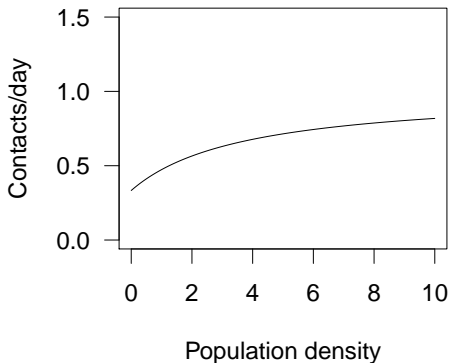
- ▶ $\beta(N) = \beta_0$
- ▶ $\mathcal{T} = \frac{\beta_0 SI}{N}$
- ▶ Also known as *frequency-dependent* transmission

Mass action



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

General

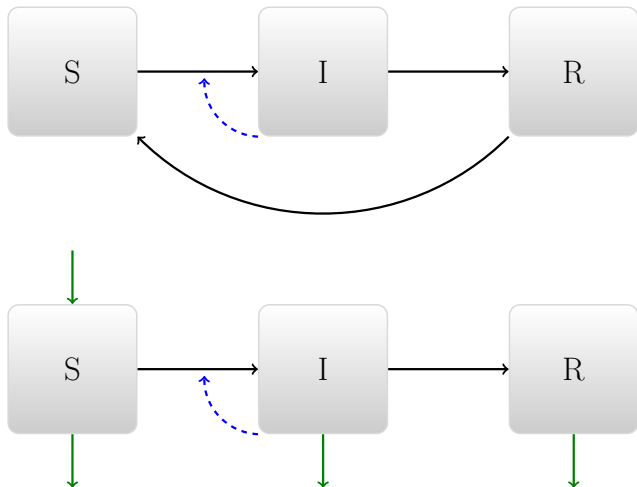


- ▶ Per-capita rate:
 - ▶ May not go to zero when N does
 - ▶ May not go to ∞ when N does

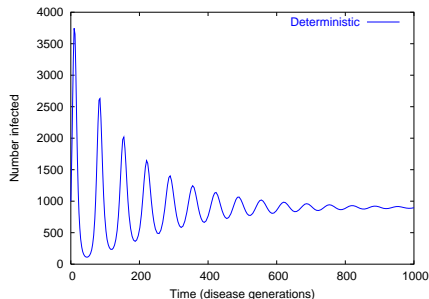
Digression – units

- ▶ $\mathcal{T} = \beta SI/N : [\text{ppl}/\text{time}]$
- ▶ $\beta : [1/\text{time}]$
 - ▶ $\beta/\gamma = \beta D : [1]$
 - ▶ Standard incidence, $\beta_0 : [1/\text{time}]$
 - ▶ Mass-action incidence, $\beta_1 : [1/(\text{people} \cdot \text{time})]$

Closing the circle

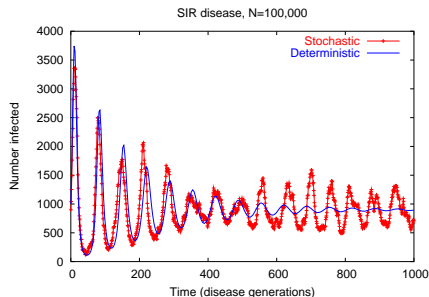


Tendency to oscillate



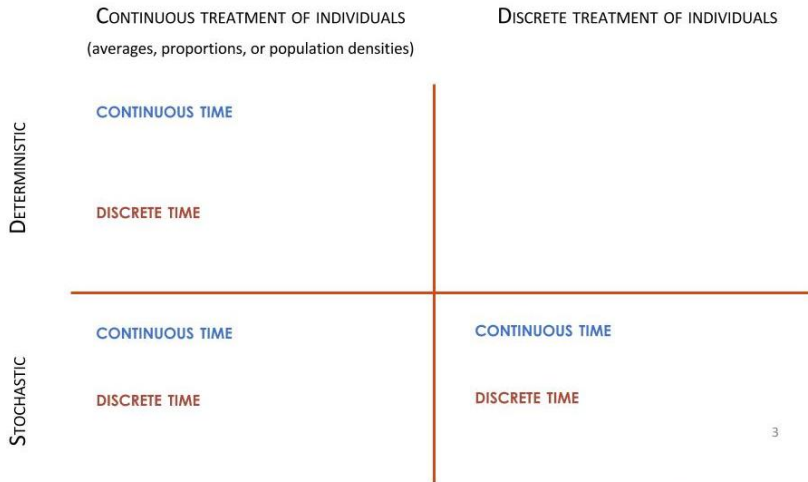
- ▶ Many susceptibles \rightarrow many infections \rightarrow few susceptibles \rightarrow few infections \rightarrow ...
- ▶ Oscillations in simple models tend to be “damped”

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



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



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